

Separate Volume

冊



出願番号 特願 2000-118776
[ST.10/C] : [JP 2000-118776]

分冊番号 2 / 2

出証番号 出証特 2002-3046778

【表335】

6). //0.00072:90:37//HOMO SAPIENS (HUMAN). //Q15428
 F-HEMBA1004509//HYPOTHETICAL 52.2 KD PROTEIN IN MPRI-GCN20 INTERGE
 NIC REGION. //6.3e-28:169:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
 T). //P43589
 F-HEMBA1004534//ENDOTHELIAL ACTIN-BINDING PROTEIN (ABP-280) (HOMNU
 SCLF FILAMIN) (FILAMIN 1). //1.3e-80:226:66//HOMO SAPIENS (HUMAN). //P21333
 F-HEMBA1004538//HYPOTHETICAL PROTEIN MJ0764. //0.96:28:35//METHANOC
 OCCUS JANNASCHII. //Q58174
 F-HEMBA1004542//METALLOTHIONEIN (MT). //0.78:36:41//GADUS MORHUA (A
 TLANTIC COD). //P51902
 F-HEMBA1004554
 F-HEMBA1004560//HYPOTHETICAL PROTEIN KIAA0281 (HA6725). //4.2e-15:5
 6:69//HOMO SAPIENS (HUMAN). //Q92556
 F-HEMBA1004573//CIRCULINSPOROZOITE PROTEIN PRECURSOR (CS). //0.65:31:
 58//PLASMODIUM BERGHEI. //P06915
 F-HEMBA1004577//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.9e-08:
 35:80//HOMO SAPIENS (HUMAN). //P39195
 F-HEMBA1004586//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//6.6e-08:
 64:54//HOMO SAPIENS (HUMAN). //P39194
 F-HEMBA1004596//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN C (HNRNP
 C) (HNRNP CORE PROTEIN C) (FRAGMENT). //0.00057:88:31//RATTUS NORVE
 GICUS (RAT). //P17132
 F-HEMBA1004604//COLLAGEN ALPHA 2(XI) CHAIN PRECURSOR (FRAGMENT). //0.
 045:37:45//MUS MUSCULUS (MOUSE). //Q64739
 F-HEMBA1004610//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.3e-11:7
 3:54//HOMO SAPIENS (HUMAN). //P39188
 F-HEMBA1004617
 F-HEMBA1004629
 F-HEMBA1004631//HYPOTHETICAL 7.8 KD PROTEIN IN WAPA-LICT INTERGENI
 C REGION. //1.0:36:38//BACILLUS SUBTILIS. //P42303
 F-HEMBA1004632//PHOTOSYSTEM I REACTION CENTRE SUBUNIT X PRECURSOR
 (LIGHT-HARVESTING 8.0 KD POLYPEPTIDE). //0.86:48:35//SYNECHOCOCCUS
 ELONGATUS NAEGELI. //P20453
 F-HEMBA1004637//HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME
 111. //1.7e-32:159:42//CAENORHABDITIS ELEGANS. //P34535
 F-HEMBA1004638//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT). //2.8
 e-06:50:46//OWENIA FUSIFORMIS. //P21260
 F-HEMBA1004666//TOXIN S6C4. //1.0:36:30//DENDROASPIS JAMESONI KAIMO
 SAE (EASTERN JAMESON'S MAMBA). //P25682
 F-HEMBA1004669//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA
 SPLICING FACTOR SRP75). //1.6e-12:105:42//HOMO SAPIENS (HUMAN). //Q0
 8170
 F-HEMBA1004670//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR. //2.5e-06:6
 2:45//HOMO SAPIENS (HUMAN). //P02452
 F-HEMBA1004672//HYPOTHETICAL PROTEIN MJ0437. //0.95:37:29//METHANOC
 OCCUS JANNASCHII. //Q57879
 F-HEMBA1004693//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYO
 SIN HEAVY CHAIN, TYPE B) (NMHC-B). //0.00035:217:23//HOMO SAPIENS
 (HUMAN). //P35580
 F-HEMBA1004697//IMMUNOGLOBULIN G BINDING PROTEIN H PRECURSOR (PROT
 EIN H). //0.058:118:30//STREPTOCOCCUS PYOGENES. //P50470
 F-HEMBA1004705//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//6.8e-09:4
 3:72//HOMO SAPIENS (HUMAN). //P39188
 F-HEMBA1004709//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//8.8e-18:
 50:84//HOMO SAPIENS (HUMAN). //P39189
 F-HEMBA1004711//ETS-RELATED PROTEIN 71 (ETS TRANSLOCATION VARIANT
 2). //0.0027:148:30//HOMO SAPIENS (HUMAN). //Q00321
 F-HEMBA1004725//CUTICLE COLLAGEN 2. //0.0051:41:41//CAENORHABDITIS
 ELEGANS. //P17656
 F-HEMBA1004730//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. //1.4e-22:21
 0:37//HOMO SAPIENS (HUMAN). //P08547
 F-HEMBA1004733//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.7e-07:5
 0:62//HOMO SAPIENS (HUMAN). //P39188
 F-HEMBA1004734//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.1
 9) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PUB1). //9.
 9e-39:143:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS). //P42743
 F-HEMBA1004736//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. //4.1e-60:21
 0:61//HOMO SAPIENS (HUMAN). //P08547
 F-HEMBA1004748
 F-HEMBA1004751//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.8e-20:8
 8:63//HOMO SAPIENS (HUMAN). //P39188
 F-HEMBA1004752//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEI
 N). //0.0043:126:34//XENODIPS LAEVIS (AFRICAN CLAWED FROG). //P17437
 F-HEMBA1004753//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//7.8e-28:
 47:78//HOMO SAPIENS (HUMAN). //P39193
 F-HEMBA1004756//HYPOTHETICAL 53.3 KD PROTEIN IN HXB-CAN1 INTERGEN
 IC REGION. //0.22:77:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P39981
 F-HEMBA1004758
 F-HEMBA1004763//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT). //1.1
 e-06:58:43//OWENIA FUSIFORMIS. //P21260
 F-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. //4.7e-65:29
 8:53//HOMO SAPIENS (HUMAN). //P08547
 F-HEMBA1004770
 F-HEMBA1004771
 F-HEMBA1004776//GRANULIN 1. //0.78:28:42//CYPRINUS CARPIO (COMMON C
 ARP). //P81013
 F-HEMBA1004778
 F-HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT). //6.9e-20:74:63//HOMO
 SAPIENS (HUMAN). //P50851
 F-HEMBA1004803//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. //1.4e-22:58:
 86//HOMO SAPIENS (HUMAN). //P08547
 F-HEMBA1004806//HYPOTHETICAL 24.3 KD PROTEIN IN PSBH-RPL11 INTERGE
 NIC REGION (ORF182). //0.72:75:33//CYANOPHORA PARADOXA. //P48324
 F-HEMBA1004807
 F-HEMBA1004816
 F-HEMBA1004820//HEMOLYMPH TRYPSIN INHIBITOR A (BPI-TYPE) (FRAGMEN
 T). //1.0:50:38//MANDUCA SEXTA (TOBACCO HAWKMOOTH) (TOBACCO HORNWORM
 N). //P26226
 F-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).
 //3.0e-76:171:91//CANIS FAMILIARIS (DOG). //Q00004
 F-HEMBA1004850//COLLAGEN ALPHA 1(XI) CHAIN (FRAGMENTS). //3.0e-05:
 64:43//BOS TAURUS (BOVINE). //P25508
 F-HEMBA1004863//TOXIN C13S1C1 PRECURSOR. //0.38:52:30//DENDROASPIS
 ANGSTICEPS (EASTERN GREEN MAMBA). //P18329
 F-HEMBA1004864//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN)
 (FRAGMENT). //0.89:24:50//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHS
 ISOLATE) (HIV-1). //P04612
 F-HEMBA1004865
 F-HEMBA1004880
 F-HEMBA1004889//SMALL PROLINE-RICH PROTEIN 11 (SPR-11) (CLONE 174
 N). //0.66:23:47//HOMO SAPIENS (HUMAN). //P22532
 F-HEMBA1004900
 F-HEMBA1004909
 F-HEMBA1004918//CHLOROPLAST 30S RIBOSOMAL PROTEIN S8 (FRAGMENT). //0.
 56:37:32//SPINACIA OLERACEA (SPINACH). //P09597
 F-HEMBA1004923//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.5e-24:4
 4:68//HOMO SAPIENS (HUMAN). //P39188
 F-HEMBA1004929//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L). //0.97:
 39:38//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN). //P15997
 F-HEMBA1004930//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. //6.6e-15:64:
 59//HOMO SAPIENS (HUMAN). //P08547
 F-HEMBA1004933//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP). //0.3
 4:58:41//HOMO SAPIENS (HUMAN). //P50552
 F-HEMBA1004934
 F-HEMBA1004944
 F-HEMBA1004954//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.
 3). //0.58:78:30//PARAMECIUM TETRAURELIA. //P15579
 F-HEMBA1004956//HYPOTHETICAL 18.8 KD PROTEIN (ORF4). //0.98:57:31//
 PARAMECIUM TETRAURELIA. //P15605
 F-HEMBA1004960//HYPOTHETICAL 12.6 KD PROTEIN (ORFJ) (RETROV EC67).
 //1.0:58:27//ESCHERICHIA COLI. //P21324
 F-HEMBA1004972
 F-HEMBA1004973//SMALL PROLINE RICH PROTEIN 11 (SPR-11) (CLONE 930
). //0.90:55:30//HOMO SAPIENS (HUMAN). //P22531
 F-HEMBA1004977
 F-HEMBA1004978
 F-HEMBA1004980//MOTILIN PRECURSOR. //0.088:79:31//MACACA MULATTA (R
 HESUS MACAQUE). //Q18811
 F-HEMBA1004983//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES). //0.
 87:51:31//BUCHNERA APHIDICOLA. //Q59176
 F-HEMBA1004995//MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RESPONSE
 E FACTOR-LIKE PROTEIN 2) (XMEF2) (RSRFR2). //0.17:52:40//HOMO SAPIENS
 (HUMAN). //Q02080
 F-HEMBA1005008//METALLOTHIONEIN (MT). //1.0:52:32//CRASSOSTREA VIRG
 INICA (EASTERN OYSTER). //P23038
 F-HEMBA1005009//ACTIN. //3.5e-27:171:38//CANDIDA ALBICANS (YEAST). //P14235
 F-HEMBA1005019//HYPOTHETICAL PROTEIN H11222. //0.13:58:31//HAEMOPHI
 LUS INFLUENZAE. //P44129
 F-HEMBA1005029//P2Y PURINOCEPTOR 5 (P2Y5) (PURINERGIC RECEPTOR 5)
 (6H1). //0.76:72:31//GALLUS GALLUS (CHICKEN). //P32250
 F-HEMBA1005035//HOMEBOX PROTEIN HB9. //0.0086:60:40//HOMO SAPIENS
 (HUMAN). //P50219
 F-HEMBA1005039//SMALL PROLINE-RICH PROTEIN 11 (SPR-11) (CLONE 174
 N). //0.47:49:32//HOMO SAPIENS (HUMAN). //P22532
 F-HEMBA1005047//RAS-RELATED PROTEIN RAB-24 (RAB-16). //1.5e-19:39:1
 00//MUS MUSCULUS (MOUSE). //P35290
 F-HEMBA1005050//COLLAGEN ALPHA 1(XI) CHAIN (FRAGMENTS). //0.074:3

【0634】

【表336】

4:44//BOS TAURUS (BOVINE).//P25508
 F-HEMBA1005062
 F-HEMBA1005066//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.1e-44:12
 6:65//HOMO SAPIENS (HUMAN).//P08547
 F-HEMBA1005075//SUPPRESSOR PROTEIN SRP40.//0.35:96:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P2583
 F-HEMBA1005079//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//3.6e-2
 0:75:64//HOMO SAPIENS (HUMAN).//P39191
 F-HEMBA1005083//COLLAGEN ALPHA 1(I1) CHAIN (FRAGMENTS).//0.00015:
 72:34//BOS TAURUS (BOVINE).//P25508
 F-HEMBA1005101//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 27C (HNRNP
 48) (HRP48.1).//4.8e-10:176:25//DROSOPHILA MELANOGASTER (FRUIT FL
 Y).//P48809
 F-HEMBA1005113
 F-HEMBA1005123//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.6e-24:
 99:60//HOMO SAPIENS (HUMAN).//P39194
 F-HEMBA1005133//HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SCA1 INTERGEN
 IC REGION.//0.11:22:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//
 P40490
 F-HEMBA1005149//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.7e-16:5
 9:71//HOMO SAPIENS (HUMAN).//P39188
 F-HEMBA1005152//GENOME POLYPROTEIN 2 [CONTAINS: HELPER COMPONENT P
 ROTEINASE (EC 3.4.22.-) (HC-PRO): 70 KD PROTEIN].//1.0:77:27//BARL
 EY YELLOW MOSAIC VIRUS (JAPANESE STRAIN 11-1) (BAYMV).//Q01207
 F-HEMBA1005159//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.
 3).//0.40:53:33//APIS MELLIFERA (HONEYBEE).//P34859
 F-HEMBA1005185//MYOSIN 18 HEAVY CHAIN.//0.011:58:48//DICTYOSTELIUM
 DISCOIDEUM (SLIME MOLD).//P34092
 F-HEMBA1005201//HYPOTHETICAL 56.6 KD PROTEIN C16C9.03 IN CHROMOSOM
 E 1.//3.9e-67:241:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//
 Q0817
 F-HEMBA1005202//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).
 //3.8e-124:257:95//CANIS FAMILIARIS (DOG).//Q00004
 F-HEMBA1005206//CUTICLE COLLAGEN I.//0.010:118:33//CAENORHABDITIS
 ELEGANS.//P08124
 F-HEMBA1005219//PTB-ASSOCIATED SPLICING FACTOR (PSF).//0.99:85:40/
 /HOMO SAPIENS (HUMAN).//P23246
 F-HEMBA1005223//HYPOTHETICAL GENE 1.05 PROTEIN.//0.31:75:28//BACTE
 RIOPHAGE T3.//P07715
 F-HEMBA1005232//HYPOTHETICAL 7.8 KD PROTEIN.//0.99:48:29//VACCINIA
 VIRUS (STRAIN WR). AND VACCINIA VIRUS (STRAIN COPENHAGEN).//P2054
 4
 F-HEMBA1005241//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.4e-28:
 138:55//HOMO SAPIENS (HUMAN).//P39193
 F-HEMBA1005244//SMALL PROLINE RICH PROTEIN 11 (SPR-11) (CLONE 930
).//0.014:39:41//HOMO SAPIENS (HUMAN).//P22531
 F-HEMBA1005251//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.55:
 15:46//DICENTRARCHUS LABRAX (EUROPEAN SEA BASS).//Q36362
 F-HEMBA1005252//EC PROTEIN HOMOLOG (ZINC-METALLOTHIONEIN CLASS 11
).//0.088:33:42//ZEA MAYS (MAIZE).//P43401
 F-HEMBA1005274
 F-HEMBA1005275//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.96:42:4
 5//HOMO SAPIENS (HUMAN).//P39188
 F-HEMBA1005293//PROBABLE COATOMER BETA' SUBUNIT (BETA'-COAT PROTEI
 N) (BETA'-COP).//0.55:98:30//CAENORHABDITIS ELEGANS.//Q20168
 F-HEMBA1005296//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//0.095:75:
 34//HOMO SAPIENS (HUMAN).//Q02817
 F-HEMBA1005304//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//5.4e-33:
 103:74//HOMO SAPIENS (HUMAN).//P39189
 F-HEMBA1005311//PERIOD CLOCK PROTEIN (FRAGMENT).//0.99:45:31//DROS
 OPHILA SALTANS (FRUIT FLY).//Q04536
 F-HEMBA1005314//HYPOTHETICAL 6.3 KD PROTEIN T19C.3 IN CHROMOSOME
 111.//0.98:30:30//CAENORHABDITIS ELEGANS.//Q10009
 F-HEMBA1005315//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.1e-05:35:
 51//HOMO SAPIENS (HUMAN).//P08547
 F-HEMBA1005318//OLFACTORY RECEPTOR-LIKE PROTEIN CORB (FRAGMENT).//
 0.57:44:38//GALLUS GALLUS (CHICKEN).//Q98913
 F-HEMBA1005331//IMMEDIATE-EARLY PROTEIN IE180.//0.57:106:33//PSEUD
 ORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675
 F-HEMBA1005338//CARTILAGE MATRIX PROTEIN PRECURSOR (MATRILIN-1).//
 1.8e-55:199:59//GALLUS GALLUS (CHICKEN).//P05099
 F-HEMBA1005353//CHLOROPLAST 30S RIBOSOMAL PROTEIN S17.//0.88:33:36
 //PORPHYRA PURPUREA.//P51305
 F-HEMBA1005359//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).
 //1.1e-68:255:48//HOMO SAPIENS (HUMAN).//P51522
 F-HEMBA1005367//ALPHA-AMYLASE INHIBITOR AAI.//1.0:25:40//AMARANTHU
 S HYPOCHONDRIACUS (PRINCE'S FEATHER).//P80403
 F-HEMBA1005372
 F-HEMBA1005374//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.0e-34:
 92:75//HOMO SAPIENS (HUMAN).//P39194
 F-HEMBA1005382//APOLIPROTEIN C-II (APO-CII).//0.99:39:33//BOS TA
 URUS (BOVINE).//P19034
 F-HEMBA1005389//HYPOTHETICAL 70.0 KD PROTEIN IN DNAK 3' REGION (ORF
 4).//0.82:164:31//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCU
 S LACTIS).//P42377
 F-HEMBA1005394//HYPOTHETICAL 8.9 KD PROTEIN IN IE0-IE1 INTERGENIC
 REGION.//0.98:44:38//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYEDROSIS V
 IRUS (ACHMPV).//P41703
 F-HEMBA1005403//SPERM HISTONE P2 PRECURSOR (PROTAMINE MP2).//0.06
 6:64:29//MUS MUSCULUS (MOUSE).//P07978
 F-HEMBA1005408//50S RIBOSOMAL PROTEIN L33.//0.77:32:25//BACILLUS S
 UBTILIS.//Q06798
 F-HEMBA1005410//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVE
 RSE TRANSCRIPTASE (EC 2.7.7.49): ENDONUCLEASE].//0.0065:38:52//MUS
 MUSCULUS (MOUSE).//P11369
 F-HEMBA1005411//TOXIN S4C8.//0.16:46:28//DENDROASPIS JAMESONI KAIN
 OSAE (EASTERN JAMESON'S MAMBA).//P25683
 F-HEMBA1005423//CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CY
 CLIN-DEPENDENT KINASE 4 INHIBITOR C) (P18-INK4C).//4.3e-09:29:96//
 HOMO SAPIENS (HUMAN).//P42773
 F-HEMBA1005426//TOXIN C10S2C2.//0.99:49:34//DENDROASPIS ANGIUSTICEP
 S (EASTERN GREEN MAMBA).//P25684
 F-HEMBA1005443//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.9e-16:7
 8:60//HOMO SAPIENS (HUMAN).//P39188
 F-HEMBA1005447//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:
 57:31//DASYPIUS NOVEMCINCTUS (NINE-BANDED ARMADILLO).//Q021329
 F-HEMBA1005468//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.
 3) (FRAGMENTS).//0.68:41:31//ARTEMIA SALINA (BRINE SHRIMP).//P1904
 0
 F-HEMBA1005469
 F-HEMBA1005472//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-39:14
 2:70//HOMO SAPIENS (HUMAN).//P08547
 F-HEMBA1005474//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//5.8e-10:
 44:68//HOMO SAPIENS (HUMAN).//P39194
 F-HEMBA1005475//U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD (U1 SNRNP
 70 KD) (SNRNP70).//9.2e-14:179:33//HOMO SAPIENS (HUMAN).//P08621
 F-HEMBA1005497
 F-HEMBA1005500//60S RIBOSOMAL PROTEIN L37.//0.11:53:33//SCHISTOSOM
 A MANSONI (BLOOD FLUKE).//Q44125
 F-HEMBA1005506
 F-HEMBA1005508
 F-HEMBA1005511//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.5e-30:
 92:73//HOMO SAPIENS (HUMAN).//P39194
 F-HEMBA1005513//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//
 2.0e-39:95:61//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q02193
 F-HEMBA1005517//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//2.1e-06:56:4
 4//MUS MUSCULUS (MOUSE).//P05142
 F-HEMBA1005518//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//5.8e-05:19
 2:33//BOS TAURUS (BOVINE).//P02453
 F-HEMBA1005520//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.0e-18:8
 7:57//HOMO SAPIENS (HUMAN).//P39188
 F-HEMBA1005526//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//5.1e-2
 2:77:54//HOMO SAPIENS (HUMAN).//P39191
 F-HEMBA1005528//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.2e-81:157:98//
 MUS MUSCULUS (MOUSE).//Q60809
 F-HEMBA1005530//POLLEN ALLERGEN AMB P 5-A PRECURSOR (AMB P 5-A).//
 0.98:19:47//AMBROSIA PSILOSTACHYA (WESTERN RAGWEED).//P43174
 F-HEMBA1005548//TRANSCRIPTION FACTOR MAF1.//1.4e-72:137:97//RATTUS
 NORVEGICUS (RAT).//P54842
 F-HEMBA1005552//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.7e-29:
 47:78//HOMO SAPIENS (HUMAN).//P39193
 F-HEMBA1005558//HYPOTHETICAL 25.6 KD PROTEIN IN ABF2-CHL12 INTERGE
 NIC REGION.//1.6e-20:202:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEA
 ST).//Q04272
 F-HEMBA1005568
 F-HEMBA1005570//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 6 (EC 1.6.5.
 3).//1.0:80:31//CAENORHABDITIS ELEGANS.//P24885
 F-HEMBA1005576//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//8.5e-58:152:
 75//HOMO SAPIENS (HUMAN).//P51805
 F-HEMBA1005577//KERATIN, HIGH-SULFUR MATRIX PROTEIN. B2A.//0.98:5
 7:36//OVIS ARIES (SHEEP).//P02438
 F-HEMBA1005581//SLIT PROTEIN PRECURSOR.//1.1e-62:254:41//DROSOPHIL
 A MELANOGASTER (FRUIT FLY).//P24014
 F-HEMBA1005582//DYNACTIN, 150 KD ISOFORM (150 KD DYNACTIN-ASSOCIATED
 POLYPEPTIDE) (DP-150) (DAP-150) (P150-GLUED).//0.0091:189:29//RAT
 TUS NORVEGICUS (RAT).//P28023
 F-HEMBA1005583//HYPOTHETICAL 41.2 KD PROTEIN IN CPS REGION (ORF7).
 //0.83:119:23//KLEBSIELLA PNEUMONIAE.//Q48453
 F-HEMBA1005588//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.9e-17:1
 08:53//HOMO SAPIENS (HUMAN).//P39188

【0635】

【表337】

F-HENBA1005593//SMALL PROLINE-RICH PROTEIN 11 (SPR-11) (CLONE 174 N).//0.23:24:54//HOMO SAPIENS (HUMAN).//P22532
 F-HENBA1005595//DYNEIN HEAVY CHAIN. CYTOSOLIC (DYHC).//2.7e-39:25:7:39//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34036
 F-HENBA1005606
 F-HENBA1005609//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.2e-20:27:96//HOMO SAPIENS (HUMAN).//P39192
 F-HENBA1005616//LATE CONTROL GENE B PROTEIN (GPB).//0.48:51:33//BACTERIOPHAGE 186.//P08711
 F-HENBA1005621//MITOTIC MAD2 PROTEIN.//1.2e-06:137:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40958
 F-HENBA1005627//HYPOTHETICAL 17.1 KD PROTEIN IN PURS 3' REGION.//0.18:100:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38898
 F-HENBA1005631
 F-HENBA1005632//HYPOTHETICAL 7.4 KD PROTEIN.//0.32:59:32//VACCINIA VIRUS (STRAIN WR).//P04309
 F-HENBA1005634//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.6e-14:9:3:58//HOMO SAPIENS (HUMAN).//P39188
 F-HENBA1005666//HYPOTHETICAL PROTEIN KIAA0129.//2.1e-05:126:25//HOMO SAPIENS (HUMAN).//Q14142
 F-HENBA1005670
 F-HENBA1005679//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.2e-08:40:72//HOMO SAPIENS (HUMAN).//P08547
 F-HENBA1005680//SMALL PROLINE-RICH PROTEIN 2-1.//0.015:19:47//HOMO SAPIENS (HUMAN).//P35326
 F-HENBA1005685
 F-HENBA1005699//EPHRIIN-B3 PRECURSOR (EPH-RELATED RECEPTOR TYROSINE KINASE LIGAND 8) (LEKX-8) (EPH-RELATED RECEPTOR TRANSMEMBRANE LIG AND ELK-L3).//4.2e-38:98:81//HOMO SAPIENS (HUMAN).//Q15768
 F-HENBA1005705//PROTEIN Q300.//0.11:23:56//MUS MUSCULUS (MOUSE).//Q02722
 F-HENBA1005717
 F-HENBA1005732//BACTENECIN 7 PRECURSOR (BACT).//0.22:55:41//OVIS ARIES (SHEEP).//P50415
 F-HENBA1005737//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT).//4.5e-18:167:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25296
 F-HENBA1005746
 F-HENBA1005755//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.4e-30:69:65//HOMO SAPIENS (HUMAN).//P08547
 F-HENBA1005765//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.8e-19:60:63//HOMO SAPIENS (HUMAN).//P39194
 F-HENBA1005780//METALLOTHIONEIN-1 (MT-1).//1.0:31:38//COLUMBA LIVIA (DOMESTIC PIGEON).//P15786
 F-HENBA1005813
 F-HENBA1005815//CALPAIN, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCULIN- ACTIVATED NEUTRAL PROTEINASE) (CAMP) (MU/M-TYPE).//1.0e-23:200:31//GALLUS GALLUS (CHICKEN).//P00789
 F-HENBA1005822//PROTEIN Q300.//0.0016:21:80//MUS MUSCULUS (MOUSE).//Q02722
 F-HENBA1005829//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.6e-33:96:73//HOMO SAPIENS (HUMAN).//P39194
 F-HENBA1005834//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.6e-22:10:3:46//MYCTICEBUS COUCANG (SLOW LORIS).//P08548
 F-HENBA1005852//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//8.8e-06:95:35//MUS MUSCULUS (MOUSE).//P05143
 F-HENBA1005853//HYPOTHETICAL PROTEIN MJ0647.//0.39:28:39//METHANOCOCCLUS JANNA SCHI.//Q58063
 F-HENBA1005884
 F-HENBA1005891//HYPOTHETICAL PROTEIN MTH137.//0.95:51:27//METHANOBACTERIUM THERMAUTOTROPHICUM.//Q26240
 F-HENBA1005894//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.6e-29:81:71//HOMO SAPIENS (HUMAN).//P39195
 F-HENBA1005909//HYPOTHETICAL 8.2 KD PROTEIN B0353.1 IN CHROMOSOME 111.//0.98:19:52//CAENORHABDITIS ELEGANS.//Q10958
 F-HENBA1005911//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.9e-27:8:6:70//HOMO SAPIENS (HUMAN).//P39188
 F-HENBA1005921//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.3e-38:99:81//HOMO SAPIENS (HUMAN).//P39194
 F-HENBA1005931//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//2.3e-17:76:51//HOMO SAPIENS (HUMAN).//P51522
 F-HENBA1005934//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/0.024:5:4:40//HOMO SAPIENS (HUMAN).//P39189
 F-HENBA1005962
 F-HENBA1005963//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP).//1.7e-32:89:79//BOS TAURUS (BOVINE).//P53620
 F-HENBA1005990//HYPOTHETICAL BHLF1 PROTEIN.//3.0e-09:180:36//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
 F-HENBA1005991//HYPOTHETICAL PROTEIN KIAA0032.//3.0e-17:107:43//HOMO SAPIENS (HUMAN).//Q15034

F-HENBA1005999
 F-HENBA1006002
 F-HENBA1006005//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B) (SPR1 B).//0.0017:45:44//MUS MUSCULUS (MOUSE).//Q62267
 F-HENBA1006031//BASIC PROLINE-RICH PEPTIDE 1B-1.//0.00016:84:39//HOMO SAPIENS (HUMAN).//P04281
 F-HENBA1006035//DNAK PROTEIN 1 (HEAT SHOCK PROTEIN 70) (HSP70).//0.43:100:27//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q55154
 F-HENBA1006036//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/6.2e-64:150:74//HOMO SAPIENS (HUMAN).//P39194
 F-HENBA1006042
 F-HENBA1006067//METALLOTHIONEIN A (MT-A).//0.86:34:41//THERMARCES CERBERUS.//P52721
 F-HENBA1006081
 F-HENBA1006090//SODIUM/GLUCOSE COTRANSPORTER 3 (NA(+)/GLUCOSE COTRANSPORTER 3) (LOW AFFINITY SODIUM-GLUCOSE COTRANSPORTER).//0.87:3:5:54//SUS SCROFA (PIG).//P31636
 F-HENBA1006091//EARLY NODULIN 20 PRECURSOR (N-20).//0.027:87:32//M. EDICAGO TRUNCATULA (BARREL MEDIC).//P33329
 F-HENBA1006100//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/8.1e-09:58:60//HOMO SAPIENS (HUMAN).//P39195
 F-HENBA1006108//HYPOTHETICAL 56.6 KD PROTEIN, IN URE2-SSU2 INTERGENIC REGION.//5.6e-16:88:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867
 F-HENBA1006121//HOMEBOX PROTEIN CDX-1 (CAUDAL-TYPE HOMEBOX PROTEIN 1).//3.4e-05:106:37//HOMO SAPIENS (HUMAN).//P47902
 F-HENBA1006124//50S RIBOSOMAL PROTEIN L33.//1.0:12:83//BACILLUS STEAROTHERMOPHILUS.//P23375
 F-HENBA1006130//SEL-10 PROTEIN.//7.7e-05:129:28//CAENORHABDITIS ELEGANS.//Q93794
 F-HENBA1006138//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.8e-13:41:73//HOMO SAPIENS (HUMAN).//P39194
 F-HENBA1006142//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/2.3e-39:101:77//HOMO SAPIENS (HUMAN).//P39192
 F-HENBA1006155//GENE 33 POLYPEPTIDE.//0.21:70:31//RATTUS NORVEGICUS (RAT).//P05432
 F-HENBA1006158
 F-HENBA1006173//PROTEIN-TYROSINE PHOSPHATASE STRIATUM-ENRICHED (EC 3.1.3.48) (STEP) (NEURAL-SPECIFIC PROTEIN-TYROSINE PHOSPHATASE) (FRAGMENT).//0.017:20:95//HOMO SAPIENS (HUMAN).//P54829
 F-HENBA1006182//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.37:31:6:1//HOMO SAPIENS (HUMAN).//P39188
 F-HENBA1006198//HOMEBOX PROTEIN HOX-83 (HOX-2.7) (H-23).//0.85:6:1:29//MUS MUSCULUS (MOUSE).//P09026
 F-HENBA1006235//50S RIBOSOMAL PROTEIN L33.//1.0:26:38//AQUIFEX AEO LICUS.//Q67756
 F-HENBA1006248//MALE SPECIFIC SPERM PROTEIN MST84B.//0.0041:64:37//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643
 F-HENBA1006252//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR DE-3.//1.0:2:2:40//DOLICHOS AXILLARIS (MACROTYLOMA AXILLARE).//P01057
 F-HENBA1006253//DISINTEGRIN ERISTICOPHIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).//0.95:19:47//ERISTICOPHIS MACMAHONI (LEAF-NOSE D VIPER).//P22826
 F-HENBA1006259
 F-HENBA1006268//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/7.0e-05:32:65//HOMO SAPIENS (HUMAN).//P39192
 F-HENBA1006272//RETROVIRUS-RELATED GAG POLYPEPTIDE (VERSION 2).//4.8e-112:248:78//HOMO SAPIENS (HUMAN).//P10264
 F-HENBA1006278//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLTRANSFERASE) (FRAGMENT).//2.5e-71:164:75//HOMO SAPIENS (HUMAN).//P51003
 F-HENBA1006283//50S RIBOSOMAL PROTEIN L32.//0.81:27:44//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P80339
 F-HENBA1006284//CUTICLE COLLAGEN 2.//0.36:42:40//CAENORHABDITIS ELEGANS.//P17656
 F-HENBA1006291//HYPOTHETICAL 43.3 KD PROTEIN IN EVGS-GLK INTERGENIC REGION.//2.4e-37:143:31//ESCHERICHIA COLI.//P76518
 F-HENBA1006293//MYELIN-OLIGODENDROCYTE GLYCOPROTEIN PRECURSOR.//0.20:134:29//RATTUS NORVEGICUS (RAT).//Q63345
 F-HENBA1006309//HYPOTHETICAL 54.2 KD PROTEIN IN ERPS-ORC6 INTERGENIC REGION.//2.1e-43:187:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38821
 F-HENBA1006310//SIGNAL TRANSDUCER CD24 PRECURSOR (HEAT STABLE ANTIGEN) (HSA) (NECTADIN).//0.71:46:39//RATTUS NORVEGICUS (RAT).//Q07490
 F-HENBA1006328//RNA POLYMERASE ALPHA SUBUNIT (EC 2.7.7.48) (NUCLEOCAPSID PHOSPHOPROTEIN).//0.44:141:24//HUMAN PARAINFLUENZA 1 VIRUS (STRAIN CI-5/73).//P32531
 F-HENBA1006334//HYPOTHETICAL TRANSCRIPTIONAL REGULATOR AF1627.//0.98:26:46//ARCHAEOGLOBUS FULGIDUS.//Q28646

【0636】

【表338】

F-HEMBA1006344//EZRIN (P81) (CYTOVILLIN) (VILLIN-2).//8.8e-08:91:36//MUS MUSCULUS (MOUSE).//P26040
 F-HEMBA1006347//MALES-ABSENT ON THE FIRST PROTEIN (EC 2.3.1.-).//9.1e-48:149:50//DROSOPHILA MELANOGASTER (FRUIT FLY).//002193
 F-HEMBA1006349//METALLOTHIONEIN-LIKE PROTEIN 1.//0.015:59:33//CASU ARINA GLAUCA (SWAMP OAK).//Q39511
 F-HEMBA1006359//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//6.8e-96:261:66//HOMO SAPIENS (HUMAN).//P28160
 F-HEMBA1006364//PUTATIVE ENDONUCLEASE CIF2.06C (EC 3.1.-.-).//0.97:60:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10348
 F-HEMBA1006377//EARLY MODULIN 20 PRECURSOR (N-20).//0.00023:110:35//MEXICAGO TRUNCATULA (BARREL MEDIC).//P93329
 F-HEMBA1006380
 F-HEMBA1006381//METALLOTHIONEIN-11.//1.0:26:38//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA).//P15114
 F-HEMBA1006398//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.3e-26:123:52//HOMO SAPIENS (HUMAN).//P08547
 F-HEMBA1006416
 F-HEMBA1006419//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.2e-24:102:50//HOMO SAPIENS (HUMAN).//P39189
 F-HEMBA1006421//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.1e-21:101:57//HOMO SAPIENS (HUMAN).//P39188
 F-HEMBA1006424//HYPOTHETICAL PROTEIN (ORF1).//0.85:55:30//BOVINE CORONAVIRUS (STRAIN MEBUS), AND BOVINE CORONAVIRUS (STRAIN QUEBEC).//P22053
 F-HEMBA1006426//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.8e-36:78:74//HOMO SAPIENS (HUMAN).//P39195
 F-HEMBA1006438//HYPOTHETICAL 8.1 KD PROTEIN (ORF65).//1.0:38:36//GUILLARDIA THETA (CRYPTOMONAS PHI).//078421
 F-HEMBA1006445//RAS-LIKE PROTEIN 3.//1.9e-06:40:47//RHIZOMUCOR RACEMOSUS (MUCOR CIRCINELLIOIDES F. LUSITANICUS).//P22280
 F-HEMBA1006446
 F-HEMBA1006461//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//4.1e-18:68:67//HOMO SAPIENS (HUMAN).//P39192
 F-HEMBA1006467
 F-HEMBA1006471
 F-HEMBA1006474//40 KD PROTEIN.//1.1e-37:231:38//BORNA DISEASE VIRUS (BDV).//Q01552
 F-HEMBA1006483//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//6.1e-38:77:74//HOMO SAPIENS (HUMAN).//P39192
 F-HEMBA1006485//HYPOTHETICAL 9.3 KD PROTEIN IN NAD3-NAD7 INTERGENIC REGION (ORF 79).//0.91:30:40//MARCHANTIA POLYMORPHA (LIVERWORT).//P38465
 F-HEMBA1006486//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.1e-12:78:51//HOMO SAPIENS (HUMAN).//P08547
 F-HEMBA1006489//FUN34 PROTEIN.//0.94:58:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32907
 F-HEMBA1006492//NADH-UBIQUINONE OXIDOREDUCTASE MWFE SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-MWFE) (CI-MWFE).//0.87:44:36//HOMO SAPIENS (HUMAN).//015239
 F-HEMBA1006494//FERRODOXIN-LIKE PROTEIN IN NIF REGION.//0.11:46:26//RHIZOBIUM LEGUMINOSARUM (BIOTIN TRIFOLI).//P42711
 F-HEMBA1006497
 F-HEMBA1006502//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.15:26:73//HOMO SAPIENS (HUMAN).//P39188
 F-HEMBA1006507//DIAPHANOUS PROTEIN.//0.0055:129:28//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48608
 F-HEMBA1006521//3-OXOACYL-ACYL CARRIER PROTEIN REDUCTASE (EC 1.1.1.100) (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE).//1.1e-32:177:41//ESCHERICHIA COLI.//P25716
 F-HEMBA1006530//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.052:84:26//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//P15583
 F-HEMBA1006535//INHIBITOR OF APOPTOSIS PROTEIN 1 (MIAP1) (MIAP-1).//6.6e-05:53:39//MUS MUSCULUS (MOUSE).//008863
 F-HEMBA1006540//PRESYNAPTIC PROTEIN SAP97 (SYNAPSE-ASSOCIATED PROTEIN 97) (DISCS, LARGE HOMOLOG 1).//2.1e-07:206:23//RATTUS NORVEGICUS (RAT).//Q62696
 F-HEMBA1006546//PROBABLY E5 PROTEIN.//0.11:70:32//HUMAN PAPILLOMAVIRUS TYPE 51.//P26553
 F-HEMBA1006559//SUPPRESSOR PROTEIN SRP40.//0.015:221:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
 F-HEMBA1006562//SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE 5).//1.5e-07:122:33//HOMO SAPIENS (HUMAN).//P10163
 F-HEMBA1006566//CELL DIVISION PROTEIN KINASE 2 (EC 2.7.1.-) (CDC2 HOMOLOG EGI PROTEIN KINASE).//0.63:53:37//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P23437
 F-HEMBA1006569//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//4.4e-06:88:39//BOS TAURUS (BOVINE).//P02465
 F-HEMBA1006579
 F-HEMBA1006583//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.011:61:40//MUS MUSCULUS (MOUSE).//P05142
 F-HEMBA1006595//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//5.6e-34:93:77//HOMO SAPIENS (HUMAN).//P39194
 F-HEMBA1006597//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.9e-26:75:74//HOMO SAPIENS (HUMAN).//P39195
 F-HEMBA1006612//SUPPRESSOR PROTEIN SRP40.//0.026:221:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
 F-HEMBA1006617//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//6.6e-20:73:63//HOMO SAPIENS (HUMAN).//P39188
 F-HEMBA1006624//HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REGION.//2.6e-31:209:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40506
 F-HEMBA1006631//HYPOTHETICAL 62.8 KD PROTEIN IN TAF145-YOR1 INTERGENIC REGION.//1.5e-15:131:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53331
 F-HEMBA1006635
 F-HEMBA1006639//POLYADENYLATE-BINDING PROTEIN 1 (POLY(A) BINDING PROTEIN 1) (PABP 1).//2.2e-11:48:75//MUS MUSCULUS (MOUSE).//P29341
 F-HEMBA1006643//LONG NEUROTOXIN CRI PRECURSOR (KAPPA NEUROTOXIN).//0.28:48:27//BUNGARUS MULTICINCTUS (MANY-BANDED KRAIT).//P15817
 F-HEMBA1006648//ZINC FINGER PROTEIN 12 (ZINC FINGER PROTEIN K0X3) (FRAGMENT).//0.26:17:47//HOMO SAPIENS (HUMAN).//P17014
 F-HEMBA1006652//60S RIBOSOMAL PROTEIN L7.//2.4e-44:206:47//MUS MUSCULUS (MOUSE).//P14148
 F-HEMBA1006653
 F-HEMBA1006659
 F-HEMBA1006665//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.018:43:58//HOMO SAPIENS (HUMAN).//P08547
 F-HEMBA1006674//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAF11-135) (TAF11135) (TAF11130).//2.9e-05:154:33//HOMO SAPIENS (HUMAN).//000268
 F-HEMBA1006676//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//3.6e-09:52:51//OMENIA FUSIFORMIS.//P21260
 F-HEMBA1006682
 F-HEMBA1006695//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.1e-06:35:65//HOMO SAPIENS (HUMAN).//P39188
 F-HEMBA1006696
 F-HEMBA1006708//HYPOTHETICAL 46.4 KD TRP-ASP REPEATS CONTAINING PROTEIN IN PNC1-TFG2 INTERGENIC REGION.//3.4e-19:104:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53196
 F-HEMBA1006709//RETINOIC ACID RECEPTOR RXR-BETA.//0.24:111:36//HOMO SAPIENS (HUMAN).//P28702
 F-HEMBA1006717
 F-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NON ERYTHROID) (FRAGMENT).//5.8e-09:111:40//HOMO SAPIENS (HUMAN).//Q01485
 F-HEMBA1006744//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//1.8e-32:84:78//HOMO SAPIENS (HUMAN).//P39191
 F-HEMBA1006754//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.3e-75:220:62//HOMO SAPIENS (HUMAN).//P08547
 F-HEMBA1006758//VASCULAR ENDOTHELIAL-CADHERIN PRECURSOR (VE-CADHERIN) (CADHERIN-5) (T84 ANTIGEN) (CD144 ANTIGEN).//0.024:110:29//HOMO SAPIENS (HUMAN).//P33151
 F-HEMBA1006767
 F-HEMBA1006779//MITOCHONDRIAL RIBOSOMAL PROTEIN S12.//0.67:19:42//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).//Q34940
 F-HEMBA1006780
 F-HEMBA1006789//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.056:98:30//MUS MUSCULUS (MOUSE).//P05143
 F-HEMBA1006795//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.9e-11:143:30//NYCTICEBUS COUCANG (SLOW LORIS).//P08548
 F-HEMBA1006796//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).//0.16:38:42//MUS MUSCULUS (MOUSE).//P70315
 F-HEMBA1006807//HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMOSOME E 111.//4.4e-75:184:77//CAENORHABDITIS ELEGANS.//P34568
 F-HEMBA1006821//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.011:20:85//HOMO SAPIENS (HUMAN).//P39194
 F-HEMBA1006824//PROTEIN B11.//0.44:27:44//VACCINIA VIRUS (STRAIN WR).//Q01229
 F-HEMBA1006832//HYPOTHETICAL 34.6 KD PROTEIN C13G5.2 IN CHROMOSOME 111.//1.0:46:36//CAENORHABDITIS ELEGANS.//P34327
 F-HEMBA1006849
 F-HEMBA1006865//ACROSIN INHIBITORS 11A AND 11B (BUS1-11).//1.0:4131//BOS TAURUS (BOVINE).//P01001
 F-HEMBA1006877//OXYSTEROL-BINDING PROTEIN.//3.7e-26:239:36//ORYCTOLAGUS CUNICULUS (RABBIT).//P16258
 F-HEMBA1006885//HYPOTHETICAL 27.2 KD PROTEIN F09E5.8 IN CHROMOSOME 11.//4.5e-38:185:43//CAENORHABDITIS ELEGANS.//P52057
 F-HEMBA1006900

【0637】

【表339】

F-HEMBA1006914//UBIQUITIN-ACTIVATING ENZYME E1-LIKE (POLYMERASE-IN
TERACTING PROTEIN 2).//5.2e-27:269:33//SACCHAROMYCES CEREVISIAE (B
AKER'S YEAST).//P52488

F-HEMBA1006921//CYTOTOXIN 3 (COMPONENT 3.20).//0.99:32:37//NAJA ME
LANOLEUCA (FOREST COBRA) (BLACK-LIPPED COBRA).//P01473

F-HEMBA1006926//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUSIAN ATROPHY P
ROTEIN).//0.0024:148:33//RATTUS NORVEGICUS (RAT).//P54258

F-HEMBA1006929//HYPOTHETICAL PROTEIN MJ0525.//0.95:35:20//METHANOC
OCUS JANNASCHII.//Q57945

F-HEMBA1006936//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PR
ECURSOR (PRP-1 / PRP-2 / PRP-4) (PIF-F / PIF-S) (PROTEIN A
/ PROTEIN C) [CONTAINS: PEPTIDE P-C].//0.074:116:31//HOMO SAPIENS
(HUMAN).//P02810

F-HEMBA1006938

F-HEMBA1006941//THIOREDOXIN H-TYPE 1 (TRX-H1).//2.1e-13:90:33//NIC
OTIANA TABACUM (COMMON TOBACCO).//P29449

F-HEMBA1006949

F-HEMBA1006973//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.75:29:
55//BOS TAURUS (BOVINE).//P25508

F-HEMBA1006976//CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-
2,3-SIALYLTRANSFERASE (EC 2.4.99.-) (BETA-GALACTOSIDE ALPHA-2,3-SI
ALYLTRANSFERASE) (ST3GAL111) (ALPHA 2,3-ST) (GAL-MAC6S) (ST2) (SIA
T4-C) (SAT-3) (ST-4).//3.9e-108:117:95//HOMO SAPIENS (HUMAN).//Q11
206

F-HEMBA1006993

F-HEMBA1006996//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGE
NIC REGION (ORF70).//0.12:51:33//ASTASIA LONGA (EUGLENOPHYCEAN ALG
A).//P34779

F-HEMBA1007002//PLATELET GLYCOPROTEIN IX PRECURSOR (GP1X) (CD42A).
//0.00095:60:33//HOMO SAPIENS (HUMAN).//P14770

F-HEMBA1007017//HYPOTHETICAL 7.2 KD PROTEIN IN CY4-DAPF INTERGENI
C REGION.//1.0:25:56//ESCHERICHIA COLI.//P39166

F-HEMBA1007018//DYNEIN LIGHT INTERMEDIATE CHAIN 1, CYTOSOLIC (LIC5
7/59) (DYNEIN LIGHT CHAIN A) (OLC-A).//8.5e-120:278:80//GALLUS GAL
LUS (CHICKEN).//Q90828

F-HEMBA1007045//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEI
N).//2.1e-12:158:29//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437

F-HEMBA1007051

F-HEMBA1007052//60S RIBOSOMAL PROTEIN L37-B (L35) (YP55).//0.94:3
7:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P51402

F-HEMBA1007062//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.93:
55:29//RHINOCEROS UNICORNIS (GREATER INDIAN RHINOCEROS).//Q96063

F-HEMBA1007066//ECLOSIN HORMONE PRECURSOR (ECDYSIS ACTIVATOR) (E
H).//0.58:49:38//BOMBYX MORI (SILK MOTH).//P25331

F-HEMBA1007073//PUTATIVE SMALL MEMBRANE PROTEIN (ORF 4).//0.86:46:
34//CANINE ENTERIC CORONAVIRUS (STRAIN INSAVC-1) (CCV).//P36696

F-HEMBA1007078//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//8.6e-29:
56:67//HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1007080//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEI
N).//0.028:122:30//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437

F-HEMBA1007085//RTGA PROTEIN (RATIO-A).//7.4e-11:221:31//DICTYOSTE
LIUM DISCOIDEUM (SLIME MOLD).//P54681

F-HEMBA1007087//HYPOTHETICAL PROTEIN MJ0162.//3.3e-29:173:36//METH
ANOCOCCUS JANNASCHII.//Q57626

F-HEMBA1007112

F-HEMBA1007113

F-HEMBA1007121//INOSITOL POLYPHOSPHATE 1-PHOSPHATASE (EC 3.1.3.57)
(IPP).//5.4e-07:90:28//HOMO SAPIENS (HUMAN).//P49441

F-HEMBA1007129//HIRUSTASIN.//0.88:37:32//HIRUDO MEDICINALIS (MEDIC
INAL LEECH).//P80302

F-HEMBA1007147//HYPOTHETICAL 12.0 KD PROTEIN IN DST1-HEM2 INTERGEN
IC REGION.//0.92:23:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//
P53182

F-HEMBA1007149//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//0.007
8:17:70//ESCHERICHIA COLI.//P05834

F-HEMBA1007151//MCHN1 PROTEIN PRECURSOR.//0.25:45:37//MUS MUSCULUS
(MOUSE).//Q62477

F-HEMBA1007174//HYPOTHETICAL 45.1 KD PROTEIN IN RP55-ZMS1 INTERGEN
IC REGION.//6.9e-18:97:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
T).//P47160

F-HEMBA1007178//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//9.8e-06:
38:65//HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1007194//GLUCOSE-6-PHOSPHATE 1-DEHYDROGENASE, CHLOROPLAST
ISOFORM PRECURSOR (EC 1.1.1.49) (G6PD).//1.0:80:32//NICOTIANA TABA
CUM (COMMON TOBACCO).//Q43793

F-HEMBA1007203//PROTEIN A22.//1.0:115:26//VARIOLA VIRUS.//P33845

F-HEMBA1007206

F-HEMBA1007224//HYPOTHETICAL 35.7 KD PROTEIN C41C4.6 IN CHROMOSOME
11.//2.4e-05:92:30//CAENORHABDITIS ELEGANS.//Q09275

F-HEMBA1007243//HYPOXANTHINE-GUANINE PHOSPHORIBOSYLTRANSFERASE (EC
2.4.2.8) (HGPRT) (HGPRTASE) (HPRT B).//3.1e-74:205:67//MUS MUSCUL
US (MOUSE).//P00493

F-HEMBA1007251//VITELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTE
IN TU-4) (PROTEIN SV23).//0.52:108:30//DROSOPHILA MELANOGASTER (FR
UIT FLY).//P13238

F-HEMBA1007256

F-HEMBA1007267//CALICIN (FRAGMENT).//0.060:88:31//HOMO SAPIENS (HU
MAN).//Q13939

F-HEMBA1007273//HYPOTHETICAL 8.1 KD PROTEIN (ORF65).//0.95:40:37//
GUILLARDIA THETA (CRYPTOMONAS PH1).//Q78421

F-HEMBA1007279//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.6e-24:9
8:64//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1007281

F-HEMBA1007288//HYPOTHETICAL 13.5 KD PROTEIN IN ZMS1-HMS1 INTERGEN
IC REGION.//0.88:11:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//
P47162

F-HEMBA1007300//CGMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE (EC
3.1.4.17) (CGB-PDE).//2.7e-43:220:41//BOS TAURUS (BOVINE).//Q28156

F-HEMBA1007301//PROCOLLAGEN ALPHA 1(I11) CHAIN PRECURSOR.//3.3e-2
2:115:33//HOMO SAPIENS (HUMAN).//P02461

F-HEMBA1007319

F-HEMBA1007320//HYPOTHETICAL 28.0 KD PROTEIN IN GLOB-RNHA INTERGEN
IC REGION.//1.0:48:37//ESCHERICHIA COLI.//P75672

F-HEMBA1007322//THREONINE DEHYDRATASE OPERON ACTIVATOR PROTEIN.//
1.0:59:33//ESCHERICHIA COLI.//P11866

F-HEMBA1007327

F-HEMBA1007341//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.1e-12:3
7:62//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1007342//PROBABLE E5 PROTEIN.//0.89:96:29//PYGMY CHIMPANZEE
PAPILLONAVIRUS TYPE 1.//Q02268

F-HEMBA1007347//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 2 PRECU
RSOR (IGFBP-2) (IBP-2) (IGF-BINDING PROTEIN 2).//0.92:62:43//OVIS
ARIES (SHEEP).//Q29400

F-HEMBA1000005//WEAK NEUROTOXIN 5.//0.98:30:33//NAJA NAJA (INDIAN
COBRA).//P29179

F-HEMBA1000008//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.7e-35:
73:84//HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1000018//HYPOTHETICAL BHLF1 PROTEIN.//0.39:90:37//EPSTEIN-B
ARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181

F-HEMBA1000024//VIRE LOCUS 9 KD VIRULENCE PROTEIN.//0.66:36:41//AG
ROBACTERIUM TUMEFACIENS.//P08061

F-HEMBA1000025//MUSCARINIC TOXIN ALPHA (MT-ALPHA).//0.46:32:40//DE
NDROASPIS POLYLEPIS POLYLEPIS (BLACK MAMBA).//P80494

F-HEMBA1000030//SUPPRESSOR PROTEIN SRP40.//5.7e-07:50:52//SACCHARO
MYCES CEREVISIAE (BAKER'S YEAST).//P32583

F-HEMBA1000036//HYPOTHETICAL 43.2 KD PROTEIN C34E10.1 IN CHROMOSOM
E 111.//2.5e-07:120:29//CAENORHABDITIS ELEGANS.//P46576

F-HEMBA1000037//HYPOTHETICAL 59.9 KD PROTEIN IN SGAI-KTR7 INTERGEN
IC REGION.//1.7e-05:71:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
T).//P40492

F-HEMBA1000039//VERY HYPOTHETICAL 11.9 KD PROTEIN C4H3.12C IN CHRO
MOSOME 1.//1.0:61:21//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//
Q10219

F-HEMBA1000044

F-HEMBA1000048//HYPOTHETICAL 15.7 KD PROTEIN IN IDH-DEOR INTERGENI
C REGION.//1.0:63:31//BACILLUS SUBTILIS.//P54942

F-HEMBA1000050//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.0e-14:
34:79//HOMO SAPIENS (HUMAN).//P39194

F-HEMBA1000054//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//5.9e-31:
45:73//HOMO SAPIENS (HUMAN).//P39193

F-HEMBA1000055//MUSCARINIC TOXIN ALPHA (MT-ALPHA).//1.0:14:57//DEN
DROASPIS POLYLEPIS POLYLEPIS (BLACK MAMBA).//P80494

F-HEMBA1000059//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.0e-21:
82:59//HOMO SAPIENS (HUMAN).//P39195

F-HEMBA1000083//CHROMOGANIN A PRECURSOR (CGA) [CONTAINS: PANCREAS
TATIN: BETA-GRANIN: WE-14].//0.87:172:28//RATTUS NORVEGICUS (RAT).
//P10354

F-HEMBA1000089//HYPOTHETICAL 9.5 KD PROTEIN IN SPEA-METK INTERGENI
C REGION (F83).//1.0:42:33//ESCHERICHIA COLI.//P46879

F-HEMBA1000099//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//7.7e-08:
31:87//HOMO SAPIENS (HUMAN).//P39189

F-HEMBA1000103//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.4e-38:13
6:58//HOMO SAPIENS (HUMAN).//P08547

F-HEMBA1000113//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.9e-13:5
7:64//HOMO SAPIENS (HUMAN).//P39188

F-HEMBA1000119//MAF PROTEIN.//3.6e-32:195:43//BACILLUS SUBTILIS.//
Q02169

F-HEMBA1000136//HYPOTHETICAL 12.7 KD PROTEIN IN PCS60-ABD1 INTERGE
NIC REGION.//0.65:71:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
//P38327

【0638】

【表340】

F-HEMBB1000141//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.00
 014:34:64//HOMO SAPIENS (HUMAN).//P20931
 F-HEMBB1000144//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/2.0e-2
 6:81:69//HOMO SAPIENS (HUMAN).//P39191
 F-HEMBB1000173//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/9.2e-29:9
 1:71//HOMO SAPIENS (HUMAN).//P39188
 F-HEMBB1000175//ANTIMICROBIAL PEPTIDE ENAP-1 (FRAGMENT).//0.97:41:
 36//EQUUS CABALLUS (HORSE).//P80930
 F-HEMBB1000198//HYPOTHETICAL 7.7 KD PROTEIN YCF33 (ORF67).//0.91:2
 1:52//PORPHYRA PURPUREA.//P51329
 F-HEMBB1000215//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.4e-08:
 39:76//HOMO SAPIENS (HUMAN).//P39192
 F-HEMBB1000217//DNA DAMAGE TOLERANCE PROTEIN RHC31 (RAD31 HOMOLOG
).//2.9e-32:174:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06
 624
 F-HEMBB1000218//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.73:
 31:38//MICROTUS PENNSYLVANICUS (MEADOW VOLE).//P24949
 F-HEMBB1000226//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME
 11.//6.5e-26:191:34//CAENORHABDITIS ELEGANS.//Q09217
 F-HEMBB1000240
 F-HEMBB1000244//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.9e-05:4
 4:61//HOMO SAPIENS (HUMAN).//P39188
 F-HEMBB1000250
 F-HEMBB1000258
 F-HEMBB1000264//CUTICLE COLLAGEN SQT-1.//0.15:89:33//CAENORHABDITI
 S ELEGANS.//P12114
 F-HEMBB1000266//TRANSLATION INITIATION FACTOR IF-2.//2.7e-06:167:2
 2//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39730
 F-HEMBB1000272//CYTOCHROME C OXIDASE POLYPEPTIDE VIB (EC 1.9.3.1)
 (AED).//0.75:30:43//BOS TAURUS (BOVINE).//P00429
 F-HEMBB1000274//CORNIFIN (SMALL PROLINE-RICH PROTEIN 1) (SPR-1) (S
 MALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).//1.0:38:36//SUS SC
 ROFA (PIG).//P35323
 F-HEMBB1000284//CALTRIN (CALCIUM TRANSPORT INHIBITOR).//1.0:56:30/
 MUS MUSCULUS (MOUSE).//Q09098
 F-HEMBB1000307
 F-HEMBB1000312
 F-HEMBB1000317//THROMBOSPONDIN 1 PRECURSOR.//3.2e-32:135:43//HOMO
 SAPIENS (HUMAN).//P07996
 F-HEMBB1000318//PUTATIVE SMALL MEMBRANE PROTEIN (NONSTRUCTURAL PRO
 TEIN NS3) (NONSTRUCTURAL 9.5 KD PROTEIN).//0.41:51:31//HUMAN CORON
 AVIRUS (STRAIN OC43).//Q04854
 F-HEMBB1000335//ZINC FINGER PROTEIN 13 (ZFP-13) (KROX-8 PROTEIN)
 (FRAGMENT).//0.82:33:45//MUS MUSCULUS (MOUSE).//P10754
 F-HEMBB1000336//ALDEHYDE OXIDASE (EC 1.2.3.1) (FRAGMENTS).//0.80:4
 4:40//ORYZOTOLAGUS CURVICULUS (RABBIT).//P80456
 F-HEMBB1000337//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA
 SPLICING FACTOR SRP75).//0.94:118:22//HOMO SAPIENS (HUMAN).//Q0817
 0
 F-HEMBB1000338//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.042:33:39/
 DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01642
 F-HEMBB1000339//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.2e-14:5
 4:55//HOMO SAPIENS (HUMAN).//P39188
 F-HEMBB1000341//GENE 74 PROTEIN (GP74).//1.0:39:33//MYCOBACTERIOPH
 AGE L5.//Q05289
 F-HEMBB1000343
 F-HEMBB1000354//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-15:8
 3:56//HOMO SAPIENS (HUMAN).//P39188
 F-HEMBB1000369//PROTEIN Q300.//0.99:27:40//MUS MUSCULUS (MOUSE).//
 Q02722
 F-HEMBB1000374//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/4.7e-34:
 56:78//HOMO SAPIENS (HUMAN).//P39189
 F-HEMBB1000376
 F-HEMBB1000391//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.0013:7
 9:35//BOS TAURUS (BOVINE).//P25508
 F-HEMBB1000399//CHECKPOINT PROTEIN RAD17.//2.8e-15:187:31//SCHIZOS
 ACCHARYOMYCES POMBE (FISSION YEAST).//P50531
 F-HEMBB1000402//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.
 3) (FRAGMENT).//0.027:60:30//LEISHMANIA TARENTOLAE (SAUROLEISHMANI
 A TARENTOLAE).//P15583
 F-HEMBB1000404//CYANELLE 50S RIBOSOMAL PROTEIN L28.//0.94:29:27//C
 YANOPHORA PARADOXA.//P48129
 F-HEMBB1000420//SPICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B5
 3).//0.023:97:35//HOMO SAPIENS (HUMAN).//Q15427
 F-HEMBB1000434//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.8e-20:
 111:54//HOMO SAPIENS (HUMAN).//P39194
 F-HEMBB1000438//HYPOTHETICAL 7.9 KD PROTEIN IN GP55-NRDC INTERGENE
 C REGION.//0.93:24:50//BACTERIOPHAGE T4.//P07076
 F-HEMBB1000441//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.4e-23:8
 5:70//HOMO SAPIENS (HUMAN).//P39188
 F-HEMBB1000449//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.88:27:
 51//HOMO SAPIENS (HUMAN).//P39195
 F-HEMBB1000455
 F-HEMBB1000472
 F-HEMBB1000480//PROTEIN STBC.//1.0:52:30//ESCHERICHIA COLI.//P1190
 5
 F-HEMBB1000487//SHORT NEUROTOXIN 1 (NEUROTOXIN ALPHA) (NEUROTOXIN
 1).//0.93:29:34//NAJA OXIANA (CENTRAL ASIAN COBRA) (OXUS COBRA).//
 P01427
 F-HEMBB1000490//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.3e-16:
 50:80//HOMO SAPIENS (HUMAN).//P39195
 F-HEMBB1000491
 F-HEMBB1000493//3A PROTEIN.//1.0:51:35//AVIAN INFECTIOUS BRONCHITI
 S VIRUS (STRAIN BEAUDETTE) (IBV).//P30237
 F-HEMBB1000510//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.7e-27:13
 2:45//HOMO SAPIENS (HUMAN).//P08547
 F-HEMBB1000518//CYTOCHROME C OXIDASE POLYPEPTIDE III (EC 1.9.3.1).
 //0.021:47:40//LEISHMANIA TARENTOLAE (SAUROLEISHMANIA TARENTOLAE).
 //P14546
 F-HEMBB1000523
 F-HEMBB1000530//COLLAGEN ALPHA 1(XIV) CHAIN PRECURSOR (LUNDULIN).//
 9.8e-14:43:83//GALLUS GALLUS (CHICKEN).//P32018
 F-HEMBB1000550//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.
 3).//0.19:97:30//TRYPANOSOMA BRUCEI BRUCEI.//P04540
 F-HEMBB1000554//MATERNAL 89.10 PROTEIN (P30 89.10).//0.94:82:25//X
 ENOPIUS LAEVIS (AFRICAN CLAWED FROG).//P40744
 F-HEMBB1000556//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUN
 IT (TAFII-135) (TAFII135) (TAFII-130) (TAFII130).//0.043:201:29//H
 OMO SAPIENS (HUMAN).//Q00268
 F-HEMBB1000564//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:5
 2:34//METRIDIDIUM SENILE (BROWN SEA ANEMONE) (FRILLED SEA ANEMONE).//
 Q047493
 F-HEMBB1000573//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/2.3e-1
 0:52:73//HOMO SAPIENS (HUMAN).//P39191
 F-HEMBB1000575//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.8e-26:
 76:76//HOMO SAPIENS (HUMAN).//P39192
 F-HEMBB1000586//NADH-UBIQUINONE OXIDOREDUCTASE MLRQ SUBUNIT (EC 1.
 6.5.3) (EC 1.6.99.3) (COMPLEX I-MLRQ) (CI-MLRQ).//0.74:23:52//HOMO
 SAPIENS (HUMAN).//Q00483
 F-HEMBB1000589//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.9e-25:
 61:75//HOMO SAPIENS (HUMAN).//P39193
 F-HEMBB1000591//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:3
 4:35//PETROMYZON MARINUS (SEA LAMPREY).//Q35537
 F-HEMBB1000592//SMALL PROLINE-RICH PROTEIN 2-1.//0.0016:49:42//HOM
 O SAPIENS (HUMAN).//P35326
 F-HEMBB1000593//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENTS).//0.0070:1
 89:32//GALLUS GALLUS (CHICKEN).//P12105
 F-HEMBB1000598//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.7e-10:11
 0:41//MYCTICEBUS COUCANG (SLOW LORIS).//P08548
 F-HEMBB1000623//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME
 111.//0.0022:98:28//CAENORHABDITIS ELEGANS.//P34284
 F-HEMBB1000630
 F-HEMBB1000631//ALPHA-2C-1 ADRENERGIC RECEPTOR (ALPHA-2C-1 ADRENOC
 EPTOR) (SUBTYPE C4).//8.8e-06:59:40//HOMO SAPIENS (HUMAN).//P18825
 F-HEMBB1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//7.3
 e-13:173:28//MUS MUSCULUS (MOUSE).//P27671
 F-HEMBB1000637//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.6e-41:
 94:82//HOMO SAPIENS (HUMAN).//P39193
 F-HEMBB1000638//INVOLUCRIN.//1.9e-06:144:29//HOMO SAPIENS (HUMAN).
 //P07476
 F-HEMBB1000643//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/8.3e-30:
 77:76//HOMO SAPIENS (HUMAN).//P39195
 F-HEMBB1000648//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.5e-37:
 58:81//HOMO SAPIENS (HUMAN).//P39189
 F-HEMBB1000652//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.2e-37:
 61:77//HOMO SAPIENS (HUMAN).//P39193
 F-HEMBB1000665//HYPOTHETICAL PROTEIN BBD24.//0.83:38:36//BORRELIA
 BURGDORFERI (LYME DISEASE SPIROCHETE).//P70845
 F-HEMBB1000671//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.8e-51:74
 71//HOMO SAPIENS (HUMAN).//P08547
 F-HEMBB1000673//HEAT-STABLE ENTEROTOXIN A3/A4 PRECURSOR (STA3/STA
 4) (ST-18) (ST-H).//0.012:37:37//ESCHERICHIA COLI.//P07965
 F-HEMBB1000684//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/3.1e-21:
 66:72//HOMO SAPIENS (HUMAN).//P39193
 F-HEMBB1000693//HUNTINGTIN ASSOCIATED PROTEIN 1 (HAP1).//5.2e-26:1
 21:49//RATTUS NORVEGICUS (RAT).//P54256
 F-HEMBB1000705
 F-HEMBB1000706
 F-HEMBB1000709//HYPOTHETICAL 5.8 KD PROTEIN.//1.0:29:44//CLOVER YE
 LLOW MOSAIC VIRUS (CYMV).//P16485

【0639】

【表341】

F-HEMBB1000725//RAS-RELATED PROTEIN RAB-8B.//7.4e-105:205:98//RATT
US NORVEGICUS (RAT).//P70550
F-HEMBB1000726//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.4e-25:
85:70//HOMO SAPIENS (HUMAN).//P39194
F-HEMBB1000738//50S RIBOSOMAL PROTEIN L33.//1.0:41:31//THERMUS AQU
ATICUS (SUBSP. THERMOPHILUS).//P35871
F-HEMBB1000749//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.3e-29:
42:85//HOMO SAPIENS (HUMAN).//P39194
F-HEMBB1000763//NIFU PROTEIN.//0.089:63:36//FRANKIA ALNI.//P46045
F-HEMBB1000770//CALTRIN-LIKE PROTEIN 11.//0.98:13:69//CAVIA PORCEL
LUS (GUINEA PIG).//P22075
F-HEMBB1000774//HIGH MOBILITY GROUP PROTEIN HMG-Y.//0.029:53:32//M
US MUSCULUS (MOUSE).//P17095
F-HEMBB1000781//MAPK/ERK KINASE 2 (EC 2.7.1.-) (MEK KINASE
2) (MEKK 2).//3.5e-75:144:98//MUS MUSCULUS (MOUSE).//Q61083
F-HEMBB1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-AOK2
INTERGENIC REGION.//2.6e-49:232:43//SACCHAROMYCES CEREVISIAE (BAKE
R'S YEAST).//P39556
F-HEMBB1000790//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.9e-16:9
3:51//HOMO SAPIENS (HUMAN).//P39188
F-HEMBB1000794
F-HEMBB1000807//MUSCARINIC ACETYLCHOLINE RECEPTOR M3.//0.54:111:27
//CALLUS GALLUS (CHICKEN).//P49578
F-HEMBB1000810
F-HEMBB1000821
F-HEMBB1000822//HYPOTHETICAL 10 KD PROTEIN (ORF 6).//0.10:50:34//M
ARCISUS MOSAIC VIRUS (MMV).//P15099
F-HEMBB1000826//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//0.00
025:73:39//HOMO SAPIENS (HUMAN).//P20931
F-HEMBB1000827//HYPOTHETICAL 7.4 KD PROTEIN.//0.89:23:52//THERMOPR
OTEUS TENAX VIRUS 1 (STRAIN KRAI) (TTV1).//P19302
F-HEMBB1000831//MALE SPECIFIC SPERM PROTEIN MST87F.//0.98:35:40//D
ROSOPHILA MELANOGASTER (FRUIT FLY).//P08175
F-HEMBB1000835//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.8e-31:96:
46//HOMO SAPIENS (HUMAN).//P08547
F-HEMBB1000840//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.0012:10
2:36//NYCTICEBUS COUCANG (SLOW LORIS).//P08548
F-HEMBB1000848//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.3e-97:23
9:70//HOMO SAPIENS (HUMAN).//P08547
F-HEMBB1000852
F-HEMBB1000870
F-HEMBB1000876//METALLOTHIONEIN (MT).//0.99:14:64//PERCA FLUVIATIL
IS (PERCH).//P52725
F-HEMBB1000883//HYPOTHETICAL 7.8 KD PROTEIN (ORF62).//0.34:60:33//
QUILLARDIA THETA (CRYPTOMONAS PH).//Q78459
F-HEMBB1000887//HISTIDINE-RICH METAL BINDING POLYPEPTIDE.//1.0:2
6:42//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//Q48251
F-HEMBB1000888
F-HEMBB1000890
F-HEMBB1000893
F-HEMBB1000908//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.0074:4
5:51//HOMO SAPIENS (HUMAN).//P39188
F-HEMBB1000910//PROBABLE ES PROTEIN.//1.0:49:36//HUMAN PAPILLOMAVI
RUS TYPE 58.//P26552
F-HEMBB1000913//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.29:56:
46//HOMO SAPIENS (HUMAN).//P39195
F-HEMBB1000915//CYTOCHROME B (EC 1.10.2.2).//2.5e-24:62:90//HOMO S
APIENS (HUMAN).//P00156
F-HEMBB1000917//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/5.9e-26:
53:66//HOMO SAPIENS (HUMAN).//P39193
F-HEMBB1000927//NEURONAL CALCIUM SENSOR 1 (NCS-1) (FREQUENIN).//3.
9e-44:182:45//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q91614
F-HEMBB1000947//SMALL PROLINE-RICH PROTEIN 2-1.//0.24:69:27//HOMO
SAPIENS (HUMAN).//P35326
F-HEMBB1000959//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/3.0e-31:
89:68//HOMO SAPIENS (HUMAN).//P39195
F-HEMBB1000973//CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.//0.96:6
6:36//BOS TAURUS (BOVINE).//Q18739
F-HEMBB1000975//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR (HISTIDINE-P
ROLINE RICH GLYCOPROTEIN) (HPRG).//0.00042:77:41//HOMO SAPIENS (HU
MAN).//P04196
F-HEMBB1000981
F-HEMBB1000985//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESS
ED PROTEIN).//1.0e-18:178:30//MUS MUSCULUS (MOUSE).//P28575
F-HEMBB1000991
F-HEMBB1000996//HYPOTHETICAL 10.1 KD PROTEIN IN RHSD-GCL INTERGENI
C REGION (ORF03).//0.58:34:35//ESCHERICHIA COLI.//P3669
F-HEMBB1001004//PROBABLE E4 PROTEIN.//0.24:110:35//HUMAN PAPILLOMA
VIRUS TYPE 58.//P26550
F-HEMBB1001008
F-HEMBB1001011//ZINC FINGER PROTEIN 7 (ZINC FINGER PROTEIN KOX4)
(ZINC FINGER PROTEIN HF.16).//3.2e-17:104:47//HOMO SAPIENS (HUMAN
).//P17097
F-HEMBB1001014//EOTAXIN PRECURSOR (EOSINOPHIL CHEMOTACTIC PROTEIN
).//1.0:58:39//RATTUS NORVEGICUS (RAT).//P97545
F-HEMBB1001020//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.4e-07:
36:75//HOMO SAPIENS (HUMAN).//P39189
F-HEMBB1001024
F-HEMBB1001037//FERREDOXIN.//1.0:52:25//MOORELLA THERMOACETICA (CL
OSTRIDIUM THERMOACETICUM).//P00203
F-HEMBB1001047
F-HEMBB1001051//PROTEIN FAN (FACTOR ASSOCIATED WITH N-SMASE ACTIVA
TION).//3.4e-21:50:100//HOMO SAPIENS (HUMAN).//Q92636
F-HEMBB1001056//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0099:115:
35//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPHPV)./
Q10341
F-HEMBB1001058//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.1e-33:
95:76//HOMO SAPIENS (HUMAN).//P39192
F-HEMBB1001060//HYPOTHETICAL 8.2 KD PROTEIN ZC21.7 IN CHROMOSOME 1
11.//1.0:38:36//CAENORHABDITIS ELEGANS.//P34591
F-HEMBB1001063
F-HEMBB1001068
F-HEMBB1001096//NOXIUSTOXIN (NTX) (TOXIN 11.11).//0.99:36:38//CENT
RUROIDES NOXIUS (MEXICAN SCORPION).//P08815
F-HEMBB1001102//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME
1.//1.1e-27:115:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q
09701
F-HEMBB1001105//CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN
PRECURSOR.//0.80:70:40//HOMO SAPIENS (HUMAN).//P28067
F-HEMBB1001112//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.
1e-126:287:85//RATTUS NORVEGICUS (RAT).//P38378
F-HEMBB1001114//HYPOTHETICAL 9.6 KD PROTEIN (ORF2).//0.84:62:27//B
ACTERIOPHAGE L2.//P42537
F-HEMBB1001117
F-HEMBB1001119//COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR.//1.6e-21:5
0:98//HOMO SAPIENS (HUMAN).//Q99715
F-HEMBB1001126//HYPOTHETICAL 55.9 KD PROTEIN EEED8.6 IN CHROMOSOME
11.//1.7e-50:184:53//CAENORHABDITIS ELEGANS.//Q09296
F-HEMBB1001133//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.4e-09:
53:62//HOMO SAPIENS (HUMAN).//P39192
F-HEMBB1001137//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC
2.7.7.6) (RPB1) (FRAGMENT).//2.0e-05:206:27//CRICETULUS GRISEUS
(CHINESE HAMSTER).//P11414
F-HEMBB1001142//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.1e-05:
46:56//HOMO SAPIENS (HUMAN).//P39193
F-HEMBB1001151//HYPOTHETICAL 33.5 KD PROTEIN C104.02C IN CHROMOSOM
E 1.//2.3e-23:109:44//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//
Q10149
F-HEMBB1001153//PROCOLLAGEN ALPHA 2(IV) CHAIN PRECURSOR.//0.75:76:
34//ASCARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).//P27393
F-HEMBB1001169//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.4e-16:
71:59//HOMO SAPIENS (HUMAN).//P39195
F-HEMBB1001175//ANKYRIN.//3.2e-12:169:31//MUS MUSCULUS (MOUSE).//Q
02357
F-HEMBB1001177//PERIODIC TRYPTOPHAN PROTEIN 2 HOMOLOG.//9.4e-07:14
8:27//HOMO SAPIENS (HUMAN).//Q15269
F-HEMBB1001182//HYPOTHETICAL 36.0 KD PROTEIN.//1.3e-09:110:31//SAC
CHAROMYCES CEREVISIAE (BAKER'S YEAST).//P54858
F-HEMBB1001199
F-HEMBB1001208//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.053:23:47//MUS
MUSCULUS (MOUSE).//P15974
F-HEMBB1001209
F-HEMBB1001210//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.14:40:37//MUS
MUSCULUS (MOUSE).//P15974
F-HEMBB1001218//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.4e-19:
49:67//HOMO SAPIENS (HUMAN).//P39194
F-HEMBB1001221//CYTOCHROME C OXIDASE POLYPEPTIDE VIIA-LIVER PRECUR
SOR (EC 1.9.3.1).//0.11:44:38//HOMO SAPIENS (HUMAN).//P14406
F-HEMBB1001234//65 KD YES-ASSOCIATED PROTEIN (YAP65).//2.0e-45:19
2:53//MUS MUSCULUS (MOUSE).//P46938
F-HEMBB1001242//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING P
ROTEIN C12G12.13C IN CHROMOSOME 1.//5.5e-37:226:41//SCHIZOSACCHARO
MYCES POMBE (FISSION YEAST).//Q09876
F-HEMBB1001249//OXALACETATE DECARBOXYLASE GAMMA CHAIN (EC 4.1.1.
3).//1.0:23:43//KLEBSIELLA PNEUMONIAE.//P13155
F-HEMBB1001253//METALLOTHIONEIN-1H (MT-1H) (METALLOTHIONEIN-O) (M
T-O).//0.14:16:43//HOMO SAPIENS (HUMAN).//P0294
F-HEMBB1001254//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.4e-12:
40:75//HOMO SAPIENS (HUMAN).//P39195
F-HEMBB1001267//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.0e-12:

【0640】

【表342】

33:78//HOMO SAPIENS (HUMAN).//P39193
 F-HEMBB1001271//HYPOTHETICAL 25.1 KD PROTEIN B0302.5 IN CHROMOSOME X.//1.0:58:37//CAENORHABDITIS ELEGANS.//Q10928
 F-HEMBB1001282//ANKYRIN HOMOLOG PRECURSOR.//9.5e-13:206:31//CHROMATIUM VINOSUM.//Q06527
 F-HEMBB1001288//COPPER HOMEOSTASIS PROTEIN CUTC.//4.6e-42:163:51//ESCHERICHIA COLI.//P46719
 F-HEMBB1001289//HYPOTHETICAL PROTEIN ORF-1137.//1.0e-05:106:26//MUS MUSCULUS (MOUSE).//P11260
 F-HEMBB1001294//GTP-BINDING PROTEIN TC10.//1.3e-34:58:94//HOMO SAPIENS (HUMAN).//P17081
 F-HEMBB1001302//HOMEBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEBOX PROTEIN 2) (CDX-3).//0.24:49:46//HOMO SAPIENS (HUMAN).//Q99626
 F-HEMBB1001304//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W10-1) (FRAGMENT).//1.0:17:70//LYCOPERSICON ESCULENTUM (TOMATO).//Q01157
 F-HEMBB1001314//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.21:104:27//DROSOPHILA ERECTA (FRUIT FLY).//P13730
 F-HEMBB1001315//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.3e-24:53:71//HOMO SAPIENS (HUMAN).//P39195
 F-HEMBB1001317//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOME 1.//0.24:90:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09782
 F-HEMBB1001326//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.36:26:50//MUS MUSCULUS (MOUSE).//P15974
 F-HEMBB1001331//HYPOTHETICAL BHLF1 PROTEIN.//1.0:127:33//EPSTEIN-BARR VIRUS (STRAIN 895-8) (HUMAN HERPESVIRUS 4).//P03181
 F-HEMBB1001335//ESCARGOT/SMALL PROTEIN HOMOLOG (FRAGMENT).//0.85:44:29//SCIARA COPROPHILA (FLUNGUS GRAT).//Q01799
 F-HEMBB1001337//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.2e-20:62:62//HOMO SAPIENS (HUMAN).//P39194
 F-HEMBB1001339//HYPOTHETICAL 17.3 KD PROTEIN CYIA11.16C.//8.2e-07:123:34//MYCOBACTERIUM TUBERCULOSIS.//Q05006
 F-HEMBB1001346//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.2e-14:60:45//HOMO SAPIENS (HUMAN).//P08547
 F-HEMBB1001348//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.6e-14:61:62//HOMO SAPIENS (HUMAN).//P39188
 F-HEMBB1001356
 F-HEMBB1001364
 F-HEMBB1001366//HISTIDINE-RICH PROTEIN.//0.87:26:42//PLASMODIUM FALCIPARUM (ISOLATE FCM17 / SENEGAL).//P14586
 F-HEMBB1001367//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//8.6e-40:146:61//HOMO SAPIENS (HUMAN).//P39192
 F-HEMBB1001369
 F-HEMBB1001380//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.9e-25:49:83//HOMO SAPIENS (HUMAN).//P39193
 F-HEMBB1001384//B34 INTERACTING DOMAIN DEATH AGONIST (BID).//0.80:95:29//MUS MUSCULUS (MOUSE).//P70444
 F-HEMBB1001387//PEA2 PROTEIN (PPF2 PROTEIN).//0.022:117:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40091
 F-HEMBB1001394//ALPHA-ADAPTIN A (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-A LARGE CHAIN) (100 KD COATED VESICLE PROTEIN A) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA A SUBUNIT).//0.38:85:31//MUS MUSCULUS (MOUSE).//P17426
 F-HEMBB1001410
 F-HEMBB1001424//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR.//0.99:37:21//ORYZA SATIVA (RICE).//P12162
 F-HEMBB1001426//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.0035:40:60//HOMO SAPIENS (HUMAN).//P39195
 F-HEMBB1001429//CYTOSOL AMINOPEPTIDASE (EC 3.4.11.1) (LEUCINE AMINOPEPTIDASE) (LAP) (LEUCYL AMINOPEPTIDASE) (PROLINE AMINOPEPTIDASE) (EC 3.4.11.5) (PROLYL AMINOPEPTIDASE).//1.1e-99:219:86//BOS TAURUS (BOVINE).//P00727
 F-HEMBB1001436//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.4e-30:57:78//HOMO SAPIENS (HUMAN).//P39195
 F-HEMBB1001443//[PYRUVATE DEHYDROGENASE (LIPOAMIDE)]-PHOSPHATASE P RECURSOR (PDP) (EC 3.1.3.43) (PYRUVATE DEHYDROGENASE PHOSPHATASE, CATALYTIC SUBUNIT) (PDPC).//2.5e-79:155:97//BOS TAURUS (BOVINE).//P35816
 F-HEMBB1001449
 F-HEMBB1001454//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//1.1e-05:196:31//HOMO SAPIENS (HUMAN).//P10161
 F-HEMBB1001458//24 KD ANTIGEN (FRAGMENT).//0.94:18:50//PLASMODIUM CHABAUDI.//P14592
 F-HEMBB1001463
 F-HEMBB1001464//PPF2L ANTIGEN (FRAGMENT).//1.0:45:28//PLASMODIUM FALCIPARUM (ISOLATE PAID ALTO / UGANDA).//P07765
 F-HEMBB1001482//GASTRULA ZINC FINGER PROTEIN XLGCF1.1 (FRAGMENT).//4.2e-10:37:43//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18712
 F-HEMBB1001500
 F-HEMBB1001521//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-39:59:72//HOMO SAPIENS (HUMAN).//P39188
 F-HEMBB1001527//HOMEBOX PROTEIN HOX-B5 (XLHBOX-4) (HOX-18) (FRAGMENT).//0.21:131:25//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P09019
 F-HEMBB1001531//GENE 32 PROTEIN (GP32).//0.88:95:30//MYCOBACTERIOPHAGE L5.//Q05241
 F-HEMBB1001535//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:31:38//LUMBRICUS TERRESTRIS (COMMON EARTHWORM).//Q34942
 F-HEMBB1001536
 F-HEMBB1001537//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//0.0063:52:50//HOMO SAPIENS (HUMAN).//P39191
 F-HEMBB1001555//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.9e-23:69:63//HOMO SAPIENS (HUMAN).//P39188
 F-HEMBB1001562//RABPHILIN-3A.//0.087:147:27//RATTUS NORVEGICUS (RAT).//P47709
 F-HEMBB1001564//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.9e-27:107:54//HOMO SAPIENS (HUMAN).//P08547
 F-HEMBB1001565//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.9e-12:51:54//HOMO SAPIENS (HUMAN).//P39194
 F-HEMBB1001585
 F-HEMBB1001586
 F-HEMBB1001588//HYPOTHETICAL 12.3 KD PROTEIN IN GAPI-MAP1 INTERGENIC REGION.//0.0031:31:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36140
 F-HEMBB1001603
 F-HEMBB1001618//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49): ENDONUCLEASE].//0.00076:47:44//MUS MUSCULUS (MOUSE).//P11369
 F-HEMBB1001619//SMALL PROLINE RICH PROTEIN 11 (SPR-11) (CLONE 930).//1.0:52:32//HOMO SAPIENS (HUMAN).//P22531
 F-HEMBB1001630
 F-HEMBB1001635//METALLOTHIONEIN-LIKE PROTEIN TYPE 2 A.//0.27:44//LYCOPERSICON ESCULENTUM (TOMATO).//Q40157
 F-HEMBB1001637//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.0042:26:73//HOMO SAPIENS (HUMAN).//P39188
 F-HEMBB1001641
 F-HEMBB1001653//SURVIVAL MOTOR NEURON PROTEIN 1.//0.51:36:47//CANIS FAMILIARIS (DOG).//Q02771
 F-HEMBB1001665//HOMEBOX PROTEIN ENGRAILED-1 (HU-EN-1).//0.0030:135:34//HOMO SAPIENS (HUMAN).//Q05925
 F-HEMBB1001668//PROBABLE 60S RIBOSOMAL PROTEIN L39.//0.99:25:44//CAENORHABDITIS ELEGANS.//P52814
 F-HEMBB1001673//HYPOTHETICAL 46.1 KD PROTEIN IN ERP5-ORC6 INTERGENIC REGION.//0.0054:128:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38823
 F-HEMBB1001684//SUPPRESSOR PROTEIN SRP40.//0.56:81:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
 F-HEMBB1001685//CYTOCHROME C OXIDASE POLYPEPTIDE VIII-HEART PRECURSOR (EC 1.9.3.1) (VIII) (IX).//1.0:21:47//BOS TAURUS (BOVINE).//P10175
 F-HEMBB1001695//MYOSIN IC HEAVY CHAIN.//8.9e-05:86:40//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569
 F-HEMBB1001704//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//9.0e-08:35:71//HOMO SAPIENS (HUMAN).//P39195
 F-HEMBB1001706//CORNIFIN (SMALL PROLINE-RICH PROTEIN 1) (SPR-1) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).//0.91:39:41//SUS SCROFA (PIC).//P35323
 F-HEMBB1001707//FERREDOXIN-LIKE PROTEIN IN NIF REGION.//1.0:43:23//BRADYRHIZOBIUM JAPONICUM.//P27394
 F-HEMBB1001717//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.3) (FRAGMENT).//1.0:71:25//LEMUR CATTAL (RING-TAILED LEMUR).//Q34878
 F-HEMBB1001735//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.0e-35:97:74//HOMO SAPIENS (HUMAN).//P39194
 F-HEMBB1001736//EUKARYOTIC TRANSLATION INITIATION FACTOR 3 BETA SUBUNIT (EIF-3 BETA) (EIF3 P116) (EIF3 P110).//0.00069:180:28//HOMO SAPIENS (HUMAN).//P55884
 F-HEMBB1001747
 F-HEMBB1001749//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.8e-43:75:70//HOMO SAPIENS (HUMAN).//P39195
 F-HEMBB1001753//PROTEIN Q300.//0.00091:16:81//MUS MUSCULUS (MOUSE).//Q02722
 F-HEMBB1001756//CYCLIN-DEPENDENT KINASES REGULATORY SUBUNIT 2 (XEP9).//0.94:35:42//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q91879
 F-HEMBB1001760
 F-HEMBB1001762//GENE 35 PROTEIN (GP35).//0.76:21:47//MYCOBACTERIOPHAGE L5.//Q05245
 F-HEMBB1001785
 F-HEMBB1001797//CHLOROPLAST 50S RIBOSOMAL PROTEIN L35.//0.99:41:31

【0641】

【表343】

//PORPHYRA PURPUREA. //P51270
 F-HEMBB1001802
 F-HEMBB1001812//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.2e-39:
 54:77//HOMO SAPIENS (HUMAN). //P39193
 F-HEMBB1001816//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.1e-19:
 97:57//HOMO SAPIENS (HUMAN). //P39194
 F-HEMBB1001831//HYPOTHETICAL 45.6 KD PROTEIN IN COXA-ALG11 INTERG
 ENIC REGION. //0.62:20:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
 T). //P53951
 F-HEMBB1001834//GLYCINE-RICH RNA-BINDING PROTEIN 1 (FRAGMENT). //0.
 0014:40:45//SORGHUM VULGARE (SORGHUM). //Q99069
 F-HEMBB1001836//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/7.1e-1
 4:85:61//HOMO SAPIENS (HUMAN). //P39191
 F-HEMBB1001839//PROBABLE E4 PROTEIN. //0.61:49:34//HUMAN PAPILLOMAV
 IRUS TYPE 6C. //P20969
 F-HEMBB1001850
 F-HEMBB1001863//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.7e-30:
 57:68//HOMO SAPIENS (HUMAN). //P39194
 F-HEMBB1001867
 F-HEMBB1001868//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH
 GLYCOPROTEIN). //0.00036:47:53//NICOTIANA TABACUM (COMMON TOBACCO).
 //P13983
 F-HEMBB1001869//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/7.0e-11:9
 5:45//HOMO SAPIENS (HUMAN). //P39188
 F-HEMBB1001872//HYPOTHETICAL 8.2 KD PROTEIN IN LEF8-FP INTERGENIC
 REGION. //1.0:34:38//AUTOGRAHA CALIFORNICA NUCLEAR POLYDROSIS VI
 RUS (ACNOPV). //P41459
 F-HEMBB1001874
 F-HEMBB1001875
 F-HEMBB1001880
 F-HEMBB1001899//GENE 11 PROTEIN. //1.0:45:31//SPIROPLASMA VIRUS SPV
 1-RBA2 B. //P15902
 F-HEMBB1001905//HYPOTHETICAL 81.7 KD PROTEIN IN MOLI-MAT2 INTERGEN
 IC REGION. //8.8e-54:216:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
 T). //P48234
 F-HEMBB1001906
 F-HEMBB1001908//MONOCYTIC LEUKEMIA ZINC FINGER PROTEIN. //6.3e-51:1
 38:80//HOMO SAPIENS (HUMAN). //Q92794
 F-HEMBB1001910
 F-HEMBB1001911
 F-HEMBB1001915//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.
 2.15) (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING
 PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E). //2.3e-27:71:70//DROS
 OPHILA MELANOGASTER (FRUIT FLY). //Q24574
 F-HEMBB1001921//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. //9.8e-13:75:
 53//HOMO SAPIENS (HUMAN). //P08547
 F-HEMBB1001922
 F-HEMBB1001925//EPITHELIAL MEMBRANE PROTEIN-1 (EMP-1) (TUMOR-ASSOC
 IATED MEMBRANE PROTEIN). //1.0:55:30//MUS MUSCULUS (MOUSE). //P47801
 F-HEMBB1001930//HYPOTHETICAL 9.6 KD PROTEIN K1002.7 IN CHROMOSOME
 111. //0.43:49:26//CAENORHABDITIS ELEGANS. //Q09412
 F-HEMBB1001944//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/5.1e-34:
 63:85//HOMO SAPIENS (HUMAN). //P39189
 F-HEMBB1001945//NONSPECIFIC LIPID-TRANSFER PROTEIN (LTP) (PHOSPHOL
 IPID TRANSFER PROTEIN) (PLTP). //0.28:45:40//AMARANTHUS CAUDATUS (L
 OVE-LIES-BLEEDING) (INCA-WHEAT). //P80450
 F-HEMBB1001947//PROTEIN UL24. //0.48:42:47//HERPES SIMPLEX VIRUS (T
 YPE 1 / STRAIN 17). //P10208
 F-HEMBB1001950//HYPOTHETICAL 42.6 KD PROTEIN IN GSHB-ANSB INTERGEN
 IC REGION (Q378). //1.6e-24:162:36//ESCHERICHIA COLI. //P52062
 F-HEMBB1001952
 F-HEMBB1001953
 F-HEMBB1001957//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.7e-11:5
 1:60//HOMO SAPIENS (HUMAN). //P39188
 F-HEMBB1001962//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/7.6e-24:1
 63:42//HOMO SAPIENS (HUMAN). //P39188
 F-HEMBB1001967//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.1e-35:
 55:80//HOMO SAPIENS (HUMAN). //P39189
 F-HEMBB1001973//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/2.1e-37:
 108:75//HOMO SAPIENS (HUMAN). //P39192
 F-HEMBB1001983//LYSIS PROTEIN (E PROTEIN) (GPE). //0.84:45:37//BACT
 ERIOPHAGE ALPHA-3. //P31280
 F-HEMBB1001988
 F-HEMBB1001990
 F-HEMBB1001996//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. //1.4e-14:98:
 40//HOMO SAPIENS (HUMAN). //P08547
 F-HEMBB1001997//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.1e-19:3
 8:73//HOMO SAPIENS (HUMAN). //P39188
 F-HEMBB1002002//CYTOCHROME C BIOGENESIS PROTEIN CCSA. //1.0:150:25/
 //PORPHYRA PURPUREA. //P51369
 F-HEMBB1002005//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/7.6e-12:
 94:40//HOMO SAPIENS (HUMAN). //P39195
 F-HEMBB1002009
 F-HEMBB1002015//HYPOTHETICAL 7.7 KD PROTEIN IN MRR-TSR INTERGENIC
 REGION (F67). //1.0:17:47//ESCHERICHIA COLI. //P39395
 F-HEMBB1002042//CYTOCHROME P450 4C1 (EC 1.14.14.1) (CYP1C1). //2.4
 e-50:139:55//BLABERUS DISCOIDALIS (TROPICAL COCKROACH). //P29981
 F-HEMBB1002043//HYPOTHETICAL 9.5 KD PROTEIN IN DHFR 3' REGION (ORF
 3). //0.052:40:42//HERPESVIRUS SAIMIRI (SUBGROUP C / STRAIN 408). //P
 22577
 F-HEMBB1002044//CELLULOSE COMPLEMENTING PROTEIN. //0.45:87:33//ACET
 OBACTER KYLINUM (ACETOBACTER PASTEURIANUS). //P37697
 F-HEMBB1002045//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (AGL). //0.78:
 18:55//HOMO SAPIENS (HUMAN). //P03928
 F-HEMBB1002049
 F-HEMBB1002050//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP
 7) [CONTAINS: BASIC PEPTIDE P-F] (FRAGMENT). //1.0e-06:188:27//HOMO
 SAPIENS (HUMAN). //P02812
 F-HEMBB1002068//HOMEOBOX PROTEIN HOX-A4 (CHOX-1.4). //0.0023:56:44/
 //GALLUS GALLUS (CHICKEN). //P17277
 F-HEMBB1002069//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH
 GLYCOPROTEIN). //0.0074:134:33//NICOTIANA TABACUM (COMMON TOBACCO).
 //P13983
 F-HEMBB1002092//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONT
 AINS: OUTER MEMBRANE PROTEIN GP70: TRANSMEMBRANE PROTEIN P20E]. //2
 .4e-07:75:40//BABOON ENDOGENOUS VIRUS (STRAIN M7). //P10269
 F-HEMBB1002094//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/1.9e-2
 4:63:82//HOMO SAPIENS (HUMAN). //P39191
 F-HEMBB1002115//EC PROTEIN HOMOLOG (ZINC-METALLOTHIONEIN CLASS 11
). //0.94:26:42//ZEA MAYS (MAIZE). //P43401
 F-HEMBB1002134//ZINC-FINGER PROTEIN NEURO-D4. //4.6e-57:176:67//RAT
 TUS NORVEGICUS (RAT). //P56163
 F-HEMBB1002139//CHLOROPLAST S0S RIBOSOMAL PROTEIN L35. //1.0:17:52/
 //PORPHYRA PURPUREA. //P51270
 F-HEMBB1002142//EARLY MODULIN 20 PRECURSOR (N-20). //0.087:52:36//M
 EDICAGO TRUNCATULA (BARREL MEDIC). //P93329
 F-HEMBB1002152//HYPOTHETICAL 12.3 KD PROTEIN IN RPL3-RPL33 INTERGE
 NIC REGION (ORF102). //5.8e-05:61:37//CYANOPHORA PARADOXA. //P15811
 F-HEMBB1002189//HYPOTHETICAL PROTEIN UL125. //1.0:77:32//HUMAN CYTO
 MEGALOVIRUS (STRAIN AD169). //P16835
 F-HEMBB1002190
 F-HEMBB1002193//TYROSINE-PROTEIN KINASE RECEPTOR TYRO3 PRECURSOR
 (TYROSINE-PROTEIN KINASE RSE) (TYROSINE-PROTEIN KINASE SKY) (TYROS
 INE-PROTEIN KINASE DTK). //1.2e-27:59:100//HOMO SAPIENS (HUMAN). //Q
 06418
 F-HEMBB1002217//ZINC FINGER PROTEIN 184 (FRAGMENT). //6.6e-22:106:5
 0//HOMO SAPIENS (HUMAN). //Q99676
 F-HEMBB1002218//PROTEIN Q300. //0.85:19:52//MUS MUSCULUS (MOUSE). //Q
 02722
 F-HEMBB1002232//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/9.6e-21:
 56:71//HOMO SAPIENS (HUMAN). //P39195
 F-HEMBB1002247
 F-HEMBB1002249//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.2e-29:
 93:69//HOMO SAPIENS (HUMAN). //P39194
 F-HEMBB1002254//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.0e-29:
 101:67//HOMO SAPIENS (HUMAN). //P39194
 F-HEMBB1002255//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 3 (EC 1.6.5.
 3). //1.0:73:28//PARAMECIUM TETRAURELIA. //P15579
 F-HEMBB1002266//GLUTAMIC ACID-RICH PROTEIN PRECURSOR. //0.0079:151:
 26//PLASMODIUM FALCIPARUM (ISOLATE FC27 / PAPUA NEW GUINEA). //P138
 16
 F-HEMBB1002280//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. //5.2e-15:18
 2:36//NYCTICEBUS COUCANG (SLOW LORIS). //P08548
 F-HEMBB1002300
 F-HEMBB1002306//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.00011:
 26:84//HOMO SAPIENS (HUMAN). //P39195
 F-HEMBB1002327//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/4.1e-11:
 41:85//HOMO SAPIENS (HUMAN). //P39189
 F-HEMBB1002329//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGEN
 IC REGION. //9.9e-17:232:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
 T). //P40032
 F-HEMBB1002340
 F-HEMBB1002342//HYPOTHETICAL 32.5 KD PROTEIN IN MSH6-BMH2 INTERGEN
 IC REGION. //3.6e-40:102:57//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
 T). //Q03835
 F-HEMBB1002358//THYMIDYLATE KINASE (EC 2.7.4.9) (DTMP KINASE). //6.
 1e-30:63:96//HOMO SAPIENS (HUMAN). //P23919
 F-HEMBB1002359//HYPOTHETICAL 7.1 KD PROTEIN C6G9.01C IN CHROMOSOME
 1. //0.97:28:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //Q9234
 6

【0642】

【表344】

F-HEMBB1002364//RETROVIRUS-RELATED POL POLYPROTEIN (FRAGMENT).//0.47:119:25//HOMO SAPIENS (HUMAN).//P12895
 F-HEMBB1002371//HYPOTHETICAL 15.5 KD PROTEIN C2F7.12 IN CHROMOSOME 1 PRECURSOR.//3.0e-05:111:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09703
 F-HEMBB1002381//PUTATIVE CUTICLE COLLAGEN C09G5.4.//0.34:105:34//CAENORHABDITIS ELEGANS.//Q09455
 F-HEMBB1002383//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.049:103:32//AQUIFEX AEOLICUS.//Q06566
 F-HEMBB1002387//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) (HEAT SHOCK PROTEIN 11).//0.18:75:28//RICKETTSIA TSUTSUGAMUSHI.//P16626
 F-HEMBB1002409//HIGH MOBILITY GROUP PROTEIN HMG-Y.//0.014:61:36//MUS MUSCULUS (MOUSE).//P17095
 F-HEMBB1002415
 F-HEMBB1002425//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.8e-18:55:70//HOMO SAPIENS (HUMAN).//P39194
 F-HEMBB1002442//LIN-10 PROTEIN.//5.1e-15:121:31//CAENORHABDITIS ELEGANS.//P34692
 F-HEMBB1002453//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.2e-32:54:75//HOMO SAPIENS (HUMAN).//P39189
 F-HEMBB1002457//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-07:31:64//HOMO SAPIENS (HUMAN).//P39188
 F-HEMBB1002458//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.92:28:53//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01642
 F-HEMBB1002477//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//0.0066:198:27//CRICETULUS CRISSEUS (CHINESE HAMSTER).//P11414
 F-HEMBB1002489//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B5 3).//0.030:182:28//HOMO SAPIENS (HUMAN).//Q15427
 F-HEMBB1002492
 F-HEMBB1002495//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//2.1e-08:41:75//HOMO SAPIENS (HUMAN).//P39192
 F-HEMBB1002502//RETROVIRUS-RELATED POL POLYPROTEIN (FRAGMENT).//0.00030:31:77//HOMO SAPIENS (HUMAN).//P12895
 F-HEMBB1002509
 F-HEMBB1002510
 F-HEMBB1002520//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.8e-36:162:50//NYCTICEBUS COUCANG (SLOW LORIS).//P08548
 F-HEMBB1002522//7 KD PROTEIN (ORF 4).//0.77:32:40//CHRYSANTHEMUM VIRIDIS B (CVRB).//P37990
 F-HEMBB1002531
 F-HEMBB1002534//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//3.1e-36:80:73//HOMO SAPIENS (HUMAN).//P39195
 F-HEMBB1002545
 F-HEMBB1002550//HOMEBOX PROTEIN HOX-D11 (HOX-4.6) (HOX-5.5).//3.8e-05:83:34//MUS MUSCULUS (MOUSE).//P23813
 F-HEMBB1002556
 F-HEMBB1002579//SPLICING FACTOR UZAF 35 KD SUBUNIT (U2 AUXILIARY FACTOR 35 KD SUBUNIT) (U2 SNRNP AUXILIARY FACTOR SMALL SUBUNIT) (FRAGMENT).//5.0e-06:27:77//SUS SCROFA (PIG).//Q29350
 F-HEMBB1002582//PROTEINASE INHIBITOR.//1.0:27:40//SOLANUM MELONGENA (EGGPLANT) (AUBERGINE).//P01078
 F-HEMBB1002590//HYPOTHETICAL PROTEIN IN MMSB 3' REGION (ORF1) (FRAGMENT).//1.9e-20:90:54//PSEUDOMONAS AERUGINOSA.//P28812
 F-HEMBB1002596
 F-HEMBB1002600//NOVEL ANTIGEN 2 (NAG-2).//1.9e-60:187:59//HOMO SAPIENS (HUMAN).//Q14817
 F-HEMBB1002601//M PROTEIN, SEROTYPE 6 PRECURSOR.//1.0:71:35//STREPTOCOCCUS PYOGENES.//P08089
 F-HEMBB1002603
 F-HEMBB1002607//SALIVARY PROLINE-RICH PROTEIN P0 (ALLELE K) (CONTAINS: PEPTIDE P-0) (FRAGMENT).//0.0032:142:33//HOMO SAPIENS (HUMAN).//P10162
 F-HEMBB1002610//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.0e-11:79:49//HOMO SAPIENS (HUMAN).//P08547
 F-HEMBB1002613//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.9e-08:41:60//HOMO SAPIENS (HUMAN).//P39188
 F-HEMBB1002614//HYPOTHETICAL 9.5 KD PROTEIN.//1.0:40:35//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20553
 F-HEMBB1002617//INSECT TOXIN 1 (BOT IT1).//1.0:44:29//BUTHUS OCCITANUS TUNETANUS (COMMON EUROPEAN SCORPION).//P55902
 F-HEMBB1002623//HYPOTHETICAL 9.7 KD PROTEIN (ORF88) (PUTATIVE DNA-BINDING PROTEIN).//0.42:31:54//BACTERIOPHAGE P4.//P12552
 F-HEMBB1002635//STRESS-ACTIVATED PROTEIN KINASE JNK3 (EC 2.7.1.-) (C-JUN N-TERMINAL KINASE 3) (MAP KINASE P49 3F12).//6.2e-17:44:95//HOMO SAPIENS (HUMAN).//P53779
 F-HEMBB1002664//SMALL NUCLEAR RIBONUCLEOPROTEIN ASSOCIATED PROTEIN 8 (SN-B) (SNRNP-B) (SM11) (FRAGMENT).//1.0:57:36//RATTUS NORVEGICUS (RAT).//P17136
 F-HEMBB1002677//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.9e-06:194:34//NYCTICEBUS COUCANG (SLOW LORIS).//P08548
 F-HEMBB1002683//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.96:56:35//LEMUR CATTAL (RING-TAILED LEMUR).//Q34879
 F-HEMBB1002684//SILLUCIN.//1.0:16:50//RHIZOMUCOR PUSILLUS.//P02885
 F-HEMBB1002686
 F-HEMBB1002692
 F-HEMBB1002697//HELIX-DESTABILIZING PROTEIN (SINGLE-STRANDED DNA BINDING PROTEIN) (GPV).//0.57:36:38//BACTERIOPHAGE FD, BACTERIOPHAGE FI, AND BACTERIOPHAGE M13.//P03669
 F-HEMBB1002699
 F-HEMBB1002702
 F-HEMBB1002705//HYPOTHETICAL 34.8 KD PROTEIN C4H3.04C IN CHROMOSOME 1.//3.6e-40:180:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10212
 F-HEMBB1002712
 F-HEMBB1000009//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.2e-32:95:75//HOMO SAPIENS (HUMAN).//P39189
 F-HEMBB1000019
 F-HEMBB1000020//DIMETHYLANILINE MONOOXYGENASE [N-OXIDE FORMING] 5 (EC 1.14.13.8) (HEPATIC FLAVIN-CONTAINING MONOOXYGENASE 5) (FMO 5) (DIMETHYLANILINE OXIDASE 5).//5.2e-12:24:100//HOMO SAPIENS (HUMAN).//P49326
 F-HEMBB1000025//BETA-2-MICROGLOBULIN PRECURSOR.//1.0:73:26//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//Q04475
 F-HEMBB1000043//HYPOTHETICAL PXL-1 PROTEIN (FRAGMENT).//0.057:130:31//BOVINE LEUKEMIA VIRUS (JAPANESE ISOLATE BLV-1) (BLV).//P03412
 F-HEMBB1000045
 F-HEMBB1000055//TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)].//7.5e-44:138:55//MUS MUSCULUS (MOUSE).//P47226
 F-HEMBB1000057//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.2e-39:92:69//HOMO SAPIENS (HUMAN).//P39194
 F-HEMBB1000069//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0044:96:34//ORGYIA PSEUDOTUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMV).//Q10341
 F-HEMBB1000084//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//5.4e-28:94:73//HOMO SAPIENS (HUMAN).//P39195
 F-HEMBB1000085//PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C (EC 6.1.1.16) (CYSTEINE--TRNA LIGASE) (CYSR5).//6.6e-38:90:51//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09860
 F-HEMBB1000092//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//6.4e-30:43:86//HOMO SAPIENS (HUMAN).//P39192
 F-HEMBB1000103//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.038:17:52//HOMO SAPIENS (HUMAN).//P22531
 F-HEMBB1000117//50S RIBOSOMAL PROTEIN L24E (HL21/HL22).//0.90:25:48//HALOARCTIA MARISMORTUI (HALOBACTERIUM MARISMORTUI).//P14116
 F-HEMBB1000129//HYPOTHETICAL BHLF1 PROTEIN.//0.0016:75:40//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
 F-HEMBB1000133
 F-HEMBB1000134//HYPOTHETICAL PROTEIN MJ0647.//1.0:41:41//METHANOCOCCUS JANNASCHII.//Q58063
 F-HEMBB1000139//GUANINE NUCLEOTIDE-BINDING PROTEIN G(1)/G(5)/G(10) GAMMA-3 SUBUNIT.//0.99:69:28//BOS TAURUS (BOVINE), AND MUS MUSCULUS (MOUSE).//P29798
 F-HEMBB1000143//CALPAIN INHIBITOR (CALPASTATIN) (FRAGMENT).//0.023:111:27//MUS MUSCULUS (MOUSE).//P51125
 F-HEMBB1000155//PUTATIVE CUTICLE COLLAGEN C09G5.5.//0.018:125:34//CAENORHABDITIS ELEGANS.//Q09455
 F-HEMBB1000163//MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT P RECURSOR (PERIPLASMIC MERCURY ION BINDING PROTEIN) (MERCURY SCAVENGER PROTEIN).//0.11:88:25//SHEWANELLA PUTREFACIENS (PSEUDOMONAS PUTREFACIENS).//Q54463
 F-HEMBB1000171
 F-HEMBB1000173//DREBRIN E.//7.6e-41:197:43//HOMO SAPIENS (HUMAN).//Q16643
 F-HEMBB1000175//GAMMA-THIONIN HOMOLOG PPT PRECURSOR.//0.92:39:38//PETUNIA INTEGRIFOLIA (VIOLET-FLOWERED PETUNIA) (PETUNIA INFLATA).//Q40901
 F-HEMBB1000183//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.4e-106:249:61//HOMO SAPIENS (HUMAN).//P51523
 F-HEMBB1000198//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.0014:35:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645
 F-HEMBB1000221
 F-HEMBB1000227//6.8 KD MITOCHONDRIAL PROTEOLIPID.//1.0:30:40//MUS MUSCULUS (MOUSE).//P56379
 F-HEMBB1000241//PHOTOSYSTEM I REACTION CENTRE SUBUNIT X (PSI-K).//1.0:40:37//PORPHYRA PURPUREA.//P51370
 F-HEMBB1000251//HYPOTHETICAL 6.8 KD PROTEIN IN FIC-PPIA INTERGENIC

【0643】

【表345】

REGION. //0.99:29:48//SALMONELLA TYPHIMURIUM. //P37771
 F-MAMMA1000254//HYPOTHETICAL 6.0 KD PROTEIN IN TH12 5' REGION. //1.0:20:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P53820
 F-MAMMA1000257//HYPOTHETICAL 50.0 KD PROTEIN IN HEML 3' REGION (ORF 2). //0.22:50:44//PSEUDOMONAS AERUGINOSA. //Q51470
 F-MAMMA1000264//CASTRIN-RELEASING PEPTIDE RECEPTOR (GRP-R) (GRP-PR EFFERING BOMBESIN RECEPTOR). //0.80:39:43//HOMO SAPIENS (HUMAN). //P30550
 F-MAMMA1000266
 F-MAMMA1000270//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/9.5e-42:95:84//HOMO SAPIENS (HUMAN). //P39189
 F-MAMMA1000277//PROCOLLAGEN ALPHA 1(I1) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN]. //0.0062:90:34//MUS MUSCULUS (MOUSE). //P28481
 F-MAMMA1000278//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT). //0.00096:59:33//HORDEUM VULGARE (BARLEY). //P17991
 F-MAMMA1000279//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/8.4e-17:56:76//HOMO SAPIENS (HUMAN). //P39195
 F-MAMMA1000284//ARYL HYDROCARBON RECEPTOR NUCLEAR TRANSLOCATOR 2 (ARNT PROTEIN 2). //0.017:146:30//MUS MUSCULUS (MOUSE). //Q61324
 F-MAMMA1000287//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.5e-32:84:58//HOMO SAPIENS (HUMAN). //P39189
 F-MAMMA1000302//C-HORDEIN (CLONE PC-919) (FRAGMENT). //1.0:42:33//HORDEUM VULGARE (BARLEY). //P17992
 F-MAMMA1000307//PROBABLE E4 PROTEIN. //0.21:71:30//RHESUS PAPILLOMA VIRUS TYPE 1 (RHPV 1). //P24832
 F-MAMMA1000309//COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN). //0.0026:141:36//HOMO SAPIENS (HUMAN). //P27658
 F-MAMMA1000312
 F-MAMMA1000313//DNA REPAIR PROTEIN RADC HOMOLOG (25 KD PROTEIN) (FRAGMENT). //0.76:52:32//STAPHYLOCOCCUS AUREUS. //P31337
 F-MAMMA1000331
 F-MAMMA1000339//50S RIBOSOMAL PROTEIN L29P. //0.78:32:46//METHANOBACTERIUM THERMAUTOTROPHICUM. //Q26117
 F-MAMMA1000340//HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION. //1.0:29:58//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P36039
 F-MAMMA1000348//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/7.5e-09:63:60//HOMO SAPIENS (HUMAN). //P39188
 F-MAMMA1000356//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.3e-05:42:52//HOMO SAPIENS (HUMAN). //P39188
 F-MAMMA1000360
 F-MAMMA1000361//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/4.4e-33:84:72//HOMO SAPIENS (HUMAN). //P39189
 F-MAMMA1000372//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/6.6e-21:53:71//HOMO SAPIENS (HUMAN). //P39193
 F-MAMMA1000385
 F-MAMMA1000388//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN). //0.40:72:36//HOMO SAPIENS (HUMAN). //P43489
 F-MAMMA1000395//RABPHILIN-3A (FRAGMENT). //0.032:125:25//MUS MUSCULUS (MOUSE). //P47708
 F-MAMMA1000402//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. //3.1e-28:6:40//HOMO SAPIENS (HUMAN). //P08547
 F-MAMMA1000410//NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-B SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-13KD-B) (C1-13KD-B) (B13). //5.9e-06:32:68//HOMO SAPIENS (HUMAN). //Q16718
 F-MAMMA1000413//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49): ENDONUCLEASE]. //6.7e-05:93:31//MUS MUSCULUS (MOUSE). //P11369
 F-MAMMA1000414
 F-MAMMA1000416//HYPOTHETICAL 32.0 KD PROTEIN CD95.2 IN CHROMOSOME 111. //4.1e-28:119:53//CAENORHABDITIS ELEGANS. //Q09232
 F-MAMMA1000421//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.7e-23:68:76//HOMO SAPIENS (HUMAN). //P39194
 F-MAMMA1000422//METALLOTHIONEIN (MT). //0.037:42:42//GADUS MORHUA (ATLANTIC COD). //P51902
 F-MAMMA1000423
 F-MAMMA1000424//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/0.048:23:73//HOMO SAPIENS (HUMAN). //P39189
 F-MAMMA1000429//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS5. //2.7e-05:110:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //Q92331
 F-MAMMA1000431//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.4e-15:85:58//HOMO SAPIENS (HUMAN). //P39194
 F-MAMMA1000444//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.3e-25:65:76//HOMO SAPIENS (HUMAN). //P39194
 F-MAMMA1000446//ZYXIN. //0.79:155:29//CALLUS GALLUS (CHICKEN). //Q04584
 F-MAMMA1000458//HYPOTHETICAL 37.7 KD PROTEIN C18B11.06 IN CHROMOSOME 1. //0.0048:46:43//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //Q09713

F-MAMMA1000468//PERIOD CLOCK PROTEIN (FRAGMENT). //0.50:20:55//DROSOPHILA ROBUSTA (FRUIT FLY). //Q03296
 F-MAMMA1000472//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.5e-17:106:55//HOMO SAPIENS (HUMAN). //P39188
 F-MAMMA1000478//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/3.9e-35:80:68//HOMO SAPIENS (HUMAN). //P39195
 F-MAMMA1000483//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.8e-24:74:77//HOMO SAPIENS (HUMAN). //P39193
 F-MAMMA1000490//TYROSINE-PROTEIN KINASE TXK (EC 2.7.1.112) (PTK-R L-18) (RESTING LYMPHOCYTE KINASE). //0.43:21:57//MUS MUSCULUS (MOUSE). //P42682
 F-MAMMA1000500//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN). //0.61:33:54//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (Z2/CDC-234 ISOLATE) (HIV-1). //P12506
 F-MAMMA1000501//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.1e-32:43:83//HOMO SAPIENS (HUMAN). //P39194
 F-MAMMA1000516
 F-MAMMA1000522//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. //0.0015:113:32//HOMO SAPIENS (HUMAN). //P08547
 F-MAMMA1000524//HYPOTHETICAL HOST RANGE 8.5 KD PROTEIN. //1.0:63:31//VACCINIA VIRUS (STRAIN WR). //P17359
 F-MAMMA1000559//METALLOTHIONEIN-1 (MT-1) (MT-1B/MT-1A). //0.31:16:50//CALLINECTES SAPIOUS (BLUE CRAB). //P55949
 F-MAMMA1000565//FERREDOXIN-TYPE PROTEIN NAF. //0.98:37:35//ESCHERICHIA COLI. //P33939
 F-MAMMA1000567//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.5e-37:95:76//HOMO SAPIENS (HUMAN). //P39195
 F-MAMMA1000576//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!/4.1e-07:34:64//HOMO SAPIENS (HUMAN). //P39191
 F-MAMMA1000583
 F-MAMMA1000585//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.5e-28:89:75//HOMO SAPIENS (HUMAN). //P39194
 F-MAMMA1000594//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.8e-24:38:71//HOMO SAPIENS (HUMAN). //P39195
 F-MAMMA1000597//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.1e-25:74:77//HOMO SAPIENS (HUMAN). //P39195
 F-MAMMA1000605//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.1e-18:83:50//HOMO SAPIENS (HUMAN). //P39195
 F-MAMMA1000612//HYPOTHETICAL 34.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN SISI-MRPL2 INTERGENIC REGION. //4.0e-42:166:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P41318
 F-MAMMA1000616
 F-MAMMA1000621
 F-MAMMA1000623//METALLOTHIONEIN-1K (MT-1K). //0.0045:25:48//HOMO SAPIENS (HUMAN). //P0296
 F-MAMMA1000625//PROLINE-RICH PROTEIN MP-3 (FRAGMENT). //0.00078:79:35//MUS MUSCULUS (MOUSE). //P05143
 F-MAMMA1000643//HYPOTHETICAL 9.3 KD PROTEIN. //1.0:25:28//MAGUARI VIRUS. //P16607
 F-MAMMA1000664
 F-MAMMA1000669//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. //4.2e-05:18:6:30//HOMO SAPIENS (HUMAN). //P08547
 F-MAMMA1000670//PROLINE-RICH PROTEIN MP-3 (FRAGMENT). //1.6e-06:19:5:30//MUS MUSCULUS (MOUSE). //P05143
 F-MAMMA1000672//VITELLOGENIC CARBOXYPEPTIDASE PRECURSOR (EC 3.4.1.6). //3.8e-28:184:35//AEDES AEGYPTI (YELLOW FEVER MOSQUITO). //P42660
 F-MAMMA1000684//DNA-BINDING PROTEIN (VIM21). //1.1e-07:55:56//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17). //P04487
 F-MAMMA1000696//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.2e-31:97:74//HOMO SAPIENS (HUMAN). //P39194
 F-MAMMA1000707//METALLOTHIONEIN-1I (MT-1I) (MT-1IB/MT-1IA). //0.31:19:42//CALLINECTES SAPIOUS (BLUE CRAB). //P55950
 F-MAMMA1000713//XYLOSE KINASE (EC 2.7.1.17) (XYLOKINASE). //1.6e-05:88:35//LACTOBACILLUS PENTOSUS. //P21939
 F-MAMMA1000714//PROTEIN-LYSINE 6-OXIDASE PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE). //0.44:126:30//RATTUS NORVEGICUS (RAT). //P16636
 F-MAMMA1000718//METALLOTHIONEIN-1IE (MT-2E). //1.0:51:31//ORYCTOLAGUS CUNICULUS (RABBIT). //P0292
 F-MAMMA1000720//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/3.3e-28:60:71//HOMO SAPIENS (HUMAN). //P39193
 F-MAMMA1000723//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. //3.7e-14:63:53//HOMO SAPIENS (HUMAN). //P08547
 F-MAMMA1000731//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2). //1.8e-43:258:43//HOMO SAPIENS (HUMAN). //O14647
 F-MAMMA1000732//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/9.9e-12:76:55//HOMO SAPIENS (HUMAN). //P39188
 F-MAMMA1000733
 F-MAMMA1000734//NPL1 PROTEIN (SEC63 PROTEIN). //2.5e-18:181:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P14906

【0644】

【表346】

F-MAMMA1000738//HYPOTHETICAL 116.5 KD PROTEIN C20G.09C IN CHROMOSOME 1.//5.4e-52:196:58//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87115

F-MAMMA1000744//!!!! ALU SUBFAMILY S81 WARNING ENTRY !!!!!//6.3e-3 6:144:47//HOMO SAPIENS (HUMAN).//P39190

F-MAMMA1000746

F-MAMMA1000752

F-MAMMA1000760//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//6.6e-29: 75:72//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1000761//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.6e-09: 59:64//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1000775

F-MAMMA1000776//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//3.3e-35: 99:74//HOMO SAPIENS (HUMAN).//P39193

F-MAMMA1000778//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.1e-19: 65:70//HOMO SAPIENS (HUMAN).//P39195

F-MAMMA1000782

F-MAMMA1000798//HYPOTHETICAL PROTEIN ORF-1137.//0.015:59:37//MUS MUSCULUS (MOUSE).//P11260

F-MAMMA1000802//MYOSIN IC-HEAVY CHAIN.//0.35:94:41//ACANTHAMOEBA CASTELLANI (AMOEBA).//P10569

F-MAMMA1000824//ACTIN 1.//0.046:60:31//ZEA MAYS (MAIZE).//P02582

F-MAMMA1000831//PROBABLE NI/FE-HYDROGENASE 1 B-TYPE CYTOCHROME SUBUNIT.//1.0:30:46//ESCHERICHIA COLI.//P19929

F-MAMMA1000839//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-28: 8 0:58//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1000841//PUTATIVE AMIDASE (EC 3.5.1.4).//1.5e-39:130:36//METHANOBACTERIUM THERMAUTOTROPICUM.//027540

F-MAMMA1000842//C-HORDEIN (CLONE PC-919) (FRAGMENT).//0.064:43:41//HORDEUM VULGARE (BARLEY).//P17992

F-MAMMA1000843

F-MAMMA1000845//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.3).//0.43:58:34//DROSOPHILA YAKUBA (FRUIT FLY).//P03895

F-MAMMA1000851//CUTICLE COLLAGEN 34.//0.019:107:29//CAENORHABDITIS ELEGANS.//P34687

F-MAMMA1000855//SPLICEDSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A6).//0.00098:149:32//HOMO SAPIENS (HUMAN).//Q15428

F-MAMMA1000856//METALLOTHIONEIN (MT).//0.63:39:41//POTAMON POTAMIO S.//P55952

F-MAMMA1000859//GLYCOPROTEIN X PRECURSOR.//0.014:192:28//EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).//P28968

F-MAMMA1000862//DISINTEGRIN KISTRIN (PLATELET AGGREGATION ACTIVATION INHIBITOR).//1.0:66:27//ACKISTRODON RHODOSTOMA (MALAYAN PIT VIPER) (CALLOSELASMIA RHODOSTOMA).//P17494

F-MAMMA1000863//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.4e-16: 4 1:68//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1000865//SALIVARY PROLINE-RICH PROTEIN 11-1 (FRAGMENT).//0.030:100:32//HOMO SAPIENS (HUMAN).//P81489

F-MAMMA1000867//APTOTOXIN IX (PARALYTIC PEPTIDE IX) (PP IX).//0.9 8:43:32//APTOSTICHUS SCHLINGERI (TRAP-DOOR SPIDER).//P49272

F-MAMMA1000875//PROLINE-RICH PEPTIDE P-B.//0.18:21:47//HOMO SAPIENS (HUMAN).//P02814

F-MAMMA1000876//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.5e-22: 85:71//HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1000877//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.2e-38: 6 2:74//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1000880//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.49:79: 32//BOS TAURUS (BOVINE).//P25508

F-MAMMA1000883//HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X.//0.87:15:60//CAENORHABDITIS ELEGANS.//Q11116

F-MAMMA1000897//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4 PRECURSOR (ITI HEAVY CHAIN H4) (INTER-ALPHA-TRYPSIN INHIBITOR FAMILY HEAVY CHAIN-RELATED PROTEIN) (PLASMA KALLIKREIN SENSITIVE GLYCOPROTEIN 120) (PK-120).//5.3e-17:130:40//HOMO SAPIENS (HUMAN).//Q14624

F-MAMMA1000905

F-MAMMA1000906

F-MAMMA1000908//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//8.0e-17:70: 62//HOMO SAPIENS (HUMAN).//P08547

F-MAMMA1000914//HYPOTHETICAL 6.2 KD PROTEIN.//0.97:36:36//THERMOPLOTUS TENAX VIRUS 1 (STRAIN KRAI) (TTV1).//P19299

F-MAMMA1000921

F-MAMMA1000931//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.6e-10: 4 9:65//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1000940//MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L32.//0.42:22: 54//RECLINOMYXAS AMERICANA.//021281

F-MAMMA1000941//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.3e-25: 5 5:69//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1000942//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.3e-08: 36:75//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1000943

F-MAMMA1000956//SMALL HISTIDINE-ALANINE-RICH PROTEIN PRECURSOR (SHARP) (ANTIGEN 57).//0.041:122:25//PLASMODIUM FALCIPARUM (ISOLATE F C27) (PAPUA NEW GUINEA).//P04930

F-MAMMA1000957//HEAT-STABLE ENTEROTOXIN A2 PRECURSOR (STA2).//0.02 4:37:37//ESCHERICHIA COLI.//Q47185

F-MAMMA1000962//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//6.0e-39: 61:78//HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1000968//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.0054: 2 9:72//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1000975//CUTICLE COLLAGEN DPY-2 PRECURSOR.//1.0:93:30//CAENORHABDITIS ELEGANS.//P35799

F-MAMMA1000979//PROLINE-RICH PEPTIDE P-B.//0.012:12:66//HOMO SAPIENS (HUMAN).//P02814

F-MAMMA1000987//HYPOTHETICAL PROTEIN LAMBDA-SP34.//1.0:47:40//MUS MUSCULUS (MOUSE).//P15973

F-MAMMA1000998

F-MAMMA1001003//PROBABLE E5 PROTEIN.//1.0:52:42//HUMAN PAPILLOMAVIRUS TYPE 33.//P06426

F-MAMMA1001008//PROGASTRIN PRECURSOR (EC 3.4.23.3) (PEPSINOGEN C) (FRAGMENT).//3.2e-14:131:35//MACACA FUSCATA FUSCATA (JAPANESE MACAQUE).//P03955

F-MAMMA1001021//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.016:61:42//STREPTOMYCES FRADIAE.//P20186

F-MAMMA1001024

F-MAMMA1001030//LUTROPIN-CHORIOGONADOTROPIC HORMONE RECEPTOR (LH/CGR) (LSH-R) (LUTEINIZING HORMONE RECEPTOR) (FRAGMENT).//2.4e-20: 234:29//GALLUS GALLUS (CHICKEN).//Q90674

F-MAMMA1001035//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.7e-15: 52:78//HOMO SAPIENS (HUMAN).//P39193

F-MAMMA1001038//NEUROTOXIN II (TOXIN RP-11) (SODIUM CHANNEL TOXIN II).//0.53:25:48//RADIANTHUS PALMOTENSIS (SEA ANEMONE) (HETERACTIS PALMOTENSIS).//P01534

F-MAMMA1001041//SPECTRIN BETA CHAIN, ERYTHROCYTE.//6.3e-18:112:43//MUS MUSCULUS (MOUSE).//P15508

F-MAMMA1001050

F-MAMMA1001059//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//1.3 e-34:187:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09747

F-MAMMA1001067//PROTEIN Q300.//0.36:12:75//MUS MUSCULUS (MOUSE).//Q02722

F-MAMMA1001073//HEPATOCYTE NUCLEAR FACTOR 3 FORKHEAD HOMOLOG 1 (HFH-1).//1.0:70:37//RATTUS NORVEGICUS (RAT).//Q63244

F-MAMMA1001074//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.00067:16 3:32//HOMO SAPIENS (HUMAN).//P08547

F-MAMMA1001075//RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1).//0.53:7 2:34//HOMO SAPIENS (HUMAN).//P29374

F-MAMMA1001078//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.0e-79:18 4:73//HOMO SAPIENS (HUMAN).//P08547

F-MAMMA1001080//IG HEAVY CHAIN PRECURSOR V-III REGION (VH26).//1.7 e-27:82:71//HOMO SAPIENS (HUMAN).//P01764

F-MAMMA1001082

F-MAMMA1001091//HYPOTHETICAL BHLF1 PROTEIN.//3.1e-05:198:32//EPSTEIN-BARR VIRUS (STRAIN 895-8) (HUMAN HERPESVIRUS 4).//P03181

F-MAMMA1001092//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.1e-21:65: 72//HOMO SAPIENS (HUMAN).//P08547

F-MAMMA1001105//OVO PROTEIN (SHAVEN BABY PROTEIN).//1.0e-18:68:48//DROSOPHILA MELANOGASTER (FRUIT FLY).//P51521

F-MAMMA1001110//PROCOLLAGEN ALPHA 1(IV) CHAIN PRECURSOR.//0.080:10 8:37//MUS MUSCULUS (MOUSE).//P02463

F-MAMMA1001126//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.3e-07: 66:45//HOMO SAPIENS (HUMAN).//P39189

F-MAMMA1001133//HYPOTHETICAL 13.2 KD PROTEIN IN RPS4A-BAT2 INTERGENIC REGION.//0.96:43:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47174

F-MAMMA1001139//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME 1.//5.4e-42:81:62//CAENORHABDITIS ELEGANS.//Q09201

F-MAMMA1001143//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.00014: 3 6:66//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1001145

F-MAMMA1001154//CSBA PROTEIN.//1.0:39:38//BACILLUS SUBTILIS.//P379 53

F-MAMMA1001161//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.2e-23: 5 3:64//HOMO SAPIENS (HUMAN).//P39188

F-MAMMA1001162//CD27L RECEPTOR PRECURSOR (T-CELL ACTIVATION ANTIGEN CD27).//0.69:86:31//MUS MUSCULUS (MOUSE).//P41272

F-MAMMA1001181//HYPOTHETICAL 81.0 KD PROTEIN C35D10.4 IN CHROMOSOME E111.//0.00010:74:47//CAENORHABDITIS ELEGANS.//Q18486

F-MAMMA1001186//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//9.0e-32: 44:86//HOMO SAPIENS (HUMAN).//P39194

F-MAMMA1001191//OCTAMER-BINDING TRANSCRIPTION FACTOR 1 (OTF-1) (N-F-A1) (FRAGMENT).//0.096:40:40//MACROPIUS EUGENII (TAMMAR WALLABY).

【0645】

【表347】

//Q28466
F-MAHMA1001198//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15) (AF-1P PROTEIN).//2.5e-75:204:70//HOMO SAPIENS (HUMAN).//P42566
F-MAHMA1001202//METALLOTHIONEIN-11 (MT-11) (MT-11B/MT-11A).//0.52:46:32//CALLINECTES SAPIIDUS (BLUE CRAB).//P55950
F-MAHMA1001203//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//7.3e-11:82:58//HOMO SAPIENS (HUMAN).//P39192
F-MAHMA1001206//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.9e-17:67:71//HOMO SAPIENS (HUMAN).//P39188
F-MAHMA1001215//9 KD PROTEIN.//1.0:51:33//HOMO SAPIENS (HUMAN).//P13994
F-MAHMA1001220//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//3.4e-37:55:87//HOMO SAPIENS (HUMAN).//P39189
F-MAHMA1001222//HYPOTHETICAL 73.6 KD PROTEIN CY49.21.//3.7e-06:16:8:38//MYCOBACTERIUM TUBERCULOSIS.//Q10690
F-MAHMA1001243
F-MAHMA1001244//TRP OPERON LEADER PEPTIDE.//1.0:18:55//SERRATIA MARCESCENS.//P03055
F-MAHMA1001249//HYPOTHETICAL 7.2 KD PROTEIN IN RPS2 3' REGION (ORF57).//0.57:23:34//ASTASIA LONGA (EUCLEOPHYCEAN ALGA).//P34774
F-MAHMA1001256//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.3e-07:79:44//HOMO SAPIENS (HUMAN).//P39188
F-MAHMA1001259//PUTATIVE DNA HELICASE II HOMOLOG (EC 3.6.1.-).//0.046:86:32//MYCOPLASMA GENITALIUM.//P47486
F-MAHMA1001260//MYOSIN HEAVY CHAIN, PERINATAL SKELETAL MUSCLE.//2.7e-05:219:27//HOMO SAPIENS (HUMAN).//P13535
F-MAHMA1001268//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.7e-27:89:67//HOMO SAPIENS (HUMAN).//P08547
F-MAHMA1001271//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUYSIAN ATROPHY PROTEIN).//4.0e-06:126:38//HOMO SAPIENS (HUMAN).//P54259
F-MAHMA1001274//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.4e-29:57:66//HOMO SAPIENS (HUMAN).//P39194
F-MAHMA1001280//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//0.27:24:54//ESCHERICHIA COLI.//P05834
F-MAHMA1001292//HYPOTHETICAL PROTEIN KIAA0176 (FRAGMENT).//1.3e-73:208:69//HOMO SAPIENS (HUMAN).//Q14681
F-MAHMA1001296//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//6.9e-22:41:80//HOMO SAPIENS (HUMAN).//P39193
F-MAHMA1001298//HYPOTHETICAL PROTEIN H10371.//0.99:29:37//HAEMOPHILUS INFLUENZAE.//P44668
F-MAHMA1001305//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (PS0-RHOGAP).//9.9e-62:222:54//HOMO SAPIENS (HUMAN).//Q07960
F-MAHMA1001322//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD).//2.1e-09:46:60//HOMO SAPIENS (HUMAN).//P20931
F-MAHMA1001324//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-): REVERSE TRANSCRIPTASE (EC 2.7.7.49): RIBONUCLEASE H (EC 3.1.26.4)].//2.5e-43:128:50//FRIEND MURINE LEUKEMIA VIRUS (ISOLATE PVC-211) (F-MULV).//P26808
F-MAHMA1001330//HEMOGLOBIN ZETA CHAIN (FRAGMENTS).//0.30:51:37//MACROPUS EUGENII (TAMMAR WALLABY).//P81044
F-MAHMA1001341//TRISTETRAPROLINE (TTP) (TIS11A) (TIS11) (ZFP-36) (GROWTH FACTOR-INDUCIBLE NUCLEAR PROTEIN NUP475).//0.024:89:39//HOMO SAPIENS (HUMAN).//P26651
F-MAHMA1001343//PROBABLE E5 PROTEIN.//0.60:64:29//HUMAN PAPILLOMAVIRUS TYPE 16.//P06927
F-MAHMA1001346//PROTEINASE INHIBITOR I1B (FRAGMENTS).//0.97:33:45//SOLANUM TUBEROSUM (POTATO).//P01082
F-MAHMA1001383//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.2e-30:86:77//HOMO SAPIENS (HUMAN).//P39194
F-MAHMA1001388//LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRC).//9.2e-91:195:92//HOMO SAPIENS (HUMAN).//P02750
F-MAHMA1001397//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.5e-19:55:69//HOMO SAPIENS (HUMAN).//P39188
F-MAHMA1001408//SALIVARY GLUE PROTEIN SGS-7 PRECURSOR.//0.60:45:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P02841
F-MAHMA1001411//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//5.8e-06:153:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640
F-MAHMA1001419//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.3e-16:99:51//HOMO SAPIENS (HUMAN).//P39194
F-MAHMA1001420//!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!!//0.0018:23:65//HOMO SAPIENS (HUMAN).//P39190
F-MAHMA1001435//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.7e-22:60:58//HOMO SAPIENS (HUMAN).//P39195
F-MAHMA1001442
F-MAHMA1001446//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.2e-23:48:75//HOMO SAPIENS (HUMAN).//P39194
F-MAHMA1001452//GENE 35 PROTEIN (GP35).//0.61:31:45//MYCOBACTERIUM
HAGE L5.//Q05245
F-MAHMA1001465//HYPOTHETICAL PROTEIN E-115.//0.0026:68:38//HUMAN ADENOVIRUS TYPE 2.//P03290
F-MAHMA1001476//URIDINE KINASE (EC 2.7.1.48) (URIDINE MONOPHOSPHOKINASE) (FRAGMENT).//3.7e-94:201:92//MUS MUSCULUS (MOUSE).//P52623
F-MAHMA1001487//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.6e-16:89:41//NYCTICEBUS COUCANG (SLOW LORIS).//P08548
F-MAHMA1001501//CALPAIN 1, LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17) (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CAMP) (MU-TYPE).//6.2e-59:86:97//HOMO SAPIENS (HUMAN).//P07384
F-MAHMA1001502//HYPOTHETICAL 11.4 KD PROTEIN (ORF1).//0.21:79:30//STREPTOMYCES FRADIAE.//P26800
F-MAHMA1001510
F-MAHMA1001522//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.67:98:31//STREPTOMYCES FRADIAE.//P20186
F-MAHMA1001547//PROBABLE MOLYBDENUM-PTERIN BINDING PROTEIN.//0.97:35:42//HAEMOPHILUS INFLUENZAE.//P45183
F-MAHMA1001551//HYPOTHETICAL PROTEIN MJ0458.1.//0.038:31:41//METHANOCOCUS JANNASCHII.//P81308
F-MAHMA1001575
F-MAHMA1001576//TUBULIN GAMMA CHAIN.//1.6e-86:162:99//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P23330
F-MAHMA1001590//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.0035:38:55//HOMO SAPIENS (HUMAN).//P39195
F-MAHMA1001600//CONNECTIVE TISSUE GROWTH FACTOR PRECURSOR.//0.85:53:33//HOMO SAPIENS (HUMAN).//P29279
F-MAHMA1001604//HYPOTHETICAL 11.1 KD PROTEIN C30D11.02C IN CHROMOSOME 1.//0.14:82:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09902
F-MAHMA1001606//HIGH MOBILITY GROUP PROTEIN HMGI-C.//8.2e-05:77:37//HOMO SAPIENS (HUMAN).//P52926
F-MAHMA1001620//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//5.5e-05:24:66//HOMO SAPIENS (HUMAN).//P39195
F-MAHMA1001627//CUTICLE COLLAGEN 40.//0.82:131:31//CAENORHABDITIS ELEGANS.//P34804
F-MAHMA1001630//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//8.6e-26:57:78//HOMO SAPIENS (HUMAN).//P39194
F-MAHMA1001633//ZINC FINGER PROTEIN 165.//6.9e-38:160:55//HOMO SAPIENS (HUMAN).//P49910
F-MAHMA1001635
F-MAHMA1001649//SPERM PROTAMINE P1.//0.39:31:41//TACHYGLOSSUS ACULEATUS ACULEATUS (AUSTRALIAN ECHIDNA).//P35311
F-MAHMA1001654//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE 1).//5.6e-06:99:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P18160
F-MAHMA1001663//VERY HYPOTHETICAL XYLU PROTEIN.//0.99:27:37//ESCHERICHIA COLI.//P05056
F-MAHMA1001670//CUTICLE COLLAGEN 1.//0.033:97:37//CAENORHABDITIS ELEGANS.//P08124
F-MAHMA1001671
F-MAHMA1001679//PROCOLLAGEN ALPHA 2(IV) CHAIN PRECURSOR.//0.92:32:50//HOMO SAPIENS (HUMAN).//P08572
F-MAHMA1001683//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.0026:147:34//STREPTOMYCES FRADIAE.//P20186
F-MAHMA1001686
F-MAHMA1001692//SMALL HYDROPHOBIC PROTEIN (SMALL PROTEIN 1A).//1.0:34:26//BOVINE RESPIRATORY SYNCYTIAL VIRUS (STRAIN A51908) (BRV).//P24616
F-MAHMA1001711//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.1e-28:56:69//HOMO SAPIENS (HUMAN).//P39194
F-MAHMA1001715//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.6e-08:39:71//HOMO SAPIENS (HUMAN).//P39188
F-MAHMA1001730//METALLOTHIONEIN-B (MTB).//1.0:17:64//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).//Q27287
F-MAHMA1001735//TUBULIN BETA-5 CHAIN (CLASS-V).//5.1e-121:213:97//GALLUS GALLUS (CHICKEN).//P09653
F-MAHMA1001740
F-MAHMA1001743//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.3e-09:100:42//HOMO SAPIENS (HUMAN).//P39195
F-MAHMA1001744//POU DOMAIN PROTEIN 2.//0.97:59:38//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//Q90270
F-MAHMA1001745//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.1e-43:199:42//HOMO SAPIENS (HUMAN).//P08547
F-MAHMA1001751//TNK-8 PROTEIN.//2.9e-15:77:36//CAENORHABDITIS ELEGANS.//P34410
F-MAHMA1001754//MALE SPECIFIC SPERM PROTEIN MST840D.//0.019:20:45//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645
F-MAHMA1001757//HYPOTHETICAL 9.2 KD PROTEIN IN RNPA 3' REGION.//0.94:30:43//PSEUDOMONAS PUTIDA.//P25753
F-MAHMA1001760//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//4.6e-3

【0646】

【表348】

4:103:59//HOMO SAPIENS (HUMAN).//P39191
 F-MAHMA1001764
 F-MAHMA1001768//HYPOTHETICAL PROTEIN UL61.//0.042:167:33//HUMAN CY
 TOMEALOVIRUS (STRAIN AD169).//P16818
 F-MAHMA1001769//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.0e-29:
 97:69//HOMO SAPIENS (HUMAN).//P39194
 F-MAHMA1001771//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//3.3e-09:123:
 32//HOMO SAPIENS (HUMAN).//P39185
 F-MAHMA1001783//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-09:5
 5:61//HOMO SAPIENS (HUMAN).//P39188
 F-MAHMA1001785//RAS-RELATED PROTEIN RABC.//1.9e-06:120:25//DICTYOS
 TELIUM DISCOIDEUM (SLIME MOLD).//P34143
 F-MAHMA1001788//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.3e-29:46:
 76//HOMO SAPIENS (HUMAN).//P08547
 F-MAHMA1001790//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.7e-24:6
 9:69//HOMO SAPIENS (HUMAN).//P39188
 F-MAHMA1001806//HYPOTHETICAL 21.2 KD PROTEIN IN TOR2-MNNA INTERGEN
 IC REGION.//0.95:58:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//
 P36042
 F-MAHMA1001812//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/8.8e-12:
 53:69//HOMO SAPIENS (HUMAN).//P39195
 F-MAHMA1001815//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.11:30:70/
 HOMO SAPIENS (HUMAN).//P08547
 F-MAHMA1001817//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.9e-16:8
 6:55//HOMO SAPIENS (HUMAN).//P39188
 F-MAHMA1001818
 F-MAHMA1001820//VITELLINE MEMBRANE PROTEIN VM26AB PRECURSOR (PROTE
 IN TU-4) (PROTEIN SY23).//0.0030:63:42//DROSOPHILA MELANOGASTER (F
 RUIT FLY).//P13238
 F-MAHMA1001824//APTOTOXIN VII (PARALYTIC PEPTIDE VII) (PP VII).//
 0.9:26:34//APTOSTICHUS SCHLINGERI (TRAP-DOOR SPIDER).//P49271
 F-MAHMA1001836//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/2.6e-35:
 77:88//HOMO SAPIENS (HUMAN).//P39195
 F-MAHMA1001837//ZINC FINGER PROTEIN 191.//1.3e-27:106:58//HOMO SAP
 IENS (HUMAN).//014754
 F-MAHMA1001848//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.0e-19:9
 2:58//HOMO SAPIENS (HUMAN).//P39188
 F-MAHMA1001851
 F-MAHMA1001854
 F-MAHMA1001858//ISOTOCIN-NEUROPHYSIN IT 1 PRECURSOR.//0.93:42:38//
 CATOSTOMUS COMMERSONI (WHITE SUCKER).//P15210
 F-MAHMA1001864//PROBABLE ABC TRANSPORTER PERMEASE PROTEIN MC189.//
 0.77:161:27//MYCOPLASMA GENITALIUM.//P47435
 F-MAHMA1001868//FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL CI
 S-TRANS ISOMERASE) (PPIASE) (EC 5.2.1.8) (PROLINE ROTAMASE) (NUCLE
 OLAR PROLINE ISOMERASE) (FKBP-70).//0.00013:219:26//SACCHAROMYCES
 CEREVISIAE (BAKER'S YEAST).//P38911
 F-MAHMA1001874//SPERM HISTONE P2 PRECURSOR (PROTAMINE MP2).//0.007
 5:76:31//MUS MUSCULUS (MOUSE).//P07978
 F-MAHMA1001878//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN (CLONE W
 10-1) (FRAGMENT).//0.020:10:80//LYCOPERSICON ESCULENTUM (TOMATO).//
 Q01157
 F-MAHMA1001880
 F-MAHMA1001890//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/5.1e-34:
 56:83//HOMO SAPIENS (HUMAN).//P39192
 F-MAHMA1001907//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.7e-12:
 44:68//HOMO SAPIENS (HUMAN).//P39194
 F-MAHMA1001908//HYPOTHETICAL 16.2 KD PROTEIN IN PRP24-RRN9 INTERGE
 NIC REGION.//0.00013:77:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
 T).//Q03525
 F-MAHMA1001931//HYPOTHETICAL 118.2 KD PROTEIN F43C1.1 IN CHROMOSOM
 E III.//0.41:106:29//CAENORHABDITIS ELEGANS.//Q09564
 F-MAHMA1001956//DCTAPEPTIDE-REPEAT PROTEIN T2.//0.00053:149:30//MU
 S MUSCULUS (MOUSE).//Q06666
 F-MAHMA1001963//HYPOTHETICAL PROTEIN IN NAC 5' REGION (ORF X) (FRAG
 MENT).//1.0:46:28//KLEBSIELLA AEROGENES.//Q08600
 F-MAHMA1001969//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.7e-34:97:
 68//HOMO SAPIENS (HUMAN).//P08547
 F-MAHMA1001970//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.2e-07:67:
 37//HOMO SAPIENS (HUMAN).//P08547
 F-MAHMA1001992//PROTEIN Q300.//0.53:14:71//MUS MUSCULUS (MOUSE).//
 Q02722
 F-MAHMA1002009//PROBABLE ES PROTEIN.//0.17:56:32//HUMAN PAPILLOMAV
 IRUS TYPE 31.//P17385
 F-MAHMA1002011//MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MAR
 CKS) (PROTEIN KINASE C SUBSTRATE, 80 KD PROTEIN, LIGHT CHAIN) (PKC
 SL) (80K-L PROTEIN).//1.0:100:31//HOMO SAPIENS (HUMAN).//P29966
 F-MAHMA1002032//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/3.1e-21:8
 6:65//HOMO SAPIENS (HUMAN).//P39188
 F-MAHMA1002033//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/8.5e-20:6
 7:58//HOMO SAPIENS (HUMAN).//P39188
 F-MAHMA1002041//MALE SPECIFIC SPERM PROTEIN MST84DC.//1.0:17:52//D
 ROSOPHILA MELANOGASTER (FRUIT FLY).//Q01644
 F-MAHMA1002042//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/0.19:45:
 46//HOMO SAPIENS (HUMAN).//P39192
 F-MAHMA1002047//TYROSINE AMINOTRANSFERASE (EC 2.6.1.5) (L-TYROSIN
 E 2-OXOGLUTARATE AMINOTRANSFERASE) (TAT).//0.0017:50:46//RATTUS NO
 RVEGICUS (RAT).//P04694
 F-MAHMA1002056//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.2e-37:
 70:77//HOMO SAPIENS (HUMAN).//P39194
 F-MAHMA1002058//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.1e-08:2
 6:76//HOMO SAPIENS (HUMAN).//P39188
 F-MAHMA1002068//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//2.0e-11:78:
 46//HOMO SAPIENS (HUMAN).//P08547
 F-MAHMA1002078//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.96:
 26:46//COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL).//P50682
 F-MAHMA1002082//SUPPRESSOR PROTEIN SRP40.//0.23:95:32//SACCHAROMYC
 ES CEREVISIAE (BAKER'S YEAST).//P32583
 F-MAHMA1002084//HYPOTHETICAL 7.5 KD PROTEIN.//1.0:40:35//VACCINIA
 VIRUS (STRAIN COPENHAGEN).//P20520
 F-MAHMA1002093
 F-MAHMA1002108//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.
 //0.00079:143:33//STREPTOMYCES FRADIAE.//P20186
 F-MAHMA1002118//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:4
 3:34//METRIDIDIUM SENILE (BROWN SEA ANEMONE) (FRILLED SEA ANEMONE)./
 Q047493
 F-MAHMA1002125//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.9e-14:
 60:68//HOMO SAPIENS (HUMAN).//P39192
 F-MAHMA1002132
 F-MAHMA1002140//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.4e-24:6
 9:65//HOMO SAPIENS (HUMAN).//P39188
 F-MAHMA1002143//SERUM PROTEIN M5E55.//2.1e-16:166:43//HOMO SAPIENS
 (HUMAN).//Q00587
 F-MAHMA1002145//36.4 KD PROLINE-RICH PROTEIN.//0.00014:84:29//LYCO
 PERSICON ESCULENTUM (TOMATO).//Q00451
 F-MAHMA1002153
 F-MAHMA1002155
 F-MAHMA1002156//METALLOPROTEINASE INHIBITOR PRECURSOR.//0.90:58:34
 //STREPTOMYCES NIGRESCENS.//P01077
 F-MAHMA1002158
 F-MAHMA1002170//40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN).//
 6.0e-66:157:70//HOMO SAPIENS (HUMAN).//P15880
 F-MAHMA1002174//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/6.5e-25:5
 6:64//HOMO SAPIENS (HUMAN).//P39188
 F-MAHMA1002198//THIOREDOXIN PEROXIDASE 1 (THIOREDOXIN-DEPENDENT PE
 ROXIDE REDUCTASE 1) (THIOL-SPECIFIC ANTIOXIDANT PROTEIN) (TSA) (PR
 P) (NATURAL KILLER CELL ENHANCING FACTOR B) (NKEF-B).//9.0e-09:28:
 100//HOMO SAPIENS (HUMAN).//P32119
 F-MAHMA1002209//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUN
 IT (TAF11-135) (TAF11-130) (TAF11130).//0.0023:132:33//
 HOMO SAPIENS (HUMAN).//Q00268
 F-MAHMA1002215//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//0.00032:6
 8:35//HOMO SAPIENS (HUMAN).//P02452
 F-MAHMA1002219//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//0.0
 079:224:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25386
 F-MAHMA1002230
 F-MAHMA1002236//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT
 (EIF-2B GTP-EXCHANGE FACTOR).//1.4e-118:151:94//RATTUS NORVEG
 ICUS (RAT).//P07054
 F-MAHMA1002243//WISKOTT-ALDRICH SYNDROME PROTEIN HOMOLOG (WASP).//
 0.028:112:33//MUS MUSCULUS (MOUSE).//P07315
 F-MAHMA1002250//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).//0.
 0012:80:32//ORYCTOLAGUS CUNICULUS (RABBIT).//P06333
 F-MAHMA1002267//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//
 0.17:139:28//TRYPAERSONIA BRUCEI BRUCEI.//P24499
 F-MAHMA1002268//60S RIBOSOMAL PROTEIN L22.//0.00026:163:30//DROSOP
 HILA MELANOGASTER (FRUIT FLY).//P50887
 F-MAHMA1002269//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//0.35:1
 4:57//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//Q48251
 F-MAHMA1002282//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/6.1e-05:
 32:65//HOMO SAPIENS (HUMAN).//P39192
 F-MAHMA1002292//TROPOMYOSIN 2.//1.4e-05:100:30//SACCHAROMYCES CERE
 VISIAE (BAKER'S YEAST).//P40414
 F-MAHMA1002293//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/6.8e-25:1
 27:44//HOMO SAPIENS (HUMAN).//P39188
 F-MAHMA1002294//ALPHA TRANS-INDUCING PROTEIN (ALPHA-TIF).//0.0001
 1:138:38//BOVINE HERPESVIRUS TYPE 1 (STRAIN PB-2).//P30020
 F-MAHMA1002297//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.15:1
 44:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
 F-MAHMA1002298//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.0e-05:40:

【0647】

【表349】

50//MUS MUSCULUS (MOUSE).//P05143
 F-MAHMA1002299//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.84:65:32//STRUTHIO CAMELUS (OSTRICH).//021405
 F-MAHMA1002308//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.3e-29:61:73//HOMO SAPIENS (HUMAN).//P39188
 F-MAHMA1002310//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.00016:70:38//MUS MUSCULUS (MOUSE).//P15265
 F-MAHMA1002311//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/9.4e-09:84:54//HOMO SAPIENS (HUMAN).//P39189
 F-MAHMA1002312//HYPOTHETICAL 10.8 KD PROTEIN IN GP30-R111 INTERGENIC REGION (URF Y).//0.48:48:33//BACTERIOPHAGE T4.//P33084
 F-MAHMA1002317
 F-MAHMA1002319//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49): ENDONUCLEASE].//0.011:128:27//MUS MUSCULUS (MOUSE).//P11369
 F-MAHMA1002322//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.2e-20:92:57//HOMO SAPIENS (HUMAN).//P39195
 F-MAHMA1002329//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.051:33:36//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P03931
 F-MAHMA1002332//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.5e-20:116:51//HOMO SAPIENS (HUMAN).//P08547
 F-MAHMA1002333//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.0017:21:4:31//BOS TAURUS (BOVINE).//P02453
 F-MAHMA1002339//COPPER-METALLOTHIONEIN (CU-MT).//0.59:42:38//HELIX POMATIA (ROMAN SNAIL) (EDIBLE SNAIL).//P55947
 F-MAHMA1002347//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.43:26:61//HOMO SAPIENS (HUMAN).//P39188
 F-MAHMA1002351//HYPOTHETICAL PROTEIN M3034.//2.3e-07:139:25//METHANOCOCUS JANNASCHII.//Q57752
 F-MAHMA1002352
 F-MAHMA1002353//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00028:31:80//HOMO SAPIENS (HUMAN).//P39188
 F-MAHMA1002355//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/4.2e-28:87:73//HOMO SAPIENS (HUMAN).//P39193
 F-MAHMA1002356//RELAXIN.//0.95:31:35//SQUALUS ACANTHIAS (SPINY DOG FISH).//P11953
 F-MAHMA1002359//CHLOROPLAST 50S RIBOSOMAL PROTEIN L33.//0.93:44:36//GUILLARDIA THETA (CRYPTOMONAS PHI).//078487
 F-MAHMA1002360//LATE L2 MU CORE PROTEIN PRECURSOR (PROTEIN X).//0.94:30:43//BOVINE ADENOVIRUS TYPE 2 (MASTADENOVIRUS BOS2).//Q96626
 F-MAHMA1002361//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.0e-08:45:68//HOMO SAPIENS (HUMAN).//P39188
 F-MAHMA1002362//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.58:23:26//LUMBRICUS TERRESTRIS (COMMON EARTHWORM).//Q34942
 F-MAHMA1002380//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.23:100:27//DROSOPHILA SIMULANS (FRUIT FLY).//P13729
 F-MAHMA1002384
 F-MAHMA1002385//HYPOTHETICAL 40.9 KD PROTEIN IN ORC2-TIP1 INTERGENIC REGION.//3.8e-14:125:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38241
 F-MAHMA1002392//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:17:58//BRANCHIOSTOMA LANCEOLATUM (COMMON LANCELET) (AMPHIOXUS).//021003
 F-MAHMA1002411//30S RIBOSOMAL PROTEIN S17.//0.85:49:32//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P73311
 F-MAHMA1002413//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3) (FRAGMENT).//0.97:41:39//DROSOPHILA AFFINIS (FRUIT FLY).//P51926
 F-MAHMA1002417//RFBP PROTEIN.//0.99:31:35//SHIGELLA FLEXNERI.//P37786
 F-MAHMA1002427//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.6e-33:135:59//HOMO SAPIENS (HUMAN).//P39194
 F-MAHMA1002428//HYPOTHETICAL PROTEIN C18.//0.97:34:44//SWINEPOX VIRUS (STRAIN KASZA) (SPV).//P32217
 F-MAHMA1002434//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/3.1e-36:56:78//HOMO SAPIENS (HUMAN).//P39189
 F-MAHMA1002446
 F-MAHMA1002454//EARLY NODULIN 20 PRECURSOR (N-20).//0.77:57:45//ME D ICAGO TRUNCATULA (BARRER MEDIC).//P3329
 F-MAHMA1002461//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//1.3e-05:193:32//CANIS FAMILIARIS (DOG).//P50551
 F-MAHMA1002470//HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION.//1.0e-75:231:60//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38795
 F-MAHMA1002475//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L4 (SNF2-BETA) (BRG-1 PROTEIN) (MITOTIC GROWTH AND TRANSCRIPTION ACTIVATOR) (BRAHMA PROTEIN HOMOLOG 1).//0.013:99:30//HOMO SAPIENS (HUMAN).//P51532
 F-MAHMA1002480//NONSTRUCTURAL PROTEIN 5B.//1.0:23:43//HUMAN CORONA VIRUS (STRAIN 229E).//P19741
 F-MAHMA1002485//STANNIOCALCIN PRECURSOR.//2.1e-23:88:46//HOMO SAPIENS (HUMAN).//P52823
 F-MAHMA1002494//MOLT-INHIBITING HORMONE (MIH).//1.0:32:37//PROCAMP ARUS CLARKII (RED SWAMP CRAYFISH).//P55848
 F-MAHMA1002498//6.7 KD PROTEIN (ORF 5).//1.0:28:42//BARLEY YELLOW DWARF VIRUS (ISOLATE PAV) (BYDV).//P09517
 F-MAHMA1002524//HYPOTHETICAL 117.8 KD PROTEIN IN STE2-FRS2 INTERGENIC REGION.//5.0e-26:222:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43571
 F-MAHMA1002530//CYTOSOLIC PHOSPHOLIPASE A2 (EC 3.1.1.4) (CPLA2) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE) / LYSOPHOSPHOLIPASE (EC 3.1.1.5).//4.5e-12:88:44//HOMO SAPIENS (HUMAN).//P47712
 F-MAHMA1002545//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.3e-29:97:71//HOMO SAPIENS (HUMAN).//P39195
 F-MAHMA1002554//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//0.46:54:40//CRICETULUS GRISEUS (CHINESE HAMSTER).//P11414
 F-MAHMA1002556//METALLOTHIONEIN 20-1 ISOFORMS A AND B (MT-20-1A AND MT-20-1B).//0.99:21:47//MYTILUS EDULIS (BLUE MUSSEL).//P80251
 F-MAHMA1002566//TRANSCRIPTION FACTOR P65 (NUCLEAR FACTOR NF-KAPPA-B P65 SUBUNIT).//0.70:130:30//MUS MUSCULUS (MOUSE).//Q04207
 F-MAHMA1002571//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (FRAGMENT).//0.54:45:51//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P35084
 F-MAHMA1002573//PARATHYMOSIN.//1.5e-07:69:46//HOMO SAPIENS (HUMAN).//P20962
 F-MAHMA1002585//MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE B/VENTRICULAR ISOFORM (FRAGMENT).//0.38:36:36//MUS MUSCULUS (MOUSE).//P09542
 F-MAHMA1002590//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.99:22:77//HOMO SAPIENS (HUMAN).//P39195
 F-MAHMA1002597//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.1e-18:44:70//HOMO SAPIENS (HUMAN).//P39194
 F-MAHMA1002598//60S RIBOSOMAL PROTEIN L7.//1.8e-16:40:100//HOMO SAPIENS (HUMAN).//P18124
 F-MAHMA1002603
 F-MAHMA1002612//30S RIBOSOMAL PROTEIN S16 (FRAGMENT).//1.0:29:37//THERMUS AQUATICUS.//007348
 F-MAHMA1002617//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.00041:81:34//RATTUS NORVEGICUS (RAT).//P10164
 F-MAHMA1002618//ESCARCOT/SMALL PROTEIN HOMOLOG (FRAGMENT).//0.11:18:50//PSYCHODA CINEREA.//Q02027
 F-MAHMA1002619//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//1.8e-13:110:40//CAENORHABDITIS ELEGANS.//Q09931
 F-MAHMA1002622//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/8.4e-05:3:58//HOMO SAPIENS (HUMAN).//P39188
 F-MAHMA1002623//PEPTIDYL-GLYCINE ALPHA-AMIDATING MONOOXYGENASE PRECURSOR (EC 1.14.17.3) (PAM).//2.6e-07:37:78//HOMO SAPIENS (HUMAN).//P19021
 F-MAHMA1002625
 F-MAHMA1002629//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.4e-19:49:73//HOMO SAPIENS (HUMAN).//P39188
 F-MAHMA1002636//COLLAGEN ALPHA 2(VI) CHAIN (FRAGMENT).//1.7e-07:189:32//HOMO SAPIENS (HUMAN).//P12110
 F-MAHMA1002637//KINESIN LIGHT CHAIN (KLC).//7.7e-54:227:52//RATTUS NORVEGICUS (RAT).//P37285
 F-MAHMA1002646//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//0.034:199:25//MUS MUSCULUS (MOUSE).//P19246
 F-MAHMA1002650//TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC HOMOLOG 2).//1.7e-07:104:32//MUS MUSCULUS (MOUSE).//P97303
 F-MAHMA1002655//SMALL PROLINE-RICH PROTEIN 11 (SPR-11) (CLONE 174 N).//1.0:25:44//HOMO SAPIENS (HUMAN).//P22532
 F-MAHMA1002662
 F-MAHMA1002665//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.3e-07:54:57//HOMO SAPIENS (HUMAN).//P39194
 F-MAHMA1002671//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL--ACTIVATING ENZYME).//1.4e-10:144:31//ESCHERICHIA COLI.//P27550
 F-MAHMA1002673//BREVICAN CORE PROTEIN PRECURSOR.//0.76:64:39//BOS TAURUS (BOVINE).//Q28062
 F-MAHMA1002684//HYPOTHETICAL 11.8 KD PROTEIN IN GP55-NRDC INTERGENIC REGION.//0.094:77:27//BACTERIOPHAGE T4.//P07079
 F-MAHMA1002685//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.0017:17:7:34//RATTUS NORVEGICUS (RAT).//P02454
 F-MAHMA1002698
 F-MAHMA1002699//HYPOTHETICAL 45.1 KD PROTEIN IN RP55-ZMS1 INTERGENIC REGION.//1.2e-28:127:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160

【0648】

【表350】

F-MAMMA1002701!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.0:14:92
//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1002708!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//7.9e-27:
52:65//HOMO SAPIENS (HUMAN).//P39193
F-MAMMA1002711!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3.7e-24:5
4:75//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1002721
F-MAMMA1002727//SOX-13 PROTEIN (FRAGMENT).//0.70:36:38//MUS MUSCU
LUS (MOUSE).//Q04891
F-MAMMA1002728//HYPOTHETICAL 6.0 KD PROTEIN.//1.0:25:44//THERMOPRO
TEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19305
F-MAMMA1002744//HYPOTHETICAL 13.4 KD PROTEIN IN ACT5-YCK1 INTERGEN
IC REGION.//1.0:52:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//
P38834
F-MAMMA1002746//HYPOTHETICAL 5.6 KD PROTEIN (ORF A-45).//1.0:22:40
//SULFOLOBUS VIRUS-LIKE PARTICLE SSV1.//P20198
F-MAMMA1002748
F-MAMMA1002754!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//5.1e-21:5
6:64//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1002758//MALE SPECIFIC SPERM PROTEIN MST840D.//0.37:14:64//
DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645
F-MAMMA1002764!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//4.7e-32:
79:60//HOMO SAPIENS (HUMAN).//P39194
F-MAMMA1002765//PARATHYROSIN.//0.79:63:28//BOS TAURUS (BOVINE).//P
08814
F-MAMMA1002769//GAR2 PROTEIN.//0.00037:192:27//SCHIZOSACCHAROMYCES
POMBE (FISSION YEAST).//P41891
F-MAMMA1002775//HYPOTHETICAL 36.7 KD PROTEIN C2F7.14C IN CHROMOSOM
E 1.//5.4e-54:240:49//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//
Q09704
F-MAMMA1002780
F-MAMMA1002782//MARGATOXIN (MGTX).//1.0:31:38//CENTRUROIDES MARGAR
ITATUS (SCORPION).//P40755
F-MAMMA1002796//ICE NUCLEATION PROTEIN.//0.0018:100:41//PSEUDOMONA
S FLUORESCENS.//P09815
F-MAMMA1002807!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//9.3e-23:1
00:59//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1002820//NEUROTOXIN IV (LQ IV).//1.0:18:50//LEIURUS QUINQU
ESTRIATUS QUINQUESTRIATUS (EGYPTIAN SCORPION).//P01489
F-MAMMA1002830!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//4.7e-24:
55:74//HOMO SAPIENS (HUMAN).//P39195
F-MAMMA1002833!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//2.6e-31:
95:73//HOMO SAPIENS (HUMAN).//P39189
F-MAMMA1002835//HYPOTHETICAL 42.1 KD PROTEIN F13G3.3 IN CHROMOSOME
1.//1.0:54:37//CAENORHABDITIS ELEGANS.//Q19417
F-MAMMA1002838!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//2.5e-27:
99:70//HOMO SAPIENS (HUMAN).//P39193
F-MAMMA1002842!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//2.3e-13:
65:63//HOMO SAPIENS (HUMAN).//P39195
F-MAMMA1002843//METALLOTHIONEIN-11 (MT-11).//0.97:19:47//MUS MUSCU
LUS (MOUSE).//P02798
F-MAMMA1002844//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENI
C REGION.//4.9e-08:119:35//AUTOPHAGA CALIFORNICA NUCLEAR POLYHEDR
OSIS VIRUS (ACNOPV).//P41479
F-MAMMA1002858//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.98:
37:37//PAN TROGLODYTES (CHIMPANZEE).//Q35647
F-MAMMA1002868!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3.8e-10:5
1:62//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1002869//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS
PROTEIN).//1.8e-95:194:78//HOMO SAPIENS (HUMAN).//P48059
F-MAMMA1002871//G-PROTEIN COUPLED RECEPTOR HOMOLOG R33.//1.0:51:35
//RAT CYTOMEGALOVIRUS (STRAIN MAASTRICHT).//012000
F-MAMMA1002880
F-MAMMA1002881//GLIOMA PATHOGENESIS-RELATED PROTEIN (RTVP-1 PROTEI
N).//3.3e-22:180:35//HOMO SAPIENS (HUMAN).//P48060
F-MAMMA1002886//MYOSIN HEAVY CHAIN 1B (MYOSIN HEAVY CHAIN 1L).//0.
00011:148:39//ACANTHAMOEBA CASTELLANII (AMOEBA).//P19706
F-MAMMA1002887
F-MAMMA1002890//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.030:
142:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
F-MAMMA1002892
F-MAMMA1002895//HYPOTHETICAL PROTEIN UL61.//0.00099:143:35//HUMAN
CYTOMEGALOVIRUS (STRAIN AD169).//P16818
F-MAMMA1002908//T-CELL RECEPTOR BETA CHAIN PRECURSOR (ANA 11).//0.
12:44:43//ORYCTOLAGUS CUNICULUS (RABBIT).//P06333
F-MAMMA1002909!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.00011:2
8:75//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1002930//BOMBYXIN A-7 PRECURSOR (BBX-A7) (4K-PROTHORACICOTR
OPIC HORMONE) (4K-PTH).//0.98:45:46//BOMBYX MORI (SILK MOTH).//P2
6730
F-MAMMA1002937//ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZ
F-1).//6.5e-24:147:34//HOMO SAPIENS (HUMAN).//P28698
F-MAMMA1002938//CERULOPLASMIN PRECURSOR (EC 1.16.3.1) (FERROXIDAS
E).//4.7e-11:44:68//MUS MUSCULUS (MOUSE).//Q61147
F-MAMMA1002941//PROTEIN Q300.//0.0076:21:61//MUS MUSCULUS (MOUSE).
//Q02722
F-MAMMA1002947//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.
//1.9e-08:152:38//STREPTOMYCES FRADIAE.//P20186
F-MAMMA1002964
F-MAMMA1002970!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//0.0057:5
5:43//HOMO SAPIENS (HUMAN).//P39189
F-MAMMA1002972//BRAIN-SPECIFIC HOMEOBOX/POU DOMAIN PROTEIN 3A (BR
N-3A) (OCT-T1) (HOMEOBOX/POU DOMAIN PROTEIN RDC-1).//0.84:53:41//H
OMO SAPIENS (HUMAN).//Q01851
F-MAMMA1002973!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//4.6e-11:
54:68//HOMO SAPIENS (HUMAN).//P39192
F-MAMMA1002982
F-MAMMA1002987//HYPOTHETICAL 11.9 KD PROTEIN IN RPC8-MFA2 INTERGEN
IC REGION.//0.17:47:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//
P53906
F-MAMMA1003003!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//8.6e-09:
30:73//HOMO SAPIENS (HUMAN).//P39195
F-MAMMA1003004!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//0.0071:4
1:58//HOMO SAPIENS (HUMAN).//P39195
F-MAMMA1003007//SPERM PROTAMINE P1.//0.0076:51:37//TACHYGLOSSUS AC
ULEATUS ACULEATUS (AUSTRALIAN ECHIDNA).//P35311
F-MAMMA1003011//HISTONE MACRO-H2A.1.//1.8e-60:175:70//RATTUS NORVE
GICUS (RAT).//Q02874
F-MAMMA1003013//ACTIN BINDING PROTEIN.//0.097:83:31//SACCHAROMYCES
EXIGUUS (YEAST).//P38479
F-MAMMA1003015
F-MAMMA1003019//MYOTUBULARIN.//0.022:56:37//HOMO SAPIENS (HUMAN).//
Q13496
F-MAMMA1003026//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0014:208:
27//OROCYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPVNPV).//
010341
F-MAMMA1003031//PROBABLE E4 PROTEIN (E1'E4).//0.14:49:32//HUMAN PA
PILLONAVIRUS TYPE 6B.//P06459
F-MAMMA1003035//HYPOTHETICAL 24.4 KD PROTEIN IN LPD 3' REGION (ORF
4).//5.1e-12:112:34//ZYMONONAS NOBILIS.//Q66114
F-MAMMA1003039!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.4e-07:6
8:54//HOMO SAPIENS (HUMAN).//P39188
F-MAMMA1003040!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!//2.8e-3
9:50:57//HOMO SAPIENS (HUMAN).//P39190
F-MAMMA1003044
F-MAMMA1003047//SPERM HISTONE P2 PRECURSOR (PROTAMINE 2).//0.18:2
5:44//BOS TAURUS (BOVINE).//P19782
F-MAMMA1003049//PROBABLE E4 PROTEIN.//0.50:67:29//HUMAN PAPILOMAV
IRUS TYPE 6C.//P20969
F-MAMMA1003055//WEAK TOXIN CM-2.//0.99:23:30//HAJA HAJE HAJE (EGYP
TIAN COBRA).//P01415
F-MAMMA1003056//EXPORTED PROTEIN 7 (FRAGMENT).//1.0:52:32//STREPTO
COCCUS PNEUMONIAE.//P35597
F-MAMMA1003057//MD6 PROTEIN.//1.5e-85:168:95//MUS MUSCULUS (MOUSE
).//Q60584
F-MAMMA1003066//REQB PROTEIN.//1.0:62:27//PSEUDOMONAS AERUGINOSA.//
Q03381
F-MAMMA1003089!!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!!//5.1e-1
5:44:77//HOMO SAPIENS (HUMAN).//P39190
F-MAMMA1003099//ENDOTHELIAL ACTIN-BINDING PROTEIN (ABP-280) (NONMU
SCL FILAMIN) (FILAMIN 1).//4.8e-20:80:62//HOMO SAPIENS (HUMAN).//
P21333
F-MAMMA1003104//PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII.//0.98:
22:40//SYNECHOCOCCUS ELONGATUS NAEGELI.//P25900
F-MAMMA1003113//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS
).//0.67:35:45//GALLUS GALLUS (CHICKEN).//P02467
F-MAMMA1003127//MYOSIN I ALPHA (MMI-ALPHA).//5.2e-34:141:56//MUS M
USCULUS (MOUSE).//P46735
F-MAMMA1003135//HYPOTHETICAL 182.0 KD PROTEIN IN NMD5-HOM6 INTERGE
NIC REGION.//3.6e-05:91:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
T).//P47170
F-MAMMA1003140
F-MAMMA1003146//MALE SPECIFIC SPERM PROTEIN MST87F.//1.0:33:36//DR
OSOPHILA MELANOGASTER (FRUIT FLY).//P08175
F-MAMMA1003150//HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOM
E 11.//4.4e-10:254:30//CAENORHABDITIS ELEGANS.//Q09625
F-MAMMA1003166//BRAIN PROTEIN H5.//4.8e-42:182:48//HOMO SAPIENS (H
UMAN).//Q43236
F-MT2RM1000001//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGE
NIC REGION (ORF70).//0.15:38:34//ASTASIA LONGA (EUGLENOPHYCEAN ALG

【表351】

A. //P34779
 F-NT2RM1000018
 F-NT2RM1000032//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L). //0.51:17:41//CYPRINUS CARPIO (COMMON CARP). //P24948
 F-NT2RM1000035//3-HYDROXY-3-METHYLGLUTARYL-COENZYME A REDUCTASE (EC 1.1.1.34) (HMG-CoA REDUCTASE). //0.00011:114:27//BLATTELLA GERMANICA (GERMAN COCKROACH). //P54960
 F-NT2RM1000037//METALLOTHIONEIN-11 (MT-11). //0.025:19:47//SCYLLA SERRATA (MUD CRAB). //P02806
 F-NT2RM1000039//VITELLINE MEMBRANE VM34CA PROTEIN PRECURSOR. //0.00083:84:33//DROSOPHILA MELANOGASTER (FRUIT FLY). //Q06521
 F-NT2RM1000055//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR. //1.1e-07:34:55//PLASMODIUM LOPHURAE. //P04929
 F-NT2RM1000059//MYOCYTE-SPECIFIC ENHANCER FACTOR 2B (SERUM RESPONSE FACTOR-LIKE PROTEIN 2) (XMEF2) (RSRFR2). //0.18:83:36//HOMO SAPIENS (HUMAN). //Q02080
 F-NT2RM1000062//PROLINE-RICH PEPTIDE P-8. //0.54:34:44//HOMO SAPIENS (HUMAN). //P02814
 F-NT2RM1000080//HYPOTHETICAL 35.7 KD PROTEIN SLR1128. //2.1e-20:119:40//SYNECHOCYSTIS SP. (STRAIN PCC 6803). //P72655
 F-NT2RM1000086//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT). //0.20:56:35//HOMO SAPIENS (HUMAN). //P10162
 F-NT2RM1000092//COLLAGEN-LIKE PROTEIN. //0.0017:44:45//HERPESVIRUS SAIMIRI (SUBGROUP C / STRAIN 488). //P22576
 F-NT2RM1000116//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT). //5.7e-07:109:28//NEUROSPORA CRASSA. //P87072
 F-NT2RM1000119//TRANSCRIPTIONAL REGULATOR IE63 (VIM63) (ICP27). //0.0050:135:32//HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN HG52). //P28276
 F-NT2RM1000127//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN). //0.032:68:32//SORGHUM VULGARE (SORGHUM). //P24152
 F-NT2RM1000131//METALLOTHIONEIN-111 (MT-111) (GROWTH INHIBITORY FACTOR) (GIF). //0.82:33:39//BOS TAURUS (BOVINE). //P37359
 F-NT2RM1000132//NADH-UBIQUINONE OXIDOREDUCTASE 13 KD-A SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-13KD-A) (CI-13KD-A). //2.7e-59:124:91//HOMO SAPIENS (HUMAN). //075380
 F-NT2RM1000153//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5). //2.5e-08:148:29//HOMO SAPIENS (HUMAN). //P49902
 F-NT2RM1000186//CALCINEURIN B SUBUNIT (PROTEIN PHOSPHATASE 2B REGULATORY SUBUNIT) (CALCINEURIN REGULATORY SUBUNIT). //1.9e-07:109:27//NEUROSPORA CRASSA. //P87072
 F-NT2RM1000187//PUTATIVE PRF-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPACIOF6.02C. //1.0e-12:94:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //Q42643
 F-NT2RM1000199//CUTICLE COLLAGEN 12 PRECURSOR. //0.46:130:33//CAENORHABDITIS ELEGANS. //P20630
 F-NT2RM1000242//PUTATIVE ATP SYNTHASE J CHAIN, MITOCHONDRIAL (EC 3.6.1.34). //0.85:38:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //Q13931
 F-NT2RM1000244//HYPOTHETICAL 131.5 KD PROTEIN CO2F12.7 IN CHROMOSOME X. //0.0055:98:36//CAENORHABDITIS ELEGANS. //Q11102
 F-NT2RM1000252//TRICHOHYALIN. //2.9e-06:88:36//OVIS ARIES (SHEEP). //P22793
 F-NT2RM1000256//GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOMERIZING] (EC 2.6.1.16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE) (GFAT). //2.9e-54:153:67//MUS MUSCULUS (MOUSE). //P47856
 F-NT2RM1000257//MAGO WASHI PROTEIN. //5.9e-64:136:89//DROSOPHILA MELANOGASTER (FRUIT FLY). //P49028
 F-NT2RM1000260
 F-NT2RM1000271//GALACTOKINASE (EC 2.7.1.6). //0.99:41:39//BACILLUS SUBTILIS. //P39574
 F-NT2RM1000272//HYPOTHETICAL 55.5 KD PROTEIN ZK1128.2 IN CHROMOSOME 111. //8.8e-25:131:45//CAENORHABDITIS ELEGANS. //Q09357
 F-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V-ATPASE 28 KD ACCESSORY PROTEIN). //2.5e-63:121:94//BOS TAURUS (BOVINE). //P39942
 F-NT2RM1000300//TREACLE PROTEIN (TREACHER COLLINS SYNDROME PROTEIN). //0.51:145:26//HOMO SAPIENS (HUMAN). //Q13428
 F-NT2RM1000314
 F-NT2RM1000318//50S RIBOSOMAL PROTEIN L23. //0.83:28:35//AQUIFEX AEOLICUS. //Q66433
 F-NT2RM1000341
 F-NT2RM1000354//HYPOTHETICAL 5.8 KD PROTEIN IN PUMA 5' REGION (ORF5). //0.95:43:37//RHODOBACTER CAPSULATUS (RHODOPEUDOMONAS CAPSULATUS). //P26159
 F-NT2RM1000355//SPERM-SPECIFIC PROTEIN PHI-1. //0.0016:73:43//MYTILUS EDULIS (BLUE MUSSEL). //Q04621
 F-NT2RM1000365//HYPOTHETICAL PROTEIN KIAA0140. //3.5e-10:83:49//HOMO SAPIENS (HUMAN). //Q14153
 F-NT2RM1000377//DUAL SPECIFICITY PROTEIN PHOSPHATASE 9 (EC 3.1.3.4) (EC 3.1.3.16) (MITOGEN-ACTIVATED PROTEIN KINASE PHOSPHATASE 4) (MAP KINASE PHOSPHATASE 4) (MKP-4). //4.9e-18:113:38//HOMO SAPIENS (HUMAN). //Q99956
 F-NT2RM1000388//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION. //0.00023:67:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P53915
 F-NT2RM1000394//HISTONE H3.3 (H3.B) (H3.3Q). //4.7e-52:71:91//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), ORYCTOLAGUS CUNICULUS (RABBIT), GALLUS GALLUS (CHICKEN), SPISULA SOLIDISSIMA (ATLANTIC SURF-CLAM), DROSOPHILA MELANOGASTER (FRUIT FLY), AND DROSOPHILA HYDEI (FRUIT FLY). //P08351
 F-NT2RM1000399//ENDOTHELIN-2 PRECURSOR (ET-2) (FRAGMENT). //0.92:24:45//CANIS FAMILIARIS (DOG). //P12064
 F-NT2RM1000421//CUTICLE COLLAGEN 2C (FRAGMENT). //0.12:93:33//HAEMOCHUS CONTORTUS. //P16252
 F-NT2RM1000430//PISTIL-SPECIFIC EXTENSIN-LIKE PROTEIN PRECURSOR (PELP). //0.13:86:31//NICOTIANA TABACUM (COMMON TOBACCO). //Q03211
 F-NT2RM1000499//HYPOTHETICAL PROTEIN KIAA0941 (FRAGMENT). //2.9e-17:75:49//HOMO SAPIENS (HUMAN). //Q15057
 F-NT2RM1000539//HYPOTHETICAL 10.4 KD PROTEIN IN FTR1-SPT15 INTERGENIC REGION. //2.9e-16:82:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P40089
 F-NT2RM1000553//GLYCOPOLIPID TRANSFER PROTEIN (GLTP). //6.4e-06:103:33//SUS SCROFA (PIG). //P17403
 F-NT2RM1000555//UMR PROTEIN. //8.7e-77:105:95//RATTUS NORVEGICUS (RAT). //P18395
 F-NT2RM1000563//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS). //0.15:20:50//HOMO SAPIENS (HUMAN). //P30808
 F-NT2RM1000623//CLARA CELL PHOSPHOLIPID-BINDING PROTEIN PRECURSOR (CCPBP) (CLARA CELLS 10 KD SECRETORY PROTEIN) (CC10). //0.17:70:34//HOMO SAPIENS (HUMAN). //P11684
 F-NT2RM1000648//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-). //2.0e-22:13:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P43636
 F-NT2RM1000661//METALLOTHIONEIN-111 (MT-111) (GROWTH INHIBITORY FACTOR) (GIF) (GIFB). //0.0060:24:33//HOMO SAPIENS (HUMAN). //P25713
 F-NT2RM1000666//COLD SHOCK PROTEIN SCOF. //9.1e-07:67:41//STREPTOMYCES COELICOLOR. //P48859
 F-NT2RM1000669//CHLOROPLAST 50S RIBOSOMAL PROTEIN L31. //0.071:69:31//PORPHYRA PURPUREA. //P51290
 F-NT2RM1000672//SIGNAL RECOGNITION PARTICLE SEC65 SUBUNIT (FRAGMENT). //0.27:42:42//KLUYVEROMYCES LACTIS (YEAST). //Q13475
 F-NT2RM1000691//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2). //4.3e-42:241:42//HOMO SAPIENS (HUMAN). //P29375
 F-NT2RM1000699//N2,N2-DIMETHYLGLUCOSAMINE TRNA METHYLTRANSFERASE PRECURSOR (EC 2.1.1.32). //0.94:48:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P15565
 F-NT2RM1000702//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 1. //0.0013:139:25//DROSOPHILA MELANOGASTER (FRUIT FLY). //P26308
 F-NT2RM1000725//BASIC PROLINE-RICH PEPTIDE P-E (18-9). //1.0:15:60//HOMO SAPIENS (HUMAN). //P02811
 F-NT2RM1000741//STATHMIN (CLONE X020) (FRAGMENT). //1.0:53:32//XENOPUS LAEVIS (AFRICAN CLAWED FROG). //Q09005
 F-NT2RM1000742//HYPOTHETICAL 24.1 KD PROTEIN IN DHFR 3' REGION (ORF 2). //1.0:54:42//HERPESVIRUS SAIMIRI (STRAIN 484-77). //P25049
 F-NT2RM1000746//HYPOTHETICAL 16.8 KD PROTEIN C29E6.04 IN CHROMOSOME 1. //0.11:87:21//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //Q09858
 F-NT2RM1000770//DXS6673E PROTEIN. //2.0e-38:190:48//HOMO SAPIENS (HUMAN). //Q14202
 F-NT2RM1000772//VEGETABLE INCOMPATIBILITY PROTEIN MET-E-1. //4.3e-12:141:30//PODOSPORA ANSERINA. //Q00808
 F-NT2RM1000780//MALE SPECIFIC SPERM PROTEIN MST87F. //0.98:34:38//DROSOPHILA MELANOGASTER (FRUIT FLY). //P08175
 F-NT2RM1000781
 F-NT2RM1000800//24.1 KD PROTEIN IN VMA12-APN1 INTERGENIC REGION. //7.9e-11:135:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P28707
 F-NT2RM1000802//ALPHA-AMYLASE INHIBITOR PAIM 1 (PIG PANCREATIC ALPHA-AMYLASE INHIBITOR OF MICROBES 1). //0.43:62:35//STREPTOMYCES OLIVACEOVIRIDIS (STREPTOMYCES CORCHORUSI). //P09921
 F-NT2RM1000811
 F-NT2RM1000826//UMR PROTEIN. //1.1e-110:144:83//RATTUS NORVEGICUS (RAT). //P18395
 F-NT2RM1000829//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L). //1.0:38:34//DROSOPHILA SIMULANS (FRUIT FLY). //P50270
 F-NT2RM1000833//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT. //1.4e-62:145:84//CANIS FAMILIARIS (DOG). //P38377
 F-NT2RM1000850//TESTIS-SPECIFIC PROTEIN KINASE 1 (EC 2.7.1.-). //7.6e-10:145:84//CANIS FAMILIARIS (DOG). //P38377

【0650】

【0 6 5 1】

【表353】

F-NT2RM2000569/!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/9.0e-08:4
3:72//HOMO SAPIENS (HUMAN).//P39188
F-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCIN
E-TRNA LIGASE) (ILERS).//9.1e-54:225:45//SYNECHOCYSTIS SP. (STRAI
N PCC 6803).//P73505
F-NT2RM2000581//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B5
3).//0.079:111:34//HOMO SAPIENS (HUMAN).//Q15427
F-NT2RM2000588//HYPOTHETICAL PROTEIN KIAA0288 (HAK116).//2.3e-09:1
93:32//HOMO SAPIENS (HUMAN).//P56524
F-NT2RM2000594//BASIC PROLINE-RICH PEPTIDE P-E (1B-9).//0.18:33:42
//HOMO SAPIENS (HUMAN).//P02811
F-NT2RM2000599//DNA (CYTOSINE-5)-METHYLTRANSFERASE (EC 2.1.1.37)
(DNA METHYLTRANSFERASE) (DNA METHASE) (MCMT) (M.MUJI).//1.5e-09:68:
45//MUS MUSCULUS (MOUSE).//P13864
F-NT2RM2000609//GRANULIN 2.//0.83:42:35//CYPRINUS CARPIO (COMMON C
ARP).//P81014
F-NT2RM2000612//ZINC FINGER PROTEIN GCS1.//7.2e-05:155:29//SACCHAR
OMYCES CEREVISIAE (BAKER'S YEAST).//P35197
F-NT2RM2000623//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//1.8e-0
9:196:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
F-NT2RM2000624//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.070:113:
27//DROSOPHILA ERECTA (FRUIT FLY).//P13730
F-NT2RM2000635//SPERM PROTAMINE P1.//0.54:47:38//ANTECHINUS STUART
11.//P42129
F-NT2RM2000636//OUTER MEMBRANE PROTEIN H.8 PRECURSOR.//0.096:62:35
//NEISSERIA GONORRHOEA.//P11910
F-NT2RM2000639//HYPOTHETICAL PROTEIN MJ0243.//0.99:32:34//METHANOC
CCUS JANNASCHII.//Q57694
F-NT2RM2000649//NEURONAL CALCIUM SENSOR 1 (NCS-1).//0.00049:70:35/
RATTUS NORVEGICUS (RAT). AND GALLUS GALLUS (CHICKEN).//P36610
F-NT2RM2000669//50S RIBOSOMAL PROTEIN L34.//1.0:34:44//BACILLUS SU
BTILIS.//P05647
F-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2).//7.0e-116:243:87/
HOMO SAPIENS (HUMAN). AND BOS TAURUS (BOVINE).//P32391
F-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN)
(RSP-1).//3.8e-21:174:35//HOMO SAPIENS (HUMAN).//Q15404
F-NT2RM2000718//HYPOTHETICAL 52.9 KD SERINE-RICH PROTEIN C11G7.01
IN CHROMOSOME 1.//0.0022:174:29//SCHIZOSACCHAROMYCES POMBE (FISSIO
N YEAST).//Q13695
F-NT2RM2000735//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//1.6e-
102:246:74//HOMO SAPIENS (HUMAN).//P28160
F-NT2RM2000740//HYPOTHETICAL 131.1 KD HELICASE IN ALG7-ENP1 INTERG
ENIC REGION.//8.5e-51:212:49//SACCHAROMYCES CEREVISIAE (BAKER'S YE
AST).//P38144
F-NT2RM2000795/!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/9.0e-41:
125:53//HOMO SAPIENS (HUMAN).//P39189
F-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-CO
P).//1.1e-128:291:89//RATTUS NORVEGICUS (RAT).//P23514
F-NT2RM2000837//CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPEN
DENT KINASE INHIBITOR P57) (P57KIP2).//3.9e-05:113:36//HOMO SAPIEN
S (HUMAN).//P49918
F-NT2RM2000951//HYPOTHETICAL 60.3 KD PROTEIN R08D7.7 IN CHROMOSOME
111.//2.5e-49:273:39//CAENORHABDITIS ELEGANS.//P30646
F-NT2RM2000952//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAM
ENT PROTEIN) (NF-H) (FRAGMENT).//0.037:234:23//RATTUS NORVEGICUS
(RAT).//P16884
F-NT2RM2000984//HYPOTHETICAL 54.7 KD PROTEIN F37A4.1 IN CHROMOSOME
111.//6.3e-44:216:43//CAENORHABDITIS ELEGANS.//P41879
F-NT2RM2001004//SYNAPSINS 1A AND 1B.//0.15:178:32//RATTUS NORVEGIC
US (RAT).//P09951
F-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.4e-87:188:90//
MUS MUSCULUS (MOUSE).//Q60809
F-NT2RM2001065//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//
0.53:122:31//TRYPAOSOMA BRUCEI BRUCEI.//P24499
F-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOM
E 111.//3.4e-13:171:30//CAENORHABDITIS ELEGANS.//P46577
F-NT2RM2001105//SPORE COAT PROTEIN SP96.//7.8e-06:141:34//DICTYOST
ELIUM DISCOIDEUM (SLIME MOLD).//P14328
F-NT2RM2001131//PROBABLE EUKARYOTIC INITIATION FACTOR C17C9.03.//
2.3e-18:249:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10475
F-NT2RM2001141//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOM
E 111.//0.050:134:26//CAENORHABDITIS ELEGANS.//P34681
F-NT2RM2001152
F-NT2RM2001177//COLLAGEN ALPHA 1(XIV) CHAIN PRECURSOR (UNDULIN).//
0.86:42:40//GALLUS GALLUS (CHICKEN).//P32018
F-NT2RM2001194//SMOOTHELIN.//4.7e-05:77:32//HOMO SAPIENS (HUMAN)./
//P53814
F-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//1.7e-18:21
8:35//MUS MUSCULUS (MOUSE).//P05143
F-NT2RM2001201//CYSTEINE STRING PROTEIN (CCCS1).//0.041:22:59//TOR

PEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P56101
F-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10)
(P-CIPI10).//1.3e-13:183:32//RATTUS NORVEGICUS (RAT).//P97924
F-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2)
(GLS) (L-GLUTAMINE AMIDOHYDROLASE).//6.5e-121:218:98//RATTUS NORV
EGICUS (RAT).//P13264
F-NT2RM2001243//HYPOTHETICAL 200.0 KD PROTEIN IN GZF3-IME2 INTERGE
NIC REGION.//0.00019:177:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
T).//P42945
F-NT2RM2001247//LEGUMIN B (FRAGMENT).//0.22:54:35//PISUM SATIVUM
(GARDEN PEA).//P14594
F-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK POINT REGULATOR).//1.
8e-109:207:98//MUS MUSCULUS (MOUSE).//P53995
F-NT2RM2001291//SMALL PROLINE RICH PROTEIN 11 (SPR-11) (CLONE 930
).//0.016:22:40//HOMO SAPIENS (HUMAN).//P22531
F-NT2RM2001306//REF(2)P PROTEIN.//0.61:51:33//DROSOPHILA MELANOGAS
TER (FRUIT FLY).//P14199
F-NT2RM2001312/!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/7.2e-11:
33:72//HOMO SAPIENS (HUMAN).//P39195
F-NT2RM2001319
F-NT2RM2001324//ZYXIN.//5.1e-22:91:38//GALLUS GALLUS (CHICKEN).//Q
04584
F-NT2RM2001345//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//7.4
e-10:159:27//PODOSPORA ANSERINA.//Q00808
F-NT2RM2001360//ACCESSORY GLAND PEPTIDE PRECURSOR (PARAGONIAL PEPT
IDE B).//1.0:27:48//DROSOPHILA MELANOGASTER (FRUIT FLY).//P05623
F-NT2RM2001370//NAPE PROTEIN.//0.98:44:31//PARACOCCLUS DENITRIFICAN
S (SUBSP. THIOSPHAERA PANTOTROPHIA).//Q56348
F-NT2RM2001393//VITELLOGENIN PRECURSOR (VTG) [CONTAINS: LIPOVITELL
IN LV-1N: LIPOVITELLIN LV-1C: LIPOVITELLIN LV-2].//0.0024:163:31//
ICHTHYOMYZON UNICUSPUS (SILVER LAMPREY).//Q91062
F-NT2RM2001420
F-NT2RM2001424//HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRP U
).//2.4e-41:140:59//HOMO SAPIENS (HUMAN).//Q00839
F-NT2RM2001499//HIGH-AFFINITY CATIONIC AMINO ACID TRANSPORTER-1 (C
AT-1) (CAT1) (SYSTEM Y+ BASIC AMINO ACID TRANSPORTER) (ECOTROPIC R
ETROVIRAL LEUKEMIA RECEPTOR HOMOLOG) (ERR) (ECOTROPIC RETROVIRUS R
ECEPTOR HOMOLOG).//3.7e-71:201:68//HOMO SAPIENS (HUMAN).//P30825
F-NT2RM2001504//CUTICLE COLLAGEN 2.//0.028:41:39//CAENORHABDITIS E
LEGANS.//P17656
F-NT2RM2001524//HYPOTHETICAL 61.3 KD PROTEIN F25B5.5 IN CHROMOSOME
111.//6.7e-47:190:42//CAENORHABDITIS ELEGANS.//Q09316
F-NT2RM2001544//TELOMERE-BINDING PROTEIN 51 KD SUBUNIT.//0.0027:13
6:33//EUPLOTES CRASSUS.//Q06184
F-NT2RM2001547//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGEN
IC REGION.//8.5e-18:91:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
T).//P40564
F-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN
(SS-A)) (RO(SS-A)).//3.9e-35:212:41//HOMO SAPIENS (HUMAN).//P19474
F-NT2RM2001582//RESA PROTEIN.//0.0033:72:27//BACILLUS SUBTILIS.//P
35160
F-NT2RM2001588//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//
1.0e-06:115:32//ZEA MAYS (MAIZE).//P14918
F-NT2RM2001592//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KER
ATIN).//0.033:156:23//HOMO SAPIENS (HUMAN).//P26371
F-NT2RM2001605//RETINOBLASTOMA BINDING PROTEIN 2 (RBBP-2).//1.1e-1
16:249:82//HOMO SAPIENS (HUMAN).//P29375
F-NT2RM2001613//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.
2e-97:192:100//RATTUS NORVEGICUS (RAT).//P38378
F-NT2RM2001632//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.0006
8:145:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
F-NT2RM2001635//NUCLEAR ENVELOPE PORE MEMBRANE PROTEIN POM 121 (PO
RE MEMBRANE PROTEIN OF 121 KD) (P145).//1.1e-39:235:47//RATTUS NOR
VEGICUS (RAT).//P52591
F-NT2RM2001637//HYPOTHETICAL BHLF1 PROTEIN.//0.075:197:29//EPSTEIN
BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
F-NT2RM2001641//NADH-CYTOCHROME B5 REDUCTASE (EC 1.6.2.2) (B5R).//
0.013:29:68//HOMO SAPIENS (HUMAN).//P00387
F-NT2RM2001648//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//3.
2e-65:132:100//CANIS FAMILIARIS (DOG).//P38377
F-NT2RM2001652//PROTEIN TRANSPORT PROTEIN SEC7.//1.6e-32:261:32//S
ACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P11075
F-NT2RM2001659//CARBOXYPEPTIDASE A INHIBITOR.//0.83:30:46//ASCARIS
SULUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).//P19399
F-NT2RM2001664//IKI3 PROTEIN.//1.3e-31:265:34//SACCHAROMYCES CEREV
ISIAE (BAKER'S YEAST).//Q06706
F-NT2RM2001668//TONB PROTEIN.//0.32:39:41//XANTHOMONAS CAMPESTRIS
(PV. CAMPESTRIS).//Q04261
F-NT2RM2001670//ZINC FINGER PROTEIN 174.//3.6e-21:172:39//HOMO SAPI
ENS (HUMAN).//Q15697

【0652】

【表354】

F-NT2RM2001671//HYPOTHETICAL 118.6 KD PROTEIN C29E6.03C IN CHROMOSOME 1.//1.6e-10:229:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09857
 F-NT2RM2001675//DIHYDRODIPICOLINATE SYNTHASE (EC 4.2.1.52) (DHDS).//1.0:184:21//METHANOCOCCUS JANNASCHII.//Q57695
 F-NT2RM2001681//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1).//0.0039:199:22//DROSOPHILA MELANOGASTER (FRUIT FLY).//P54399
 F-NT2RM2001688//HYPOTHETICAL 28.1 KD PROTEIN IN SIPU-PBPC INTERGENIC REGION.//2.6e-21:162:33//BACILLUS SUBTILIS.//P42966
 F-NT2RM2001695//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/4.9e-41:60:81//HOMO SAPIENS (HUMAN).//P39194
 F-NT2RM2001696//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//9.8e-16:126:38//AUTOPHAGA CALIFORNICA NUCLEAR POLYHEDRUS VIRUS (ACMPV).//P41479
 F-NT2RM2001698//PENAEIDIN-3B PRECURSOR (P3-B).//0.36:52:34//PENAEUS VANNAMEI (PENAEID SHRIMP) (EUROPEAN WHITE SHRIMP).//P81059
 F-NT2RM2001699//TRANSCRIPTION INITIATION FACTOR TFIID 30 KD SUBUNIT (TAF11-30) (TAF1130).//0.0012:79:40//HOMO SAPIENS (HUMAN).//Q12962
 F-NT2RM2001700//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC (EC 1.3.99.-) (VLCAD) (FRAGMENT).//1.0e-30:140:53//MUS MUSCULUS (MOUSE).//P50544
 F-NT2RM2001705//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.5e-33:95:75//HOMO SAPIENS (HUMAN).//P39195
 F-NT2RM2001716//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DALS INTERGENIC REGION PRECURSOR.//0.010:116:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47179
 F-NT2RM2001718//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB.//0.0002:9:77:37//BACILLUS SUBTILIS.//P39217
 F-NT2RM2001723//POSTERIOR PITUITARY PEPTIDE.//0.94:26:53//BOS TAURUS (BOVINE).//P01154
 F-NT2RM2001727//ET PROTEIN.//0.91:46:34//HUMAN PAPILLOMAVIRUS TYPE 23.//P50781
 F-NT2RM2001730//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE K02C4.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//4.9e-07:139:29//CAENORHABDITIS ELEGANS.//Q09931
 F-NT2RM2001743//PROENKEPHALIN A PRECURSOR.//0.75:65:35//CAVIA PORCELLUS (GUINEA PIG).//P47969
 F-NT2RM2001753//HYPOTHETICAL PROTEIN KIAA0210.//1.5e-14:119:36//HOMO SAPIENS (HUMAN).//Q92609
 F-NT2RM2001760//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//8.3e-58:119:99//CANIS FAMILIARIS (DOG).//P38377
 F-NT2RM2001768//HYPOTHETICAL PROTEIN UL25.//0.45:77:32//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16761
 F-NT2RM2001771//ZINC FINGER PROTEIN 135.//4.6e-80:224:60//HOMO SAPIENS (HUMAN).//P52742
 F-NT2RM2001782//MANNOSE-1-PHOSPHATE QUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-PHOSPHATE QUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//7.0e-06:61:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41940
 F-NT2RM2001784//HYPOTHETICAL PROTEIN UL61.//0.00070:145:33//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818
 F-NT2RM2001785//LIMOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESATURASE).//1.5e-08:127:32//SYNCHOCYSTIS SP. (STRAIN PCC 6803).//Q08871
 F-NT2RM2001797//ZINC FINGER PROTEIN 135.//1.6e-73:267:49//HOMO SAPIENS (HUMAN).//P52742
 F-NT2RM2001800//HYPOTHETICAL HELICASE MG018/MG017/MG016 HOMOLOG.//3.9e-12:171:33//MYCOPLASMA PNEUMONIAE.//P75093
 F-NT2RM2001803//IK13 PROTEIN.//1.6e-38:283:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06706
 F-NT2RM2001805//COLD SHOCK-LIKE PROTEIN CSPP.//0.51:46:32//SALMONELLA TYPHIMURUM.//Q03793
 F-NT2RM2001813//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C14B1.4 IN CHROMOSOME III.//5.0e-05:82:32//CAENORHABDITIS ELEGANS.//Q17963
 F-NT2RM2001823//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 2 (CHD-2).//3.6e-49:233:45//HOMO SAPIENS (HUMAN).//Q14647
 F-NT2RM2001839//RETICULOCALBIN 1 PRECURSOR.//5.2e-65:222:56//HOMO SAPIENS (HUMAN).//Q15293
 F-NT2RM2001840//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.6e-33:102:68//HOMO SAPIENS (HUMAN).//P39194
 F-NT2RM2001855//BASPI PROTEIN.//0.054:120:30//HOMO SAPIENS (HUMAN).//P80723
 F-NT2RM2001867//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION.//4.1e-19:88:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867
 F-NT2RM2001879//HYPOTHETICAL 47.3 KD PROTEIN C22G7.07C IN CHROMOSOME 1.//5.9e-15:76:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09800
 F-NT2RM2001886//HYPOTHETICAL 126.9 KD PROTEIN C22G7.04 IN CHROMOSOME 1.//1.4e-41:249:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09798
 F-NT2RM2001896//HYPOTHETICAL 83.2 KD PROTEIN IN KAR4-PBM1 INTERGENIC REGION.//2.1e-59:197:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25582
 F-NT2RM2001903//HYPOTHETICAL PROTEIN MJ0263.//0.070:132:31//METHANOCOCCUS JANNASCHII.//Q06917
 F-NT2RM2001930//THROMBOSPONDIN 2 PRECURSOR.//7.1e-05:53:47//MUS MUSCULUS (MOUSE).//Q03350
 F-NT2RM2001935//PUTATIVE CUTICLE COLLAGEN F55C10.3.//0.00046:116:35//CAENORHABDITIS ELEGANS.//Q21184
 F-NT2RM2001936//32.3 KD PROTEIN IN CWP1-MBRI INTERGENIC REGION.//4.5e-27:216:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P28320
 F-NT2RM2001950//HIRUDIN HVI (BUFRUDIN).//0.59:43:34//HIRUDINARIA MANILLENSIS (BUFFALO LEECH).//P81492
 F-NT2RM2001982//GUANINE NUCLEOTIDE-BINDING PROTEIN G(11)/G(S)/G(O) GAMMA-8 SUBUNIT (G GAMMA-C).//0.72:35:42//BOS TAURUS (BOVINE).//P50154
 F-NT2RM2001983//PROLINE-RICH PEPTIDE P-B.//0.00035:23:52//HOMO SAPIENS (HUMAN).//P02814
 F-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77).//8.6e-24:197:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P37838
 F-NT2RM2001997
 F-NT2RM2001998//IMMEDIATE-EARLY PROTEIN IE180.//0.076:92:27//PSEUDORABIES VIRUS (STRAIN INDIANA-FURKHAUSER / BECKER) (PRV).//P11675
 F-NT2RM2002004//SLF1 PROTEIN.//3.5e-06:235:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12034
 F-NT2RM2002014//HYPOTHETICAL PROTEIN H10568.//2.1e-17:235:29//HAEMOPHILUS INFLUENZAE.//P71353
 F-NT2RM2002030//GLUCOSAMINE--FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE [ISOMERIZING] (EC 2.6.1.16) (HEXOSEPHOSPHATE AMINOTRANSFERASE) (D-FRUCTOSE-6-PHOSPHATE AMINOTRANSFERASE) (GFAT).//9.5e-105:271:76//MUS MUSCULUS (MOUSE).//P47856
 F-NT2RM2002049//SMALL PROLINE-RICH PROTEIN 2-1.//0.099:41:41//HOMO SAPIENS (HUMAN).//P35326
 F-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.//0.012:217:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q07878
 F-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//1.1e-09:65:53//MUS MUSCULUS (MOUSE).//Q61990
 F-NT2RM2002091//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.072:74:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214
 F-NT2RM2002100//ATP-DEPENDENT RNA HELICASE ROK1.//4.5e-50:289:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P45818
 F-NT2RM2002109//NT-3 GROWTH FACTOR RECEPTOR PRECURSOR (EC 2.7.1.112) (TRK TYROSINE KINASE) (GP145-TRK) (TRK-C).//1.4e-14:203:32//RATTUS NORVEGICUS (RAT).//Q03351
 F-NT2RM2002128//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//0.0025:139:31//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437
 F-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.//9.2e-20:42:73//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//P47805
 F-NT2RM2002145//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT 12 PRECURSOR.//0.0085:200:26//TRITICUM AESTIVUM (WHEAT).//P08488
 F-NT2RM2002178//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//5.8e-05:56:39//BOS TAURUS (BOVINE).//P25508
 F-NT2RM2002580//CCAAT-BINDING TRANSCRIPTION FACTOR SUBUNIT A (CBF-A) (NF-Y PROTEIN CHAIN B) (NF-YB) (CAAT-BOX DNA BINDING PROTEIN SUBUNIT B).//2.9e-14:96:37//PETROMYZON MARINUS (SEA LAMPREY).//P25210
 F-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//8.6e-95:271:67//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25167
 F-NT2RM4000027//INTERFERON-ACTIVATABLE PROTEIN 202 (IFI-202).//0.9:72:31//MUS MUSCULUS (MOUSE).//P15091
 F-NT2RM4000030//LASI PROTEIN.//1.4e-14:184:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36146
 F-NT2RM4000046//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//0.99:120:28//RATTUS NORVEGICUS (RAT).//P13941
 F-NT2RM4000061
 F-NT2RM4000085//ATP-DEPENDENT RNA HELICASE A (NUCLEAR DNA HELICASE II) (NDH II) (DEAD BOX PROTEIN 9) (MDEL-5).//8.5e-40:263:38//MUS MUSCULUS (MOUSE).//Q70133
 F-NT2RM4000086//HYPOTHETICAL PROTEIN H11497.//1.0:27:37//HAEMOPHILUS INFLUENZAE.//P44221
 F-NT2RM4000104//ZINC FINGER PROTEIN 134.//1.0e-26:64:56//HOMO SAPIENS (HUMAN).//P52741
 F-NT2RM4000139//PREPROTEIN TRANSLOCASE SECE SUBUNIT.//0.99:38:42//

【0653】

【表355】

THERMOTOGA MARITIMA. //P35874
 F-NT2RM4000155//THREONYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.3) (THREONINE--TRNA LIGASE) (THRS). //6.3e-34:181:40//HOMO SAPIENS (HUMAN). //P26639
 F-NT2RM4000156//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN). //4.6e-12:142:33//NICOTIANA TABACUM (COMMON TOBACCO). //P13983
 F-NT2RM4000167//KINESIN-LIKE PROTEIN KIF4. //3.4e-123:269:91//MUS MUSCULUS (MOUSE). //P33174
 F-NT2RM4000169//M PROTEIN, SEROTYPE 2.2 PRECURSOR. //9.7e-10:229:26//STREPTOCOCCUS PYOGENES. //P50469
 F-NT2RM4000191//P68-LIKE PROTEIN. //2.1e-11:104:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P24783
 F-NT2RM4000197//CUTICLE PROTEIN CP463 (CPCP463). //0.84:29:37//CANCER PAGURUS (ROCK CRAB). //P81587
 F-NT2RM4000199//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT). //1.8e-06:187:34//HOMO SAPIENS (HUMAN). //P10162
 F-NT2RM4000200//HYPOTHETICAL 9.4 KD PROTEIN IN FLAL 3' REGION (ORF 3). //0.52:42:40//BACILLUS LICHENIFORMIS. //P22754
 F-NT2RM4000202//COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN). //0.0044:168:32//ORYZOLAGUS CUNICULUS (RABBIT). //P14282
 F-NT2RM4000210//EXTENSIN PRECURSOR. //0.27:129:27//DAUCUS CAROTA (CARROT). //P06599
 F-NT2RM4000215//MAX16 PROTEIN. //2.0e-65:234:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P10962
 F-NT2RM4000229//GAR2 PROTEIN. //0.13:217:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //P41891
 F-NT2RM4000233//TRANSMEMBRANE PROTEIN SEX PRECURSOR. //0.047:108:30//HOMO SAPIENS (HUMAN). //P51805
 F-NT2RM4000244//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L). //0.67:59:27//BALAENOPTERA PHYSAULUS (FINBACK WHALE) (COMMON RORQUAL). //P24947
 F-NT2RM4000251//PROLINE-RICH PROTEIN MP-3 (FRAGMENT). //0.0059:108:35//MUS MUSCULUS (MOUSE). //P05143
 F-NT2RM4000265//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//8.1e-38:70:70//HOMO SAPIENS (HUMAN). //P39188
 F-NT2RM4000290//TRANSDUCIN-LIKE ENHANCER PROTEIN 3 (ESG3). //1.6e-15:209:94//HOMO SAPIENS (HUMAN). //Q04726
 F-NT2RM4000324//PRESPORE PROTEIN DP87 PRECURSOR. //0.14:136:30//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD). //Q04503
 F-NT2RM4000327//HYPOTHETICAL 8.9 KD PROTEIN IN 1E0-1E1 INTERGENIC REGION. //0.91:73:28//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYEDROSIS VIRUS (ACNPV). //P41703
 F-NT2RM4000344//YME1 PROTEIN HOMOLOG (EC 3.4.24.-). //9.4e-78:241:55//CAENORHABDITIS ELEGANS. //P54813
 F-NT2RM4000349//CYSTEINE STRING PROTEIN (CCCS). //0.055:22:59//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY). //P56101
 F-NT2RM4000354//LETHAL(2) DENTICLELESS PROTEIN (DTL83 PROTEIN). //4.6e-26:208:35//DROSOPHILA MELANOGASTER (FRUIT FLY). //Q24371
 F-NT2RM4000356//COAT PROTEIN. //0.11:105:36//SATELLITE TOBACCO MOSAIC VIRUS (TMV). //P17574
 F-NT2RM4000366//IMMEDIATE-EARLY PROTEIN. //1.2e-05:215:24//HERPESVIRUS SAIMIRI (STRAIN 11). //Q01042
 F-NT2RM4000368//HYPOTHETICAL 7.3 KD PROTEIN IN RPBA-GP46 INTERGENIC REGION. //0.54:46:36//BACTERIOPHAGE RB69. //Q64300
 F-NT2RM4000386//RHSC PROTEIN PRECURSOR. //0.0096:162:29//ESCHERICHIA COLI. //P16918
 F-NT2RM4000395//HYPOTHETICAL 52.9 KD PROTEIN IN SAPI55-YMR31 INTERGENIC REGION. //4.5e-66:256:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P43616
 F-NT2RM4000414//HYPOTHETICAL 6.0 KD PROTEIN IN TH112 5' REGION. //0.13:33:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P53820
 F-NT2RM4000421//MRNA TRANSPORT REGULATOR NTR10. //5.0e-13:171:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //Q99189
 F-NT2RM4000425//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//2.1e-25:46:80//HOMO SAPIENS (HUMAN). //P39193
 F-NT2RM4000433//CUTICLE COLLAGEN 3A3. //2.5e-06:77:38//HAEMONCHUS CONTORTUS. //P16253
 F-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME 1. //4.3e-09:215:22//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //Q10297
 F-NT2RM4000471//TRNA SPLICING PROTEIN SPL1. //6.7e-73:163:65//CANDIDA ALBICANS (YEAST). //P87185
 F-NT2RM4000486//COLLAGEN ALPHA 2(VI) CHAIN PRECURSOR. //0.0012:121:34//GALLUS GALLUS (CHICKEN). //P15988
 F-NT2RM4000496//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RNA POLYMERASE II SUBUNIT 1). //5.9e-09:175:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //P36594
 F-NT2RM4000511//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR. //0.020:122:31//DROSOPHILA SIMULANS (FRUIT FLY). //P13729
 F-NT2RM4000514//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6). //0.46:68:32//ARTEMIA SANFRANCISCANA (BRINE SHRIMP) (ARTEMIA FRANCIS CANA). //Q37708
 F-NT2RM4000515//GAR2 PROTEIN. //3.2e-05:198:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //P41891
 F-NT2RM4000520//HYPOTHETICAL 7.5 KD PROTEIN (ORF 63). //0.011:55:38//SPINACIA OLERACEA (SPINACH). //P08974
 F-NT2RM4000531//ZINC FINGER PROTEIN 169 (FRAGMENT). //3.6e-44:244:42//HOMO SAPIENS (HUMAN). //Q14929
 F-NT2RM4000532//PUTATIVE MEMBRANE PROTEIN 53. //1.0:47:34//HERPESVIRUS SAIMIRI (STRAIN 11). //Q01049
 F-NT2RM4000534//HYPOTHETICAL 5.9 KD PROTEIN IN URBA-PUTA INTERGENIC REGION. //0.75:26:46//ESCHERICHIA COLI. //P56614
 F-NT2RM4000585//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P16: CORE PROTEIN P26]. //0.019:86:34//HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE SBLISY) (HIV-2). //P12450
 F-NT2RM4000590//RING CANAL PROTEIN (KELCH PROTEIN). //5.0e-23:224:29//DROSOPHILA MELANOGASTER (FRUIT FLY). //Q04652
 F-NT2RM4000595//HYPOTHETICAL 54.9 KD PROTEIN CO2F5.7 IN CHROMOSOME 111. //3.8e-62:226:50//CAENORHABDITIS ELEGANS. //P34284
 F-NT2RM4000603//SRC SUBSTRATE CORTACTIN (AMPLAXIN) (EMSI ONCOGENE). //0.077:132:22//HOMO SAPIENS (HUMAN). //Q14247
 F-NT2RM4000611//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PROTEIN C1481.4 IN CHROMOSOME 111. //1.9e-06:82:32//CAENORHABDITIS ELEGANS. //Q17963
 F-NT2RM4000616//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL--ACTIVATING ENZYME). //5.3e-79:213:62//ESCHERICHIA COLI. //P27550
 F-NT2RM4000674//HYPOTHETICAL SYMPORTER SLL1374. //1.3e-11:147:32//SYNECHOCYSTIS SP. (STRAIN PCC 6803). //P74168
 F-NT2RM4000689
 F-NT2RM4000698//CHORION CLASS HIGH-CYSTEINE HCA PROTEIN 12 PRECURSOR (HC-A.12). //0.26:45:33//BOMBYX MORI (SILK MOTH). //P05687
 F-NT2RM4000700//THIOPHENE AND FURAN OXIDATION PROTEIN THOF. //0.95:165:25//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE). //P53364
 F-NT2RM4000712//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10 E11.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME). //2.2e-82:152:63//CAENORHABDITIS ELEGANS. //P34547
 F-NT2RM4000717//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR. //0.80:54:40//DROSOPHILA SIMULANS (FRUIT FLY). //P13729
 F-NT2RM4000733//OCTAPEPTIDE-REPEAT PROTEIN T2. //1.5e-08:139:28//MUS MUSCULUS (MOUSE). //Q06666
 F-NT2RM4000734//GASTRULA ZINC FINGER PROTEIN XLCGF26.1 (FRAGMENT). //7.2e-20:205:28//XENOPUS LAEVIS (AFRICAN CLAWED FROG). //P18715
 F-NT2RM4000741//SPERM PROTAMINE P1. //0.89:52:38//ISODON MACROURUS (SHORT-NOSED BANDICOOT). //P42136
 F-NT2RM4000751//ZINC FINGER PROTEIN 26 (ZFP-26) (MKR3 PROTEIN) (FRAGMENT). //5.2e-77:246:52//MUS MUSCULUS (MOUSE). //P10076
 F-NT2RM4000764//KERATIN, GLYCINE/TYROSINE-RICH OF HAIR. //0.062:33:42//OVIS ARIES (SHEEP). //Q02958
 F-NT2RM4000778
 F-NT2RM4000779//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185). //0.014:53:45//VOLVOX CARTERI. //P21997
 F-NT2RM4000787//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1). //0.00011:73:39//MUS MUSCULUS (MOUSE). //P98063
 F-NT2RM4000790//SPORE COAT PROTEIN SP96. //0.00083:157:29//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD). //P14328
 F-NT2RM4000795//CHOLINESTERASE PRECURSOR (EC 3.1.1.8) (ACYLCHOLINE ACYLHYDROLASE) (CHOLINE ESTERASE II) (BUTYRYLCHOLINE ESTERASE) (PSEUDACHOLINESTERASE). //7.4e-41:271:36//HOMO SAPIENS (HUMAN). //P06276
 F-NT2RM4000796//5-METHYLCYTOSINE-SPECIFIC RESTRICTION ENZYME B (EC 3.1.21.-). //0.28:82:30//ESCHERICHIA COLI. //P15005
 F-NT2RM4000798//PROTEIN TRANSPORT PROTEIN SEC7. //4.7e-38:165:48//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P11075
 F-NT2RM4000813//METALLOTHIONEIN-1B. //0.0025:25:44//OVIS ARIES (SHEEP). //P09577
 F-NT2RM4000820
 F-NT2RM4000833//HYPOTHETICAL PROTEIN MJ1136. //6.5e-42:208:41//METHANOCOCCUS JANNASCHII. //Q58536
 F-NT2RM4000848//BRAIN-SPECIFIC HOMEOBOX/POU DOMAIN PROTEIN 3A (BRN-3A) (BRN-3.0). //0.0060:159:33//MUS MUSCULUS (MOUSE). //P17208
 F-NT2RM4000852//SMALL PROLINE-RICH PROTEIN 2B (SPR-2B). //0.0076:1:3:69//HOMO SAPIENS (HUMAN). //P35325
 F-NT2RM4000855//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//0.0060:68:44//HOMO SAPIENS (HUMAN). //P39194
 F-NT2RM4000887//RTS1 PROTEIN (SCS1 PROTEIN). //0.23:153:24//SACCHAR

【0654】

【表356】

OMYCES CEREVISIAE (BAKER'S YEAST). //P38903
 F-NT2RM4000895//HYPOTHETICAL 53.5 KD PROTEIN IN PHO2-POL3 INTERGENIC REGION. //3.3e-09:80:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P43123
 F-NT2RM4000950//HYPOTHETICAL PROTEIN MJ0572. //0.090:68:29//METHANO COCCUS JANNASCHII. //Q57992
 F-NT2RM4000971//KINESIN LIGHT CHAIN (KLC). //0.79:201:24//LOLIGO PE ALEII (LONGFIN SQUID). //P45825
 F-NT2RM4000979//MYOSIN REGULATORY LIGHT CHAIN 2, NONSARCOMERIC (MYOSIN ILC). //1.2e-07:25:96//HOMO SAPIENS (HUMAN). //P19105
 F-NT2RM4000996//ZINC FINGER PROTEIN 37 (ZFP-37) (MALE GERM CELL SPECIFIC ZINC FINGER PROTEIN). //1.4e-56:253:46//MUS MUSCULUS (MOUSE). //P17141
 F-NT2RM4001002
 F-NT2RM4001016//GAG POLYPEPTIDE [CONTAINS: CORE PROTEIN P15: INNER COAT PROTEIN P12: CORE SHELL PROTEIN P30]. //0.25:101:31//FBR MURINE OSTEOSARCOMA VIRUS. //P29175
 F-NT2RM4001032//CUTICLE COLLAGEN 2. //2.6e-07:130:39//CAENORHABDITIS ELEGANS. //P17656
 F-NT2RM4001047//MO25 PROTEIN. //5.6e-107:252:80//MUS MUSCULUS (MOUSE). //Q06138
 F-NT2RM4001054//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT. //9.0e-109:209:94//CANIS FAMILIARIS (DOG). //P38377
 F-NT2RM4001084//HYPOTHETICAL TRANSCRIPTIONAL REGULATOR IN UXR-1AD A INTERGENIC REGION. //0.57:95:30//ESCHERICHIA COLI. //P39376
 F-NT2RM4001092//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME III. //2.5e-47:231:47//CAENORHABDITIS ELEGANS. //Q09531
 F-NT2RM4001116//HYPOTHETICAL 216.3 KD PROTEIN R06F6.8 IN CHROMOSOME I. //1.3e-08:243:23//CAENORHABDITIS ELEGANS. //Q09417
 F-NT2RM4001140//HOMEODOMAIN PROTEIN MSH-D. //1.1e-13:103:38//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO). //Q01704
 F-NT2RM4001151//SYNAPSINS 1A AND 1B (BRAIN PROTEIN 4.1). //0.26:96:34//HOMO SAPIENS (HUMAN). //P17600
 F-NT2RM4001155//ADRENAL MEDULLA 50 KD PROTEIN. //3.6e-103:201:91//BOS TAURUS (BOVINE). //Q27969
 F-NT2RM4001160//GLUTATHIONE S-TRANSFERASE (EC 2.5.1.18) (CLASS-PH I) (FRAGMENTS). //1.0:33:33//BRASSICA OLERACEA (CAULIFLOWER). //P48438
 F-NT2RM4001187//PREPROTEIN TRANSLOCASE SECA SUBUNIT. //0.44:158:27//MYCOPLASMA GENITALIUM. //P47318
 F-NT2RM4001191//LONG NEUROTOXIN 2 (TOXIN C). //0.99:44:43//ASTROTIA STOKESII (STOKES'S SEA SNAKE) (DIOSTERA STOKESII). //P01381
 F-NT2RM4001200//ZINC FINGER PROTEIN 135. //2.2e-82:245:59//HOMO SAPIENS (HUMAN). //P52742
 F-NT2RM4001203//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION. //0.028:94:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P53214
 F-NT2RM4001204//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A6). //0.0096:182:34//HOMO SAPIENS (HUMAN). //Q15428
 F-NT2RM4001217//RING CANAL PROTEIN (KELCH PROTEIN). //2.1e-21:221:29//DROSOPHILA MELANOGASTER (FRUIT FLY). //Q04652
 F-NT2RM4001256//CBP3 PROTEIN PRECURSOR. //0.30:55:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P21560
 F-NT2RM4001258//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556. //0.00031:132:39//STREPTOMYCES FRADIAE. //P20186
 F-NT2RM4001309//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAGMENT). //0.048:132:28//HOMO SAPIENS (HUMAN). //P02812
 F-NT2RM4001313//PHOSPHATIDYLINOSITOL 3-KINASE VPS34-LIKE (EC 2.7.1.137) (PI3-KINASE) (PTDINS-3-KINASE) (PI3K). //2.6e-37:124:65//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD). //P54676
 F-NT2RM4001316//ACYL-COA DEHYDROGENASE, MEDIUM-CHAIN SPECIFIC PRECURSOR (EC 1.3.99.3) (MCAD). //1.7e-10:185:30//RATTUS NORVEGICUS (RAT). //P08503
 F-NT2RM4001320//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG). //1.5e-08:197:26//MUS MUSCULUS (MOUSE). //P52734
 F-NT2RM4001340//UTR4 PROTEIN (UNKNOWN TRANSCRIPT 4 PROTEIN). //7.7e-14:82:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P32626
 F-NT2RM4001344//HYPOTHETICAL GTP-BINDING PROTEIN IN POP2-HOLI INTERGENIC REGION. //3.3e-16:128:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P53742
 F-NT2RM4001347//HYPOTHETICAL 76.9 KD PROTEIN IN RPM2-TUB1 INTERGENIC REGION. //0.067:111:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //Q04511
 F-NT2RM4001371
 F-NT2RM4001382//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR. //1.0e-08:82:39//PLASMODIUM LOPHURAE. //P04929
 F-NT2RM4001384
 F-NT2RM4001410//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR. //2.1e-08:185:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P32323
 F-NT2RM4001411//EARLY MODULIN 20 PRECURSOR (M-20). //5.3e-05:105:38//MEDICAGO TRUNCATULA (BARREL MEDIC). //P93329
 F-NT2RM4001412//GTPASE-ACTIVATING PROTEIN (GAP) (RAS P21 PROTEIN ACTIVATOR) (PI20GAP) (RASGAP). //6.2e-17:109:41//RATTUS NORVEGICUS (RAT). //P50804
 F-NT2RM4001414//ZINC FINGER PROTEIN 177. //8.3e-06:54:50//HOMO SAPIENS (HUMAN). //Q13360
 F-NT2RM4001437//ALU SUBFAMILY SC WARNING ENTRY !!!!! //2.1e-24:87:65//HOMO SAPIENS (HUMAN). //P39192
 F-NT2RM4001444//PROBABLE ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS) (FRAGMENT). //2.6e-45:197:47//CLOSTRIDIUM INTENSIVUM. //Q94425
 F-NT2RM4001454//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT). //0.0060:95:29//HOMO SAPIENS (HUMAN). //Q15057
 F-NT2RM4001455//PROBABLE E5B PROTEIN. //0.41:44:36//HUMAN PAPILLOMA VIRUS TYPE 68. //P06461
 F-NT2RM4001483//ZINC FINGER PROTEIN 136. //1.7e-28:85:64//HOMO SAPIENS (HUMAN). //P52737
 F-NT2RM4001489//PTB-ASSOCIATED SPLICING FACTOR (PSF). //0.086:111:34//HOMO SAPIENS (HUMAN). //P23246
 F-NT2RM4001519//ACID UREASE ALPHA SUBUNIT (EC 3.5.1.5) (UREA AMIDE HYDROLASE). //0.82:51:47//LACTOBACILLUS FERMENTUM. //P26929
 F-NT2RM4001522//TROPOMYOSIN. //0.030:117:23//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //Q02088
 F-NT2RM4001557
 F-NT2RM4001565//HYPOTHETICAL 44.3 KD PROTEIN CIF7.07C IN CHROMOSOME I. //0.99:42:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //Q09919
 F-NT2RM4001566//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE). //0.054:190:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P08640
 F-NT2RM4001569//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT-LIKE PROTEIN (ACTIVATED PROTEIN KINASE C RECEPTOR HOMOLOG). //0.72:64:31//TRYPAANOSOMA BRUCEI BRUCEI. //Q94775
 F-NT2RM4001582
 F-NT2RM4001592//DNA REPAIR PROTEIN RAD9. //0.00037:198:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P14737
 F-NT2RM4001594//IMMEDIATE-EARLY PROTEIN IE180. //1.9e-05:147:34//PS ELDORABIES VIRUS (STRAIN KAPLAN) (PRV). //P33479
 F-NT2RM4001597//THIOL-DISULFIDE INTERCHANGE PROTEIN TLPA (CYTOCHROME C BIOGENESIS PROTEIN TLPA). //5.7e-06:122:29//BRADYRHOBIUM JAPONICUM. //P43221
 F-NT2RM4001605//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140). //1.7e-128:249:96//RATTUS NORVEGICUS (RAT). //P37199
 F-NT2RM4001611//S1S2 PROTEIN (HALOTOLERANCE PROTEIN HAL3). //1.5e-35:128:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P36024
 F-NT2RM4001629//MAGUK P55 SUBFAMILY MEMBER 3 (MPP3 PROTEIN) (DISC 5, LARGE HOMOLOG 3). //5.8e-42:254:37//HOMO SAPIENS (HUMAN). //Q13368
 F-NT2RM4001650//HOMEODOMAIN PROTEIN HOX-A4 (HOX-1.4). //0.62:19:57//GALLUS GALLUS (CHICKEN). //P17277
 F-NT2RM4001662//PROTEIN KINASE C, ALPHA TYPE (EC 2.7.1.-) (PKC-ALPHA). //0.29:90:32//HOMO SAPIENS (HUMAN). //P17252
 F-NT2RM4001666//HYPOTHETICAL 48.6 KD PROTEIN IN ALPA-GAP INTERGENIC REGION. //1.1e-31:137:44//ESCHERICHIA COLI. //P37339
 F-NT2RM4001682//PROBABLE 60S RIBOSOMAL PROTEIN L22. //0.98:55:29//CAENORHABDITIS ELEGANS. //P52819
 F-NT2RM4001710//HYPOTHETICAL PROTEIN KIAA0039 (FRAGMENT). //0.56:113:28//HOMO SAPIENS (HUMAN). //Q15054
 F-NT2RM4001714//SEPTIN 2 HOMOLOG (FRAGMENT). //1.4e-108:255:77//HOMO SAPIENS (HUMAN). //Q14141
 F-NT2RM4001715//HYPOTHETICAL PROTEIN C19G10.16 IN CHROMOSOME I (FRAGMENT). //2.1e-36:148:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //Q10342
 F-NT2RM4001731//HYPOTHETICAL 54.9 KD PROTEIN C02F5.7 IN CHROMOSOME III. //1.1e-05:90:33//CAENORHABDITIS ELEGANS. //P34284
 F-NT2RM4001741//TALIN. //1.1e-106:208:99//MUS MUSCULUS (MOUSE). //P26039
 F-NT2RM4001746//EBNA-1 NUCLEAR PROTEIN. //1.6e-09:155:38//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4). //P03211
 F-NT2RM4001754//COLLAGEN ALPHA 5(V) CHAIN PRECURSOR. //0.93:158:33//HOMO SAPIENS (HUMAN). //P29400
 F-NT2RM4001758//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.-). //5.1e-113:277:79//HOMO SAPIENS (HUMAN). //P27448
 F-NT2RM4001776//MYOSIN I ALPHA (MMI-ALPHA). //2.2e-73:262:54//MUS MUSCULUS (MOUSE). //P46735
 F-NT2RM4001783//ZINC FINGER PROTEIN HRX (ALL-1) (FRAGMENT). //5.3e-26:169:39//MUS MUSCULUS (MOUSE). //P55200

【0655】

[表357]

F-NT2RM4001810//MALE SPECIFIC SPERM PROTEIN MST84DB.//2.3e-05:68:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643
 F-NT2RM4001813//RHODOCETIN ALPHA SUBUNIT.//2.3e-05:115:34//AGK1STR ODOM RHODOSTOMA (MALAYAN PIT VIPER) (CALLOSELASMA RHODOSTOMA).//P81397
 F-NT2RM4001819//CELL SURFACE GLYCOPROTEIN EMR1 PRECURSOR (EMR1, HORMONE RECEPTOR) (CELL SURFACE GLYCOPROTEIN F4/80).//1.7e-06:159:25//MUS MUSCULUS (MOUSE).//Q61549
 F-NT2RM4001823//ZINC FINGER PROTEIN ZIC1 (ZINC FINGER PROTEIN OF THE CEREBELLUM 1).//2.6e-18:114:40//MUS MUSCULUS (MOUSE).//P46684
 F-NT2RM4001828//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//4.0e-81:253:59//HOMO SAPIENS (HUMAN).//P51523
 F-NT2RM4001836//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//0.21:176:30//NEPHILA CLAVIPES (ORB SPIDER).//P46804
 F-NT2RM4001841//PROLINE-RICH PEPTIDE P-8.//0.046:27:40//HOMO SAPIENS (HUMAN).//P02814
 F-NT2RM4001842//HYPOTHETICAL 7.0 KD PROTEIN B0388.1 IN CHROMOSOME 111.//0.98:35:42//CAENORHABDITIS ELEGANS.//Q11104
 F-NT2RM4001856//HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGENIC REGION.//2.3e-37:242:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39722
 F-NT2RM4001858//T-BOX PROTEIN VEGT (T-BOX PROTEIN BRAT) (T-BOX PROTEIN ANTIPODEAN).//1.8e-23:78:64//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P87377
 F-NT2RM4001865//NEURONAL CALCIUM SENSOR 2 (NCS-2).//0.012:83:28//CAENORHABDITIS ELEGANS.//P36609
 F-NT2RM4001876//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DALS INTERGENIC REGION PRECURSOR.//3.8e-10:242:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47179
 F-NT2RM4001880//EC PROTEIN HOMOLOG.//0.22:59:32//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P93746
 F-NT2RM4001905//60S RIBOSOMAL PROTEIN L40 (CEP52).//0.57:20:60//HOMO SAPIENS (HUMAN), RATTUS NORVEGICUS (RAT), AND GALLUS GALLUS (CHICKEN).//P14793
 F-NT2RM4001922
 F-NT2RM4001930//PUTATIVE GLUCOSYLTRANSFERASE C08B11.8 (EC 2.4.1.-).//5.5e-45:167:53//CAENORHABDITIS ELEGANS.//Q09226
 F-NT2RM4001938//RTOA PROTEIN (RATIO-A).//0.0036:120:32//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P54681
 F-NT2RM4001940//IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-1 (FRAGMENT).//0.32:31:48//HOMO SAPIENS (HUMAN).//P78415
 F-NT2RM4001953//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//2.2e-43:56:85//HOMO SAPIENS (HUMAN).//P39192
 F-NT2RM4001965//IG ALPHA-1 CHAIN C REGION.//0.56:73:34//GORILLA GORILLA GORILLA (LOWLAND GORILLA).//P20758
 F-NT2RM4001969//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE 18-6; PEPTIDE P-H].//0.0016:140:27//HOMO SAPIENS (HUMAN).//P04280
 F-NT2RM4001979//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.9e-21:103:51//HOMO SAPIENS (HUMAN).//P51523
 F-NT2RM4001984//HYPOTHETICAL PROTEIN LAMBDA-SP5.//0.0034:50:40//MUS MUSCULUS (MOUSE).//P15974
 F-NT2RM4001987//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRREG PROTEIN).//6.9e-17:115:31//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q08180
 F-NT2RM4002013//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHROMOSOME V.//0.0062:117:28//CAENORHABDITIS ELEGANS.//Q23256
 F-NT2RM4002018//SPORE COAT PROTEIN SP96.//4.3e-06:203:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P14328
 F-NT2RM4002034//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131).//0.78:132:25//HOMO SAPIENS (HUMAN).//P98171
 F-NT2RM4002044//VITELLOGENIN 1 PRECURSOR (MINOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LVI); PHOSVITIN (PV); LIPOVITELLIN II (LVI); YCP42].//0.062:201:24//GALLUS GALLUS (CHICKEN).//P87498
 F-NT2RM4002054//DUPLICATE PROCYCLIN.//0.0079:44:52//TRYPAANOSOMA BRUCEI BRUCEI.//P14044
 F-NT2RM4002055//PUTATIVE Z PROTEIN.//0.82:39:30//OVIS ARIES (SHEEP).//P08105
 F-NT2RM4002062//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//7.0e-37:80:52//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P36419
 F-NT2RM4002063//SARCOSINE OXIDASE (EC 1.5.3.1).//2.2e-25:216:31//BACILLUS SP. (STRAIN NS-129).//P23342
 F-NT2RM4002066//HYPOTHETICAL PROTEIN KIAA0192 (FRAGMENT).//1.1e-9:4:260:71//HOMO SAPIENS (HUMAN).//Q93074
 F-NT2RM4002067//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.5e-15:51:70//HOMO SAPIENS (HUMAN).//P39188
 F-NT2RM4002073//ELASTIN PRECURSOR (TROPOLASTIN).//4.9e-05:88:36//HOMO SAPIENS (HUMAN).//P15502
 F-NT2RM4002075//RING CANAL PROTEIN (KELCH PROTEIN).//7.2e-43:220:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
 F-NT2RM4002093//POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 1) (HNRNP 1) (57 KD RNA-BINDING PROTEIN PPTB-1).//1.8e-93:255:72//HOMO SAPIENS (HUMAN).//P26599
 F-NT2RM4002109//KINESIN-LIKE PROTEIN KIF4.//3.7e-101:260:78//MUS MUSCULUS (MOUSE).//P33174
 F-NT2RM4002128//HYPOTHETICAL PROTEIN IN CYCB 3' REGION PRECURSOR (ORF2) (FRAGMENT).//0.91:49:32//PARACOCCLUS DENITRIFICANS.//P29969
 F-NT2RM4002140//GROUCHO PROTEIN (ENHANCER OF SPLIT W9/10).//0.36:104:22//DROSOPHILA MELANOGASTER (FRUIT FLY).//P16371
 F-NT2RM4002145//SLIT PROTEIN PRECURSOR.//8.6e-13:127:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//P24014
 F-NT2RM4002146//MAGO HASHI PROTEIN.//7.9e-69:143:91//DROSOPHILA MELANOGASTER (FRUIT FLY).//P49028
 F-NT2RM4002161//DUAL SPECIFICITY PROTEIN PHOSPHATASE (EC 3.1.3.48) (EC 3.1.3.16).//0.0062:99:26//CHLAMYDOMONAS EUCAMETOS.//Q39491
 F-NT2RM4002174//MRP PROTEIN.//4.5e-50:183:55//ESCHERICHIA COLI.//P21590
 F-NT2RM4002189//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//2.6e-14:233:29//HOMO SAPIENS (HUMAN).//Q02817
 F-NT2RM4002194//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//0.92:108:28//HOMO SAPIENS (HUMAN).//P51805
 F-NT2RM4002205//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEFG).//5.8e-39:122:72//RATTUS NORVEGICUS (RAT).//Q07803
 F-NT2RM4002213//HYPOTHETICAL 88.4 KD PROTEIN B0464.7 IN CHROMOSOME 111.//9.9e-27:110:43//CAENORHABDITIS ELEGANS.//Q03565
 F-NT2RM4002226//GTPASE ACTIVATING PROTEIN ROTUND.//1.3e-21:147:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//P40809
 F-NT2RM4002251//PROTEIN EF-7 (FRAGMENT).//0.0082:45:42//MUS MUSCULUS (MOUSE).//P97805
 F-NT2RM4002256//COLD-REGULATED PROTEIN 1 (FRAGMENT).//0.00015:114:42//HORDEUM VULGARE (BARLEY).//P23251
 F-NT2RM4002266//CUTICLE COLLAGEN 2.//0.00013:142:33//CAENORHABDITIS ELEGANS.//P17656
 F-NT2RM4002278//HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-T1F4631 INTERGENIC REGION.//1.0e-40:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53288
 F-NT2RM4002281
 F-NT2RM4002287//GAR2 PROTEIN.//0.00055:225:23//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891
 F-NT2RM4002294//HYPOTHETICAL PROTEIN KIAA0281 (HA6725).//1.1e-60:152:75//HOMO SAPIENS (HUMAN).//Q92556
 F-NT2RM4002301//GENERAL STRESS PROTEIN CTC (FRAGMENT).//0.56:43:39//BACILLUS CALDOLYTICUS.//P42832
 F-NT2RM4002323//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.0080:73:35//BOS TAURUS (BOVINE).//P02313
 F-NT2RM4002339//METALLOTHIONEIN 10-111 (MT-10-111).//0.67:34:38//MYTILUS EDULIS (BLUE MUSSEL).//P80248
 F-NT2RM4002344//METALLOTHIONEIN-1 (MT-1).//0.84:41:31//MUS MUSCULUS (MOUSE).//P02802
 F-NT2RM4002373//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT DY10 PRECURSOR.//0.0019:190:28//TRITICUM AESTIVUM (WHEAT).//P10387
 F-NT2RM4002374//SE5 ANTIGEN.//0.0059:170:32//RATTUS NORVEGICUS (RAT).//Q63003
 F-NT2RM4002383//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//0.13:17:88//HOMO SAPIENS (HUMAN).//P39193
 F-NT2RM4002390
 F-NT2RM4002398//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODPI PROTEIN).//0.034:110:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38074
 F-NT2RM4002409//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE--COA LIGASE) (ACYL--ACTIVATING ENZYME).//4.0e-20:179:31//METHANOTRIX SOEHNENII.//P27095
 F-NT2RM4002438//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//1.7e-15:41:95//HOMO SAPIENS (HUMAN).//P39194
 F-NT2RM4002446//CRYPTOIN-RELATED PROTEIN 4C-1 PRECURSOR (CRS4C).//0.0058:24:50//MUS MUSCULUS (MOUSE).//P17534
 F-NT2RM4002452//METALLOTHIONEIN 10-11 (MT-10-11).//0.83:48:37//MYTILUS EDULIS (BLUE MUSSEL).//P80247
 F-NT2RM4002457//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//4.9e-07:52:63//HOMO SAPIENS (HUMAN).//P39192
 F-NT2RM4002460//C-HORDEIN (CLONE PC-919) (FRAGMENT).//0.92:43:30//HORDEUM VULGARE (BARLEY).//P17992
 F-NT2RM4002479//RNA HELICASE-LIKE PROTEIN DB10.//1.7e-28:200:41//NICOTIANA SYLVESTRIS (WOOD TOBACCO).//P46942
 F-NT2RM4002482//HYPOTHETICAL 65.9 KD PROTEIN YP065W.//8.8e-26:123:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12514
 F-NT2RM4002493//LARVAL CUTICLE PROTEIN 1 PRECURSOR.//0.17:126:27//DROSOPHILA MIRANDA (FRUIT FLY).//P91627

[0656]

【表358】

F-NT2RM4002499/!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.4e-34:92:80//HOMO SAPIENS (HUMAN).//P39194
 F-NT2RM4002504/!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/3.4e-19:55:83//HOMO SAPIENS (HUMAN).//P39189
 F-NT2RM4002527//ND-40 REPEAT PROTEIN MS12.//3.0e-07:193:27//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//022468
 F-NT2RM4002532//AEROLYSIN REGULATORY PROTEIN.//0.97:19:47//AEROMONAS SOBRIA.//P09165
 F-NT2RM4002534//MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L32 PRECURSOR (YML32).//0.76:86:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25348
 F-NT2RM4002558//LONG-CHAIN FATTY ACID TRANSPORT PROTEIN (FATP).//4.2e-55:204:50//MUS MUSCULUS (MOUSE).//Q60714
 F-NT2RM4002565//CHYMOTRYPSIN/ELASTASE ISOINHIBITORS 2 TO 5.//1.0:1:6:62//ASCARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).//P07852
 F-NT2RM4002567//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION.//2.7e-10:184:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40032
 F-NT2RM4002571//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN-UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-GALNAc:POLYPEPTIDE, N-ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAc-T1).//2.4e-25:124:47//HOMO SAPIENS (HUMAN).//Q10472
 F-NT2RM4002593//HYPOTHETICAL 9.1 KD PROTEIN IN TETB-EXOA INTERGENIC REGION.//0.95:36:38//BACILLUS SUBTILIS.//P37509
 F-NT2RM4002594//MSPI PROTEIN HOMOLOG.//9.0e-68:227:60//CAENORHABDITIS ELEGANS.//P54815
 F-NT2RM4002623//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS).//3.3e-54:243:47//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P73851
 F-NT2RP1000018//SUPPRESSOR PROTEIN SRP40.//0.0023:131:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
 F-NT2RP1000035//RING CANAL PROTEIN (KELCH PROTEIN).//1.0e-06:63:34//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
 F-NT2RP1000040//LETHAL NEUROTOXIN TX1.//0.69:21:47//PHONEUTRIA NIGRIVENTER (BRAZILIAN ARMED SPIDER).//P17727
 F-NT2RP1000063//HYPOTHETICAL 25.1 KD PROTEIN IN SMC3-MRPL8 INTERGENIC REGION.//3.8e-14:130:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40359
 F-NT2RP1000086//HYPOTHETICAL 9.4 KD PROTEIN IN RNPA-THOF INTERGENIC REGION.//0.16:44:40//ESCHERICHIA COLI.//P22847
 F-NT2RP1000101//45.8 KD PROTEIN IN SHM1-MRPL37 INTERGENIC REGION.//1.9e-06:74:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38344
 F-NT2RP1000111//COPI REGULATORY PROTEIN (FUSCA PROTEIN FUS1).//2.7e-19:135:36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P43254
 F-NT2RP1000112//DUAL SPECIFICITY PROTEIN KINASE TTK (EC 2.7.1.-) (PYT).//1.2e-39:91:62//HOMO SAPIENS (HUMAN).//P33981
 F-NT2RP1000124//ATP-DEPENDENT PROTEASE LA 2 (EC 3.4.21.53).//0.074:131:24//MYXOCOCCUS XANTHUS.//P36774
 F-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//1.5e-49:18:6:56//MUS MUSCULUS (MOUSE).//P51859
 F-NT2RP1000163//METALLOTHIONEIN (MT).//0.98:41:34//PLEURONECTES PLATESSA (PLAICE).//P07216
 F-NT2RP1000170//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.85:64:35//HOMO SAPIENS (HUMAN).//P10162
 F-NT2RP1000174//IMMEDIATE-EARLY PROTEIN IE180.//0.00056:89:37//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479
 F-NT2RP1000191//NIFU PROTEIN.//0.53:78:35//FRANKIA ALNI.//P46045
 F-NT2RP1000202//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NON ERYTHROID) (FRAGMENT).//9.1e-21:148:39//HOMO SAPIENS (HUMAN).//Q01485
 F-NT2RP1000243//HYPOTHETICAL PROTEIN MJ1136.//1.4e-37:219:36//METHANOCOCCUS JANNASCHII.//Q58536
 F-NT2RP1000259//HYPOTHETICAL PROTEIN TP0318.//0.18:25:44//TREPONEMA PALLIDUM.//Q83338
 F-NT2RP1000272//SPLICING FACTOR, ARGININE/SERINE-RICH 3 (PRE-MIRNA SPLICING FACTOR SRP20) (X16 PROTEIN).//1.6e-18:133:36//HOMO SAPIENS (HUMAN), AND MUS MUSCULUS (MOUSE).//P23152
 F-NT2RP1000324
 F-NT2RP1000326//HYPOTHETICAL 29.8 KD PROTEIN ZC97.1 IN CHROMOSOME 111.//1.0e-23:129:36//CAENORHABDITIS ELEGANS.//P34599
 F-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//2.5e-45:147:57//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32447
 F-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//4.8e-14:119:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25343
 F-NT2RP1000357//TRYPTOPAN-INDUCED GENE EXPRESSION-ACCELERATING FACTOR (T-DAF) (FRAGMENT).//1.0:43:32//TRYPTANOSOMA CRUZI.//Q26327
 F-NT2RP1000358//HYPOTHETICAL 84.4 KD PROTEIN IN RPC2/RET1 3' REGION.//7.9e-28:244:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39744

F-NT2RP1000363//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//2.2e-07:178:30//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437
 F-NT2RP1000376//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//1.5e-20:254:31//HOMO SAPIENS (HUMAN).//P16157
 F-NT2RP1000409//CYTOCHROME C3 (CYTOCHROME C7) (C551.5).//1.0:34:26//DESULFURIMONAS ACETOXIDANS (CHLOROPSEUDOMONAS ETHYLICA).//P00137
 F-NT2RP1000413//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAPI PROTEIN).//3.7e-131:230:97//RATTUS NORVEGICUS (RAT).//P55161
 F-NT2RP1000416//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.83:54:40//DROSOPHILA SIMULANS (FRUIT FLY).//P13729
 F-NT2RP1000418//HYPOTHETICAL 9.9 KD PROTEIN IN GCVT-SPO11AA INTERGENIC REGION.//0.24:91:35//BACILLUS SUBTILIS.//P49779
 F-NT2RP1000439//HYPOTHETICAL 100.5 KD PROTEIN C189.04 IN CHROMOSOME 1.//0.13:172:22//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10429
 F-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN).//1.9e-08:167:24//HOMO SAPIENS (HUMAN).//Q08257
 F-NT2RP1000460//NUCLEAR MOVEMENT PROTEIN NUDC.//1.0e-18:149:34//EMERICELLA NIDULANS (ASPERGILLUS NIDULANS).//P17624
 F-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME 111.//1.3e-43:180:47//CAENORHABDITIS ELEGANS.//P34580
 F-NT2RP1000478//TUBULIN BETA-6 CHAIN (CLASS-VI).//1.5e-45:85:63//GALLUS GALLUS (CHICKEN).//P09207
 F-NT2RP1000481//HYPOTHETICAL 5.8 KD PROTEIN IN PUHA 5' REGION (ORF55).//0.083:21:47//RHODOBACTER CAPSULATUS (RHODOPSEUDOMONAS CAPSULATA).//P26159
 F-NT2RP1000493//POSSIBLE DNA-REPAIR PROTEIN XP-E (POSSIBLE XERODERMA PIGMENTOSUM GROUP E PROTEIN) (UV-DAMAGED DNA-BINDING PROTEIN) (UV-DBB).//6.6e-11:139:31//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET).//P33194
 F-NT2RP1000513//60S RIBOSOMAL PROTEIN L22.//0.017:92:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//P50887
 F-NT2RP1000522//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//0.0055:86:36//MUS MUSCULUS (MOUSE).//Q61068
 F-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.2e-09:69:36//CRICETULUS GRISEUS (CHINESE HAMSTER).//P49020
 F-NT2RP1000574//HOMEOBOX PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//6.0e-39:141:65//MUS MUSCULUS (MOUSE).//P97367
 F-NT2RP1000577//PUTATIVE ATP-DEPENDENT RNA HELICASE YOL031W.//0.00016:48:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12389
 F-NT2RP1000581//VON WILLEBRAND FACTOR PRECURSOR.//0.00017:61:50//HOMO SAPIENS (HUMAN).//P04275
 F-NT2RP1000609//LINOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESATURASE).//4.4e-07:128:31//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q08871
 F-NT2RP1000629//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//4.2e-70:167:86//MUS MUSCULUS (MOUSE).//P35585
 F-NT2RP1000630//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR.//0.0011:238:21//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47179
 F-NT2RP1000677//COLLAGEN ALPHA 1(XVI) CHAIN PRECURSOR.//0.99:71:33//HOMO SAPIENS (HUMAN).//Q07092
 F-NT2RP1000688/!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/0.0024:1:94//HOMO SAPIENS (HUMAN).//P39193
 F-NT2RP1000695//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME 111.//2.2e-30:185:37//CAENORHABDITIS ELEGANS.//Q18262
 F-NT2RP1000701//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//3.2e-65:128:93//RATTUS NORVEGICUS (RAT).//P54319
 F-NT2RP1000721//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAF11-135) (TAF1135) (TAF1130).//2.3e-06:139:34//HOMO SAPIENS (HUMAN).//Q00268
 F-NT2RP1000730//MYOSIN LIGHT CHAIN 1, SLOW-TWITCH MUSCLE B/VENTRICULAR ISOFORM (FRAGMENT).//0.89:40:40//MUS MUSCULUS (MOUSE).//P09542
 F-NT2RP1000733//METALLOTHIONEIN-LIKE PROTEIN CR55.//0.024:24:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41902
 F-NT2RP1000738//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1 / PRP-3) (PRP-2 / PRP-4) (PIF-F / PIF-S) (PROTEIN A / PROTEIN C) (CONTAINS: PEPTIDE P-CJ).//0.040:82:36//HOMO SAPIENS (HUMAN).//P02810
 F-NT2RP1000746//HYPOTHETICAL 27.1 KD PROTEIN UFD4-CAP1 INTERGENIC REGION.//2.0e-30:170:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33201
 F-NT2RP1000767//PSEUDOMONAS PEPSIN PRECURSOR (EC 3.4.23.37) (PEPSTAT

【表359】

IN-INSENSITIVE CARBOXYL PROTEINASE).//0.99:75:34//PSEUDOMONAS SP. (STRAIN 101).//P42790
 F-NT2RP1000782//CELL SURFACE GLYCOPROTEIN A15 (T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA ASSOCIATED ANTIGEN 1) (TALLA-1) (MEMBRANE COMPONENT, X CHROMOSOME, SURFACE MARKER 1).//2.3e-23:159:35//HOMO SAPIENS (HUMAN).//P41732
 F-NT2RP1000796//CORNIFIN (SMALL PROLINE-RICH PROTEIN 1) (SPR-1) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SPRP).//0.00018:79:32//SU S SCROFA (PIG).//P35323
 F-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P5 0-RHOGAP).//3.1e-37:89:64//HOMO SAPIENS (HUMAN).//Q07960
 F-NT2RP1000833//SMALL PROLINE RICH PROTEIN 11 (SPR-11) (CLONE 930).//0.32:29:48//HOMO SAPIENS (HUMAN).//P22531
 F-NT2RP1000834//2-ARYLPYRROLYL-COA EPIMERASE (EC 5.-.-.-).//6.4e-67:202:68//RATTUS NORVEGICUS (RAT).//P70473
 F-NT2RP1000836//HYPOTHETICAL 7.3 KD PROTEIN IN 100 KD PROTEIN REGION.//1.0:35:54//HUMAN ADENOVIRUS TYPE 41.//P23691
 F-NT2RP1000846//SMALL PROLINE-RICH PROTEIN 2-1.//0.013:35:48//HOMO SAPIENS (HUMAN).//P35326
 F-NT2RP1000851//PERIOD CLOCK PROTEIN (FRAGMENT).//0.082:28:57//DROSOPHILA SALTANS (FRUIT FLY).//Q04536
 F-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//2.5e-26:19 0:30//MUS MUSCULUS (MOUSE).//Q03566
 F-NT2RP1000860//POTENTIAL TRANSCRIPTIONAL ADAPTOR.//0.13:86:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q02336
 F-NT2RP1000902//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME 111.//7.6e-11:200:35//CAENORHABDITIS ELEGANS.//Q09531
 F-NT2RP1000915//HYPOTHETICAL GTP-BINDING PROTEIN IN PBI40-PAC2 INTERGENIC REGION.//1.4e-06:88:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40010
 F-NT2RP1000916//SUPPRESSOR PROTEIN SRP40.//0.40:90:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
 F-NT2RP1000943//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//0.099:75:34//HOMO SAPIENS (HUMAN).//Q02817
 F-NT2RP1000944//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//7.6e-06:65:41//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMPV).//Q10341
 F-NT2RP1000947//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E217) (KB 2).//3.6e-12:27:77//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P51669
 F-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//2.8e-15:169:28//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
 F-NT2RP1000958//HYPOTHETICAL GTP-BINDING PROTEIN IN PBI40-PAC2 INTERGENIC REGION.//4.2e-16:162:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40010
 F-NT2RP1000959//CORNIFIN A (SMALL PROLINE-RICH PROTEIN 1A) (SPR-1A) (SPRK).//0.0031:34:44//HOMO SAPIENS (HUMAN).//P35321
 F-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//1.5e-52:110:95//HOMO SAPIENS (HUMAN).//P19338
 F-NT2RP1000980//LIGHT-HARVESTING PROTEIN 8-1015, ALPHA CHAIN PRECURSOR (ANTENNA PIGMENT PROTEIN, ALPHA CHAIN).//0.87:37:45//RHODOPSEUDOMONAS VIRIDIS.//P04123
 F-NT2RP1000988
 F-NT2RP1001011//PROTEIN P19.//0.96:30:50//BACTERIOPHAGE PRD1.//P17638
 F-NT2RP1001013//DNA-BINDING PROTEIN 65 (PROTEIN GP65).//1.0:20:45//BACTERIOPHAGE T4.//P16012
 F-NT2RP1001014
 F-NT2RP1001033//TUBULIN GAMMA CHAIN.//2.5e-16:112:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P25295
 F-NT2RP1001073//HYPOTHETICAL 10.4 KD PROTEIN IN FTR1-SPT15 INTERGENIC REGION.//7.6e-16:82:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40089
 F-NT2RP1001079//SARCOSINE OXIDASE (EC 1.5.3.1).//4.8e-15:95:40//ARTHROBACTER SP. (STRAIN TE1826).//P40873
 F-NT2RP1001080//PROBABLE ATP-DEPENDENT RNA HELICASE DBP9.//2.4e-29:126:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06218
 F-NT2RP1001113//SMALL PROLINE-RICH PROTEIN 2-1.//0.49:38:39//HOMO SAPIENS (HUMAN).//P35326
 F-NT2RP1001173//RHOMBOTIN-1 (CYSTEINE RICH PROTEIN TTG-1) (T-CELL TRANSLOCATION PROTEIN 1) (LIM-ONLY PROTEIN 1).//0.99:54:37//HOMO SAPIENS (HUMAN).//P25800
 F-NT2RP1001177//HISTONE MACRO-H2A.1.//1.6e-29:85:76//RATTUS NORVEGICUS (RAT).//Q02874
 F-NT2RP1001185
 F-NT2RP1001199//NEUROTOXIN 1.//1.0:23:47//CENTRUROIDES SCULPTURATUS (BARK SCORPION).//P01491
 F-NT2RP1001247//TRANSFORMING GROWTH FACTOR BETA 4 PRECURSOR (TGF-BETA 4) (ENDOMETRIAL BLEEDING-ASSOCIATED FACTOR).//3.3e-08:28:89//HOMO SAPIENS (HUMAN).//Q00292
 F-NT2RP1001248//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.33:49:28//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HI V-1).//P18804
 F-NT2RP1001253//GLUCOSAMINE-6-PHOSPHATE ISOMERASE (EC 5.3.1.10) (GLUCOSAMINE-6-PHOSPHATE DEAMINASE) (GNPDA) (OSCILLIN) (K1A0060).//3.8e-46:115:81//HOMO SAPIENS (HUMAN).//P46926
 F-NT2RP1001286//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (ICE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-34 GALACTOSIDE-BINDING LECTIN).//0.16:48:37//MUS MUSCULUS (MOUSE).//P16110
 F-NT2RP1001294//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//6.1e-05:92:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12024
 F-NT2RP1001302//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.2e-05:92:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12024
 F-NT2RP1001310//PROBABLE E4 PROTEIN.//0.99:109:26//HUMAN PAPILLOMA VIRUS TYPE 5.//P06924
 F-NT2RP1001311//SODIUM/HYDROGEN EXCHANGER 5 (NA(+)/H(+) EXCHANGER 5) (NHE-5) (FRAGMENT).//0.99:94:31//HOMO SAPIENS (HUMAN).//Q14940
 F-NT2RP1001313//CYTOCHROME B5.//9.0e-13:92:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40312
 F-NT2RP1001361//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B).//1.2e-47:117:74//BOS TAURUS (BOVINE).//Q02827
 F-NT2RP1001385//CELL DIVISION PROTEIN FTSN.//0.64:107:28//ESCHERICHIA COLI.//P29131
 F-NT2RP1001395//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS).//0.25:35:45//GALLUS GALLUS (CHICKEN).//P02467
 F-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//2.2e-41:129:67//CAENORHABDITIS ELEGANS.//P91917
 F-NT2RP1001424//UREASE ACCESSORY PROTEIN UREF (FRAGMENT).//0.87:24:45//ESCHERICHIA COLI.//Q03286
 F-NT2RP1001432//CYSTEINE PROTEINASE INHIBITOR B (CYSTATIN B) (SCB).//1.0:35:42//HELIANTHUS ANNUUS (COMMON SUNFLOWER).//Q10993
 F-NT2RP1001449//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (HMS KERATIN).//0.053:37:37//OVIS ARIES (SHEEP).//P26372
 F-NT2RP1001457//HYPOTHETICAL 57.0 KD TRP-ASP REPEATS CONTAINING PROTEIN IN CPR4-SSK22 INTERGENIC REGION.//2.9e-16:159:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25382
 F-NT2RP1001466//HYPOTHETICAL PROTEIN MJ0284.//5.3e-15:162:35//METHANOCOCCUS JANNASCHII.//Q57732
 F-NT2RP1001475//HYPOTHETICAL 195.1 KD PROTEIN IN DNA43-UB11 INTERGENIC REGION.//0.69:119:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40457
 F-NT2RP1001482//PROTEASOME COMPONENT C9 (EC 3.4.99.46) (MACROPAIN SUBUNIT C9) (MULTICATALYTIC ENDOPEPTIDASE COMPLEX SUBUNIT C9).//1.0:58:32//HOMO SAPIENS (HUMAN).//P25789
 F-NT2RP1001494//MALE STERILITY PROTEIN 2.//2.4e-12:84:42//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q08891
 F-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IP 5).//6.3e-37:94:52//SPIRODELA POLYRRHIZA.//P42803
 F-NT2RP1001546//LEUKOCYTE SURFACE ANTIGEN CD53 (CELL SURFACE GLYCOPROTEIN CD53).//9.3e-11:98:29//HOMO SAPIENS (HUMAN).//P19397
 F-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA).//2.2e-64:159:84//MUS MUSCULUS (MOUSE).//P47758
 F-NT2RP1001616//HYPOTHETICAL 13.5 KD PROTEIN C45G9.7 IN CHROMOSOME 111.//9.2e-05:49:42//CAENORHABDITIS ELEGANS.//Q09506
 F-NT2RP1001665//REGB PROTEIN.//0.99:29:37//PSEUDOMONAS AERUGINOSA.//Q03381
 F-NT2RP2000001//SMALL PROLINE-RICH PROTEIN 2-1.//0.64:36:41//HOMO SAPIENS (HUMAN).//P35326
 F-NT2RP2000006//DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40).//1.7e-19:74:52//HOMO SAPIENS (HUMAN).//P25685
 F-NT2RP2000007//TROPOMYOSIN, FIBROBLAST AND EPITHELIAL MUSCLE-TYPE (TM36) (TME1) (TM1).//0.93:126:23//HOMO SAPIENS (HUMAN).//P06468
 F-NT2RP2000008//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN K031) (K1A0065) (HA0946) (FRAGMENT).//4.2e-35:156:54//HOMO SAPIENS (HUMAN).//Q06730
 F-NT2RP2000027//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.95:41:39//MACACA FASCICULARIS (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).//P50665
 F-NT2RP2000032//BAX PROTEIN, CYTOPLASMIC ISOFORM GAMMA.//1.0:35:34//HOMO SAPIENS (HUMAN).//Q07815
 F-NT2RP2000040//BASIC PROLINE-RICH PEPTIDE 1B-1.//0.0024:58:36//HOMO SAPIENS (HUMAN).//P04281
 F-NT2RP2000045//DNAJ PROTEIN.//1.1e-12:42:66//THERMUS AQUATICUS (S

【0658】

【表360】

UBSP. THERMOPHILUS). //Q56237
 F-NT2RP2000054//CONADOLIBERIN 111 PRECURSOR (CONADOTROPIN-RELEASEIN C HORMONE 111) (GHRH-111) (LH-RH 111) (LULIBERIN 111). //0.20:46:36
 //ONCORYNCHUS MASOU (CHERRY SALMON) (MASU SALMON). //P30973
 F-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP- EPSILON). //1.3e-18:45:100//MUS MUSCULUS (MOUSE). //P49446
 F-NT2RP2000067//HOMEBOX PROTEIN HOX-A5 (S12-B) (FRAGMENT). //0.71:44:40//SALMO SALAR (ATLANTIC SALMON). //P09637
 F-NT2RP2000070//INSULIN. //0.94:30:43//HYSTRIX CRISTATA (CRESTED PORCUPINE). //P01328
 F-NT2RP2000076//ETS-LIKE PROTEIN POINTED P1 (D-ETS-2). //0.0013:76:40//DROSOPHILA MELANOGASTER (FRUIT FLY). //P51022
 F-NT2RP2000077//U1 SMALL NUCLEAR RIBONUCLEOPROTEIN C (U1-C). //0.2:4:49:40//HOMO SAPIENS (HUMAN). //P09234
 F-NT2RP2000079//PLATELET FACTOR 4 (PF-4). //0.15:52:30//SUS SCROFA (PIG). //P30034
 F-NT2RP2000088//HYPOTHETICAL 13.6 KD PROTEIN IN SPT4-ROM1 INTERGENIC REGION. //1.0:36:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P53245
 F-NT2RP2000091//HYPOTHETICAL PROTEIN H10149 PRECURSOR. //0.22:38:47//HAEMOPHILUS INFLUENZAE. //P43953
 F-NT2RP2000097//VIRUS ATTACHMENT PROTEIN (O61R). //0.75:33:36//AFRICAN SWINE FEVER VIRUS (STRAIN BATHV) (ASFV). //P32510
 F-NT2RP2000098
 F-NT2RP2000108//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!! //2.4e-09:50:70//HOMO SAPIENS (HUMAN). //P39195
 F-NT2RP2000114//WISKOTT-ALDRICH SYNDROME PROTEIN (WASP). //0.024:5:2:44//HOMO SAPIENS (HUMAN). //P42768
 F-NT2RP2000120//5.8 KD PROTEIN IN HMC OPERON (ORF 4). //0.67:37:32//DESULFOVIBRIO VULGARIS (STRAIN HILDEBOROUGH). //P33391
 F-NT2RP2000126//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1). //1.5e-23:94:47//HOMO SAPIENS (HUMAN). //Q14646
 F-NT2RP2000133//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B5 3). //5.6e-10:82:39//HOMO SAPIENS (HUMAN). //Q15427
 F-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN). //6.7e-89:96:98//MUS MUSCULUS (MOUSE). //P35585
 F-NT2RP2000153//PEPTIDYLPROLYL ISOMERASE CYP-1 (EC 5.2.1.8) (PEPTIDYLPROLYL CIS-TRANS ISOMERASE) (CYCLOPHILIN) (PPIASE). //1.7e-05:13:6:33//BRUGIA MALAYI. //Q27450
 F-NT2RP2000157//ML02 PROTEIN. //2.7e-06:62:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //Q09329
 F-NT2RP2000161//DIS3 PROTEIN HOMOLOG. //2.7e-33:173:45//CAENORHABDITIS ELEGANS. //Q17632
 F-NT2RP2000173//HYPOTHETICAL 10.5 KD PROTEIN IN S00A-COMGA INTERGENIC REGION. //0.99:62:25//BACILLUS SUBTILIS. //P54499
 F-NT2RP2000175//MALE SPECIFIC SPERM PROTEIN MST840B. //0.19:41:43//DROSOPHILA MELANOGASTER (FRUIT FLY). //Q01643
 F-NT2RP2000183//DIHYDROXYRIMIDINASE RELATED PROTEIN-2 (DRP-2) (NEURAL SPECIFIC PROTEIN NSP60). //4.1e-19:114:44//BOS TAURUS (BOVINE). //Q02675
 F-NT2RP2000195//ATP SYNTHASE PROTEIN B (EC 3.6.1.34) (A6L). //0.99:30:33//MICROTUS PENNSYLVANICUS (MEADOW VOLE). //P24949
 F-NT2RP2000205//MERCURIC TRANSPORT PROTEIN PERIPLASMIC COMPONENT P RECURSOR (PERIPLASMIC MERCURY ION BINDING PROTEIN) (MERCURY SCAVENGER PROTEIN). //0.098:88:25//SHEWANELLA PUTREFACIENS (PSEUDOMONAS PUTREFACIENS). //Q54463
 F-NT2RP2000208//MALE SPECIFIC SPERM PROTEIN MST840D. //0.020:19:57//DROSOPHILA MELANOGASTER (FRUIT FLY). //Q01645
 F-NT2RP2000224//PUTATIVE CUTICLE COLLAGEN C09G5.4. //0.0058:159:32//CAENORHABDITIS ELEGANS. //Q09455
 F-NT2RP2000232//P55-C-FOS PROTO-ONCOGENE PROTEIN (FRAGMENT). //1.0:44:38//OVIS ARIES (SHEEP). //Q02761
 F-NT2RP2000233//GASTRIN/CHOLECYSTOKININ TYPE B RECEPTOR (CCK-B RECEPTOR) (CCK-8R). //0.34:53:43//CANIS FAMILIARIS (DOG). //P30552
 F-NT2RP2000239//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLOVE PRP2 5) (FRAGMENT). //0.019:69:33//RATTUS NORVEGICUS (RAT). //P10164
 F-NT2RP2000248//OVOMUCOID (FRAGMENT). //0.88:18:55//POLYPECTRON EM PHANUM (PALAWAN PEACOCK-PHEASANT). //P52250
 F-NT2RP2000257//PUTATIVE MITOCHONDRIAL CARRIER Y1006W. //6.4e-09:8:3:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P40556
 F-NT2RP2000258//MYOSIN II HEAVY CHAIN, NON MUSCLE. //0.081:217:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD). //P08799
 F-NT2RP2000270//!!!! ALU SUBFAMILY J WARNING ENTRY !!!! //2.4e-17:8:0:57//HOMO SAPIENS (HUMAN). //P39188
 F-NT2RP2000274//HYPOTHETICAL 5.8 KD PROTEIN. //0.082:22:45//CLOVER YELLOW MOSAIC VIRUS (CYMV). //P16485
 F-NT2RP2000283//HYPOTHETICAL 83.6 KD PROTEIN R0503.2 IN CHROMOSOME 111. //0.39:38:34//CAENORHABDITIS ELEGANS. //P34535
 F-NT2RP2000288
 F-NT2RP2000289//HYPOTHETICAL 9.4 KD PROTEIN IN RNPA-THDF INTERGENIC REGION. //0.40:38:42//ESCHERICHIA COLI. //P22847
 F-NT2RP2000297//ZINC FINGER PROTEIN 85 (ZINC FINGER PROTEIN HPF4) (MTF1). //2.3e-62:206:47//HOMO SAPIENS (HUMAN). //Q03923
 F-NT2RP2000298//CUTICLE COLLAGEN 12 PRECURSOR. //0.55:81:40//CAENORHABDITIS ELEGANS. //P20630
 F-NT2RP2000310//RUBREDOXIN (RD). //0.13:43:41//TREPONEMA PALLIDUM. //Q083956
 F-NT2RP2000327//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L). //1.0:4:6:30//GADUS MORHUA (ATLANTIC COD). //P15996
 F-NT2RP2000328//HYPOTHETICAL 86.6 KD PROTEIN IN PFK1-TDS4 INTERGENIC REGION. //2.0e-21:198:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P53313
 F-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3). //1.8e-91:155:92//BOS TAURUS (BOVINE). //P08760
 F-NT2RP2000337//PROTEIN A54. //0.75:48:35//VACCINIA VIRUS (STRAIN WR), AND VACCINIA VIRUS (STRAIN COPENHAGEN). //P21072
 F-NT2RP2000346//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN M YD116. //9.7e-13:114:42//MUS MUSCULUS (MOUSE). //P17564
 F-NT2RP2000369//CALTRIN (CALCIUM TRANSPORT INHIBITOR). //0.98:47:34//MUS MUSCULUS (MOUSE). //Q09098
 F-NT2RP2000412//SHORT NEUROTOXIN D PRECURSOR. //0.66:57:36//APISYRUS LAEVIS (OLIVE SEA SNAKE). //P19960
 F-NT2RP2000414//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F). //1.0e-27:96:67//HOMO SAPIENS (HUMAN). //P52597
 F-NT2RP2000420//ZINC FINGER PROTEIN 191. //0.16:47:38//HOMO SAPIENS (HUMAN). //Q14754
 F-NT2RP2000422//PUTATIVE PHOSPHOACETYLGLUCOSAMINE MUTASE (EC 5.4.2.3) (ACETYLGLUCOSAMINE PHOSPHOMUTASE) (N-ACETYLGLUCOSAMINE-PHOSPHATE MUTASE). //3.6e-19:148:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //Q09687
 F-NT2RP2000438//TUBULIN GAMMA CHAIN. //0.86:190:27//RETICULOMYXA F1 LOSA. //P54405
 F-NT2RP2000448//OXYSTEROL-BINDING PROTEIN. //3.7e-13:140:42//HOMO SAPIENS (HUMAN). //P22059
 F-NT2RP2000459//NEURONAL PROTEIN 3.1 (P311 PROTEIN). //1.0:45:35//HOMO SAPIENS (HUMAN). //Q16612
 F-NT2RP2000488//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! //0.062:2:5:68//HOMO SAPIENS (HUMAN). //P39194
 F-NT2RP2000503
 F-NT2RP2000510//TOXIN IV-5. //1.0:51:33//TITYUS BAHIANENSIS (BRAZILIAN SCORPION). //P56608
 F-NT2RP2000516//SLYX PROTEIN. //1.0:52:32//ESCHERICHIA COLI. //P30857
 F-NT2RP2000523//PHORBOLIN 1 (FRAGMENTS). //1.4e-06:36:47//HOMO SAPIENS (HUMAN). //P31941
 F-NT2RP2000603//ALPHA/BETA-GLIADIN PRECURSOR (PROLAMIN) (CLASS A-11). //0.93:119:26//TRITICUM AESTIVUM (WHEAT). //P04723
 F-NT2RP2000617//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE). //0.0:56:16:62//OVIS ARIES (SHEEP), AND CAPRA HIRCUS (GOAT). //P04102
 F-NT2RP2000634//NEDD-4 PROTEIN (EC 6.3.2.-) (KIAA0093) (FRAGMENT). //1.8e-05:128:28//HOMO SAPIENS (HUMAN). //P46934
 F-NT2RP2000644//HYPOTHETICAL PROTEIN H11566 PRECURSOR. //0.85:48:39//HAEMOPHILUS INFLUENZAE. //P44257
 F-NT2RP2000656//EARLY GROWTH RESPONSE PROTEIN 1 (EGR-1) (NERVE GROWTH FACTOR-INDUCED PROTEIN A) (NGF1-A). //1.0:111:24//RATTUS NORVEGICUS (RAT). //P08154
 F-NT2RP2000658//URONATE ISOMERASE (EC 5.3.1.12) (GLUCURONATE ISOMERASE) (URONIC ISOMERASE). //0.49:79:31//ESCHERICHIA COLI. //P42607
 F-NT2RP2000668//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (45 KD-MEROZOITE SURFACE ANTIGEN). //0.020:115:30//PLASMODIUM FALCIPARUM (ISOLATE 3D7). //P50498
 F-NT2RP2000678//!!!! ALU SUBFAMILY J WARNING ENTRY !!!! //0.00085:3:8:68//HOMO SAPIENS (HUMAN). //P39188
 F-NT2RP2000704//!!!! ALU SUBFAMILY J WARNING ENTRY !!!! //2.2e-17:5:5:74//HOMO SAPIENS (HUMAN). //P39188
 F-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE) (ASPRS). //8.9e-47:106:59//TREPONEMA PALLIDUM. //Q083950
 F-NT2RP2000715
 F-NT2RP2000731//CONIDIATION-SPECIFIC PROTEIN 10. //0.094:31:41//NEUROSPORA CRASSA. //P10713
 F-NT2RP2000758//!!!! ALU SUBFAMILY J WARNING ENTRY !!!! //0.00027:3:1:74//HOMO SAPIENS (HUMAN). //P39188
 F-NT2RP2000764//NIFS PROTEIN. //2.7e-27:175:47//ANABAENA SP. (STRAIN PCC 7120). //P12623
 F-NT2RP2000809//HYPOTHETICAL PROTEIN MG381 HOMOLOG. //0.91:85:25//MYCOPLASMA PNEUMONIAE. //P75219

【0659】

【表361】

F-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).
//2.8e-07:133:31//MUS MUSCULUS (MOUSE).//Q99104
F-NT2RP2000814//40S RIBOSOMAL PROTEIN S27A.//0.93:44:38//LYCOPERSI-
CON ESCULENTUM (TOMATO), AND SOLANUM TUBEROSUM (POTATO).//P27083
F-NT2RP2000816//HYPOTHETICAL 88.4 KD PROTEIN B0464.7 IN CHROMOSOME
111.//3.3e-21:123:39//CAENORHABDITIS ELEGANS.//Q03565
F-NT2RP2000819//TROPOMYOSIN 5, CYTOSKELETAL TYPE.//1.0:71:30//MUS
MUSCULUS (MOUSE).//P21107
F-NT2RP2000841//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//0.00
11:133:26//MUS MUSCULUS (MOUSE).//P27671
F-NT2RP2000842//LYSOPHOSPHATIDIC ACID RECEPTOR (EDG-2).//6.4e-13:2
2:95//HOMO SAPIENS (HUMAN).//Q92633
F-NT2RP2000845//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR (MSTI).//0.9
2:24:41//MEDICAGO SCUTELLATA (SNAIL MEDIC).//P80321
F-NT2RP2000863//N-MYC PROTO-ONCOGENE PROTEIN.//0.010:148:27//XENOP-
US LAEVIS (AFRICAN CLAWED FROG).//P24793
F-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2.//4.0
e-100:199:94//HOMO SAPIENS (HUMAN).//Q60841
F-NT2RP2000892//PROCOLLAGEN ALPHA 1(I1) CHAIN PRECURSOR [CONTAINS:
CHONDROCALCIN].//0.43:45:44//MUS MUSCULUS (MOUSE).//P28481
F-NT2RP2000931//MATRIN 3.//2.8e-46:104:92//RATTUS NORVEGICUS (RAT
).//P43244
F-NT2RP2000932//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DE-
PENDENT RNAASE) (RNASE L) (RIBONUCLEASE 4) (FRAGMENT).//3.9e-07:11
3:31//MUS MUSCULUS (MOUSE).//Q05921
F-NT2RP2000938//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSH
111D).//0.026:59:45//RATTUS NORVEGICUS (RAT).//Q01956
F-NT2RP2000943//HYPOTHETICAL PROTEIN KIA0079 (HA3543).//5.9e-18:1
61:42//HOMO SAPIENS (HUMAN).//P53992
F-NT2RP2000965//INNER CENTROMERE PROTEIN (INCENP).//0.062:156:25//
GALLUS GALLUS (CHICKEN).//P53352
F-NT2RP2000970//EC PROTEIN HOMOLOG.//1.0:50:30//ARABIDOPSIS THALIA
NA (MOUSE-EAR CRESS).//P93746
F-NT2RP2000985//HYPOTHETICAL 96.8 KD PROTEIN IN SIS2-MTD1 INTERGEN-
IC REGION.//2.5e-06:53:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
T).//P36159
F-NT2RP2000987//INSECT TOXIN 4 (INSECT TOXIN AAH IT4).//1.0:32:34//
ANDROCTONUS AUSTRALIS HECTOR (SAHARA SCORPION).//P21150
F-NT2RP2001036//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.2e-33:
65:81//HOMO SAPIENS (HUMAN).//P39193
F-NT2RP2001044//HIRUSTASIN.//0.97:15:66//HIRUDO MEDICINALIS (MEDIC-
INAL LEECH).//P80302
F-NT2RP2001056//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.0e-24:
85:65//HOMO SAPIENS (HUMAN).//P39194
F-NT2RP2001065//BOWMAN-BIRK TYPE SEED TRYPSIN AND CHYMOTRYPSIN INH-
IBITOR (BTCI).//0.41:50:32//VIGNA UNGUICULATA (COWPEA).//P17734
F-NT2RP2001070//PROBABLE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.
4.3.5) (PNP/PMP OXIDASE) (FPPA PROTEIN).//6.2e-18:64:48//MYXOCOCCU
S XANTHUS.//P21159
F-NT2RP2001081//SYNAPTOTAGMIN IV.//7.8e-16:94:46//RATTUS NORVEGICU
S (RAT).//P50232
F-NT2RP2001094//METALLOTHIONEIN-I (MT-I).//1.0:24:33//RATTUS NORVE-
GICUS (RAT).//P02803
F-NT2RP2001119//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//7.5e-11:
61:63//HOMO SAPIENS (HUMAN).//P39195
F-NT2RP2001127//XEL69 PROTEIN (SMCX PROTEIN) (FRAGMENTS).//1.0e-4
7:155:58//MUS MUSCULUS (MOUSE).//P41230
F-NT2RP2001137//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS).//0.10:68:
39//BOS TAURUS (BOVINE).//P25508
F-NT2RP2001149//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-13:8
1:59//HOMO SAPIENS (HUMAN).//P39188
F-NT2RP2001168//PROTEIN KINASE C SUBSTRATE 80 KD PROTEIN (FRAGMENT
S).//0.0071:77:33//RATTUS NORVEGICUS (RAT).//P20468
F-NT2RP2001173//CYTOSKELETON-ASSOCIATED PROTEIN CKAP1 (TUBULIN FOL-
DING COFACTOR B).//1.0:36:41//HOMO SAPIENS (HUMAN).//Q99426
F-NT2RP2001174//ZINC FINGER PROTEIN 137.//7.2e-11:65:43//HOMO SAPI-
ENS (HUMAN).//P52743
F-NT2RP2001196//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 (EC 1.6.5.
3).//1.0:95:26//CAPRA HIRCUS (GOAT).//Q36346
F-NT2RP2001218//HYPOTHETICAL 59.2 KD PROTEIN IN M0B1-SGA1 INTERGEN-
IC REGION.//0.00024:80:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
T).//P40486
F-NT2RP2001226//RABPHILIN-3A (FRAGMENT).//4.6e-05:121:39//MUS MUSC-
ULUS (MOUSE).//P47708
F-NT2RP2001233//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.2e-61:15
3:56//HOMO SAPIENS (HUMAN).//P16415
F-NT2RP2001245//SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN).//
4.9e-05:230:21//HOMO SAPIENS (HUMAN).//Q15431
F-NT2RP2001268//HOMEOBOX PROTEIN CEH-32.//0.23:159:25//CAENORHABDI-
TIS ELEGANS.//Q23175

F-NT2RP2001277
F-NT2RP2001290//BETA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-BETA) (S
NAP-ALPHA HOMOLOG) (BRAIN PROTEIN 147) (FRAGMENT).//1.0e-86:131:97
//MUS MUSCULUS (MOUSE).//P28663
F-NT2RP2001295
F-NT2RP2001312//N-ACETYLGLUCOSAMINE-6-SULFATASE PRECURSOR (EC 3.1.
6.14) (G6S) (GLUCOSAMINE-6-SULFATASE).//0.64:80:33//CAPRA HIRCUS
(GOAT).//P50426
F-NT2RP2001327//TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 1, EN-
DOTHelial (B12 PROTEIN).//1.0e-36:118:65//HOMO SAPIENS (HUMAN).//Q
13829
F-NT2RP2001328//PROBABLE E5 PROTEIN.//1.0:46:41//HUMAN PAPILLOMAVI-
RUS TYPE 33.//P06426
F-NT2RP2001347//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//4.5e-19:
66:62//HOMO SAPIENS (HUMAN).//P39193
F-NT2RP2001366//SPERM-SPECIFIC PROTEIN PH1-1.//0.66:55:32//MYTILUS
EDULIS (BLUE MUSSEL).//Q04621
F-NT2RP2001378//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN KV3.3 (KSH
111D) (FRAGMENT).//0.060:78:33//HOMO SAPIENS (HUMAN).//Q14003
F-NT2RP2001381//26S PROTEASE REGULATORY SUBUNIT 8 (SUG1 HOMOLOG)
(XSUG1).//1.0:167:26//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P4647
0
F-NT2RP2001392//KERATIN, HIGH-SULFUR MATRIX PROTEIN, 111A3.//0.008
0:82:32//OVIS ARIES (SHEEP).//P02441
F-NT2RP2001394//POLYHOMEOCTIC-PROXIMAL CHROMATIN PROTEIN.//0.024:3
9:53//DROSOPHILA MELANOGASTER (FRUIT FLY).//P39769
F-NT2RP2001397//G2/MITOTIC-SPECIFIC CYCLIN B2.//1.4e-46:125:78//ME-
SOCRICETUS AURATUS (GOLDEN HAMSTER).//P37883
F-NT2RP2001420//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP
3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE 18-6: PEPTIDE P-H].//0.00
018:113:38//HOMO SAPIENS (HUMAN).//P04280
F-NT2RP2001423//HYPOTHETICAL 9.4 KD PROTEIN IN GP31-CD INTERGENIC
REGION (ORF A).//0.90:23:43//BACTERIOPHAGE T4.//P17307
F-NT2RP2001427//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.2e-11:3
8:68//HOMO SAPIENS (HUMAN).//P39188
F-NT2RP2001436//DYNEIN LIGHT INTERMEDIATE CHAIN 2, CYTOSOLIC (LIC3
3/55) (LIC-2).//0.25:124:28//RATTUS NORVEGICUS (RAT).//Q62698
F-NT2RP2001440//14-3-3 PROTEIN GAMMA (PROTEIN KINASE C INHIBITOR P
ROTEIN-1) (KCIP-1).//4.8e-62:145:90//RATTUS NORVEGICUS (RAT).//P35
214
F-NT2RP2001445
F-NT2RP2001449//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 1
00 KD SUBUNIT (CPSF 100 KD SUBUNIT).//9.5e-118:226:95//BOS TAURUS
(BOVINE).//Q10568
F-NT2RP2001450
F-NT2RP2001467//SHORT NEUROTOXIN 1 (TOXIN V-11-1).//1.0:25:40//BLU-
GARUS FASCIATUS (BANDED KRAIT).//P10808
F-NT2RP2001506
F-NT2RP2001511//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOM
E 111.//0.49:124:29//CAENORHABDITIS ELEGANS.//P34681
F-NT2RP2001520//VITAMIN D-DEPENDENT CALCIUM-BINDING PROTEIN, INTES-
TINAL (CABP) (CALBINDIN D9K).//0.035:71:33//HOMO SAPIENS (HUMAN).//
P29377
F-NT2RP2001526
F-NT2RP2001536//METALLOTHIONEIN-I (MT-I).//1.0:19:42//COLUMBA LIVI-
A (DOMESTIC PIGEON).//P15786
F-NT2RP2001560//CUTICLE COLLAGEN 12 PRECURSOR.//0.0018:144:35//CAE-
NORHABDITIS ELEGANS.//P20630
F-NT2RP2001569//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.7e-31:
102:67//HOMO SAPIENS (HUMAN).//P39194
F-NT2RP2001576//SMP3 PROTEIN.//0.00016:75:36//SACCHAROMYCES CEREVI-
SIAE (BAKER'S YEAST).//Q04174
F-NT2RP2001581//TRANSMEMBRANE PROTEIN SEX PRECURSOR.//0.040:46:36//
HOMO SAPIENS (HUMAN).//P51805
F-NT2RP2001597//PROBABLE E4 PROTEIN.//0.00042:113:34//HUMAN PAPILL-
OMAVIRUS TYPE 5.//P06924
F-NT2RP2001601
F-NT2RP2001613//HOMEOBOX PROTEIN SAX-1 (CHOX-3) (FRAGMENT).//0.14:
59:32//GALLUS GALLUS (CHICKEN).//P19601
F-NT2RP2001628//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.056:
140:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
F-NT2RP2001634//ALPHA-CATENIN.//7.1e-12:152:35//DROSOPHILA MELANO-
GASTER (FRUIT FLY).//P35220
F-NT2RP2001660//HYPOTHETICAL 80.4 KD PROTEIN IN SMC3-MRPL8 INTERGE-
NIC REGION.//0.43:119:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST
).//P40358
F-NT2RP2001663//ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE
HYDRO-LYASE) (NON- NEURAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATA-
SE).//1.2e-26:126:56//HOMO SAPIENS (HUMAN).//P06733
F-NT2RP2001675//HYPOTHETICAL 107.7 KD PROTEIN IN RP50 5' REGION (OR

【0660】

【表362】

F1) //0.25:148:25//CAMPYLOBACTER JEJUNI.//Q46089
 F-NT2RP2001677//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP2 S) (FRAGMENT) //0.010:101:31//RATTUS NORVEGICUS (RAT).//P10164
 F-NT2RP2001678//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.6e-18:8 3:61//HOMO SAPIENS (HUMAN).//P39188
 F-NT2RP2001699//PROTEIN C14.//0.98:51:31//VACCINIA VIRUS (STRAIN C OPENHAGEN).//P21045
 F-NT2RP2001720//MERZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2) (ALL ELIC FORM 1).//0.16:145:30//PLASMODIUM FALCIPARUM (ISOLATE CAMP / MALAYSIA).//Q99317
 F-NT2RP2001721//MALE-SPECIFIC LETHAL-2 PROTEIN.//0.00090:48:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//P50534
 F-NT2RP2001740//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.50:43:25//BOS TAURUS (BOVINE).//P20072
 F-NT2RP2001748//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.77:111:28//HOMO SAPIENS (HUMAN).//P10162
 F-NT2RP2001762
 F-NT2RP2001813//PHOTOSYSTEM I REACTION CENTRE SUBUNIT VIII (PSI-1) //1.0:22:40//PICEA ABIES (NORWAY SPRUCE) (PICEA EXCELSA).//Q4704 0
 F-NT2RP2001839//SCY1 PROTEIN.//6.0e-17:204:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53009
 F-NT2RP2001861//DISK21 PROTEIN (FRAGMENT).//0.31:56:39//MUS MUSCULUS (MOUSE).//Q61466
 F-NT2RP2001869//CORNEODESMOSIN (S PROTEIN) (FRAGMENT).//0.97:78:30 //SUS SCROFA (PIG).//Q19084
 F-NT2RP2001876//ALLOGRAFT INFLAMMATORY FACTOR-1 (AIF-1) (IONIZED CALCIUM BINDING ADAPTER MOLECULE 1).//3.5e-36:106:66//HOMO SAPIENS (HUMAN).//P55008
 F-NT2RP2001883//CATHEPSIN L (EC 3.4.22.15).//0.95:29:41//OVIS ARIES (SHEEP).//Q10991
 F-NT2RP2001898//TYPE II INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE PRECURSOR (EC 3.1.3.56) (SPYASE) (FRAGMENT).//1.6e-84:185:88//HOMO SAPIENS (HUMAN).//P32019
 F-NT2RP2001900//ACTIN-LIKE PROTEIN ARPS.//1.1e-17:180:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53946
 F-NT2RP2001907//HYPHAL WALL PROTEIN 1 (CELL ELONGATION PROTEIN 2).//0.13:108:27//CANDIDA ALBICANS (YEAST).//Q46593
 F-NT2RP2001926//HYPOTHETICAL 7.6 KD PROTEIN YCF33.//0.55:57:26//CYANOPHORA PARADOXA.//P48273
 F-NT2RP2001936
 F-NT2RP2001943//HYPOTHETICAL 57.7 KD PROTEIN IN AIP1-CTF13 INTERGENIC REGION.//1.8e-13:208:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04305
 F-NT2RP2001946//HYPOTHETICAL 13.0 KD PROTEIN IN ALGR3 3' REGION.//0.59:76:28//PSEUDOMONAS AERUGINOSA.//P21485
 F-NT2RP2001947//ZINC FINGER PROTEIN DAN (M03).//0.53:68:29//RATTUS NORVEGICUS (RAT).//Q06880
 F-NT2RP2001969//CHLOROPLAST 30S RIBOSOMAL PROTEIN S18.//0.0015:52:34//CHLORELLA VULGARIS.//P56353
 F-NT2RP2001976//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//9.5e-07:201:22//MUS MUSCULUS (MOUSE).//Q99104
 F-NT2RP2001985//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//0.016:90:32//MUS MUSCULUS (MOUSE).//P05142
 F-NT2RP2001991//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73.//8.0e-14:47:76//RATTUS NORVEGICUS (RAT).//Q08469
 F-NT2RP2002025//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (N R-CAM) (BRAVO).//2.9e-30:211:42//GALLUS GALLUS (CHICKEN).//P35331
 F-NT2RP2002032//FLOCCULANT-ACTIVE PROTEINS MO2.1 AND MO2.2.//0.23:20:40//MORINGA OLEIFERA (HORSE RADISH TREE) (MORINGA PTERYGOSPERMA).//P24303
 F-NT2RP2002033//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.88:27:62//HOMO SAPIENS (HUMAN).//P39193
 F-NT2RP2002041
 F-NT2RP2002046//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN S MS1) (PROTEIN KINASE A INTERFERENCE PROTEIN).//1.0:85:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36027
 F-NT2RP2002047
 F-NT2RP2002058//DOM34 INTERACTING PROTEIN 2.//9.4e-25:165:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12220
 F-NT2RP2002066//TIGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN 1).//5.7e-12:108:41//HOMO SAPIENS (HUMAN).//Q07157
 F-NT2RP2002070//CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) (FRAGMENT).//0.88:28:50//ASTERINA PECTINIFERA (STARFISH).//P11958
 F-NT2RP2002076//TRP-ASP REPEATS CONTAINING PROTEIN RBA-2.//0.0031:124:27//CAENORHABDITIS ELEGANS.//P90916
 F-NT2RP2002078//KERATIN, GLYCINE/TYROSINE-RICH OF HAIR.//0.82:30:4 0//OVIS ARIES (SHEEP).//Q02958
 F-NT2RP2002079//OUTER DENSE FIBER PROTEIN.//0.34:41:39//HOMO SAPIENS (HUMAN).//Q14990
 F-NT2RP2002099//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U).//5.2e-08:81:48//HOMO SAPIENS (HUMAN).//Q00839
 F-NT2RP2002105//COLLAGEN 1(X) CHAIN PRECURSOR.//0.0012:100:34//BOS TAURUS (BOVINE).//P23206
 F-NT2RP2002124//EARLY GROWTH RESPONSE PROTEIN 1 (EGR-1) (KROX24) (TRANSCRIPTION FACTOR ETR103) (ZINC FINGER PROTEIN 225) (AT225).//0.74:72:31//HOMO SAPIENS (HUMAN).//P18146
 F-NT2RP2002137//NEUROTOXIN B-II.//1.0:27:44//CEREBRATULUS LACTEUS (MILKY RIBBON WORM).//P01526
 F-NT2RP2002154//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (ICE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-34 GALACTOSIDE-BINDING LECTIN).//0.0029:112:34//MUS MUSCULUS (MOUSE).//P16110
 F-NT2RP2002172
 F-NT2RP2002185//UBIQUITIN-LIKE PROTEIN DSK2.//1.8e-07:87:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48510
 F-NT2RP2002192
 F-NT2RP2002193//CUTICLE COLLAGEN 40.//0.0062:70:37//CAENORHABDITIS ELEGANS.//P34804
 F-NT2RP2002208//PEROXISOME ASSEMBLY PROTEIN PEX10 (PEROXIN-10).//0.00011:45:40//HOMO SAPIENS (HUMAN).//Q06063
 F-NT2RP2002219
 F-NT2RP2002231//V-TYPE SODIUM ATP SYNTHASE SUBUNIT E (EC 3.6.1.34) (NA(+)-TRANSLLOCATING ATPASE SUBUNIT E).//1.0:68:32//ENTEROCOCCUS HIRAE.//P43436
 F-NT2RP2002235//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP34.5).//0.0022:66:45//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN CVG-2).//P37318
 F-NT2RP2002252//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT).//0.071:110:31//CRICETULUS GRAISEUS (CHINESE HAMSTER).//P11414
 F-NT2RP2002256//CYTOCHROME P450 26 (EC 1.14.-.-) (RETINOIC ACID-METABOLIZING CYTOCHROME) (P450RA1) (RETINOIC ACID 4-HYDROXYLASE).//3.1e-31:75:84//MUS MUSCULUS (MOUSE).//Q55127
 F-NT2RP2002259//L-MYC-1 PROTO-ONCOGENE PROTEIN.//1.9e-17:41:90//HOMO SAPIENS (HUMAN).//P12524
 F-NT2RP2002270//HYPOTHETICAL 26.0 KD PROTEIN IN CYB5-LEU4 INTERGENIC REGION.//2.1e-27:164:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53930
 F-NT2RP2002292//IMMEDIATE-EARLY PROTEIN RSP40.//0.018:107:23//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P24827
 F-NT2RP2002312//PHOSPHATIDATE CYTIDYLYLTRANSFERASE (EC 2.7.7.41) (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP-PHOSPHATIDATE CYTIDYLYLTRANSFERASE) (CDP-DAG SYNTHASE).//1.4e-52:174:55//HOMO SAPIENS (HUMAN).//Q92903
 F-NT2RP2002316//HISTONE H1.C6/H1.C9.//1.0:40:40//TRYPANOSOMA CRUZI.//P40269
 F-NT2RP2002325//PEROXISOMAL MEMBRANE PROTEIN PMP30A (PMP31) (PEROXIN-11A).//2.2e-06:145:26//CANDIDA BOIDINI (YEAST).//Q00316
 F-NT2RP2002333//HYPOTHETICAL 39.1 KD PROTEIN IN RNBP-SOHA INTERGENIC REGION (ORF 3).//0.30:86:32//ESCHERICHIA COLI.//P23524
 F-NT2RP2002373//SYNAPSINS IA AND IB.//0.080:145:31//BOS TAURUS (BOVINE).//P17599
 F-NT2RP2002385//ENV POLYPROTEIN PRECURSOR (COAT POLYPROTEIN) [CONTAINS: KNOB PROTEIN GP70; SPIKE PROTEIN P15E; R PROTEIN].//0.021:6 6:28//MINK CELL FOCUS-FORMING MURINE LEUKEMIA VIRUS (ISOLATE CI-3).//P03388
 F-NT2RP2002394
 F-NT2RP2002408//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.00030:10 7:37//BOS TAURUS (BOVINE).//P02453
 F-NT2RP2002426
 F-NT2RP2002439//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//0.00032:79:32//PLASMODIUM BERGHEI (STRAIN ANKA).//P23093
 F-NT2RP2002442//HESA PROTEIN.//6.0e-16:163:30//PLECTONEMA BORYANUM.//P46037
 F-NT2RP2002457
 F-NT2RP2002464//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME 1.//9.3e-18:165:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10264
 F-NT2RP2002475//CYSTEINE-RICH HEART PROTEIN (HCRHP).//0.91:45:35//HOMO SAPIENS (HUMAN).//P50238
 F-NT2RP2002479//ATP-BINDING CASSETTE TRANSPORTER 7 PRECURSOR (ABC TRANSPORTER 7 PROTEIN).//6.8e-96:186:94//HOMO SAPIENS (HUMAN).//Q7 5027
 F-NT2RP2002498//HYPOTHETICAL MERCURIC RESISTANCE PROTEIN MERC.//0.65:37:45//PSEUDOMONAS AERUGINOSA.//P04139
 F-NT2RP2002503//ZINC FINGER PROTEIN 45 (BRC1744).//1.3e-31:124:59/

【0661】

【表363】

/HOMO SAPIENS (HUMAN).//Q02386
 F-NT2RP2002504//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN N UP155) (155 KD NUCLEOPORIN) (P140).//1.2e-123:240:92//RATTUS NORVEGICUS (RAT).//P37199
 F-NT2RP2002520//ACIDIC PROLINE-RICH PROTEIN HP43A PRECURSOR.//0.9 4:83:28//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//P06680
 F-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//4.0e-10:194:23//CAENORHABDITIS ELEGANS.//Q11073
 F-NT2RP2002546
 F-NT2RP2002549//G2/MITOTIC-SPECIFIC CYCLIN C13-1 (A-LIKE CYCLIN) (FRAGMENT).//0.98:65:30//DAUCUS CAROTA (CARROT).//P25010
 F-NT2RP2002591//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.6e-19:60:61//HOMO SAPIENS (HUMAN).//P51523
 F-NT2RP2002595//ANNEXIN VII (SYNEXIN).//1.2e-15:121:49//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q92125
 F-NT2RP2002606//PROTEIN TRANSPORT PROTEIN SEC2.//0.00034:98:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P17065
 F-NT2RP2002609//HYPOTHETICAL 52.0 KD PROTEIN IN CLB6-SPT6 INTERGENIC REGION.//0.00022:79:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53264
 F-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 1 (EC 2.1.1.-).//6.2e-37:180:44//RATTUS NORVEGICUS (RAT).//Q63009
 F-NT2RP2002621//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.98:37:35//LEMUR CATTI (RING-TAILED LEMUR).//Q34879
 F-NT2RP2002643//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACTOR ICP34.5).//0.042:77:32//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN M CH-10).//P37319
 F-NT2RP2002672//PROTEIN Q300.//0.0018:41:43//MUS MUSCULUS (MOUSE).//Q02722
 F-NT2RP2002701//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME 1.//3.6e-17:100:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701
 F-NT2RP2002706//IMMEDIATE-EARLY PROTEIN IE180.//0.00027:139:33//PS EUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479
 F-NT2RP2002710//SH3-BINDING PROTEIN 3BP-1.//6.9e-09:96:40//MUS MUSCULUS (MOUSE).//P55194
 F-NT2RP2002727//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN).//3.6e-20:160:36//RATTUS NORVEGICUS (RAT).//P49816
 F-NT2RP2002736
 F-NT2RP2002740
 F-NT2RP2002741//RHO1 GTP-GTP EXCHANGE PROTEIN 2.//2.0e-07:178:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P51862
 F-NT2RP2002750//ALU SUBFAMILY S02 WARNING ENTRY !!!//1.6e-09:43:72//HOMO SAPIENS (HUMAN).//P39191
 F-NT2RP2002752//LOW CALCIUM RESPONSE LOCUS PROTEIN T.//0.95:33:39//YERSINIA PSEUDOTUBERCULOSIS.//Q00932
 F-NT2RP2002753//ENDOGLUCANASE EG-1 PRECURSOR (EC 3.2.1.4) (ENDO-1, 4-BETA-GLUCANASE) (CELLULOSE).//0.71:78:33//TRICHOPTERIS LONGIBRACH IATUM.//Q12714
 F-NT2RP2002769//50 KD SPICULE MATRIX PROTEIN PRECURSOR.//0.44:76:32//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).//P11994
 F-NT2RP2002778
 F-NT2RP2002800//CRABBIN.//0.99:20:50//CRABE ABYSSINICA (ABYSSINIAN CRAB).//P01542
 F-NT2RP2002839//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP 7) [CONTAINS: BASIC PEPTIDE P-F] (FRAGMENT).//0.010:87:31//HOMO SAPIENS (HUMAN).//P02812
 F-NT2RP2002857//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP 3).//0.00018:57:45//RATTUS NORVEGICUS (RAT).//P04474
 F-NT2RP2002862//HYPOTHETICAL 27.1 KD PROTEIN UFD4-CAP1 INTERGENIC REGION.//7.2e-27:140:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33201
 F-NT2RP2002880//DNA REPAIR PROTEIN RAD32.//0.83:67:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09683
 F-NT2RP2002891//HOMEOBOX PROTEIN DLX-2 (DLX-5) (FRAGMENT).//0.99:70:24//RATTUS NORVEGICUS (RAT).//Q64204
 F-NT2RP2002925//ALPHA-10 ADRENERGIC RECEPTOR (ALPHA 10-ADRENERGIC RECEPTOR) (ALPHA-1A ADRENERGIC RECEPTOR).//0.31:48:43//HOMO SAPIENS (HUMAN).//P25100
 F-NT2RP2002928//CELL DIVISION CONTROL PROTEIN 40.//2.8e-26:142:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P04968
 F-NT2RP2002929//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME 11.//2.0e-31:186:35//CAENORHABDITIS ELEGANS.//Q18964
 F-NT2RP2002939//ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-INHIBITABLE ADENYLATE CYCLASE).//0.0022:98:39//CANIS FAMILIARIS (DOG).//P30803
 F-NT2RP2002954//U2 SMALL NUCLEAR RIBONUCLEOPROTEIN A' (U2 SNRNP-A').//0.0019:107:30//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P4333

【0662】

【表364】

MELANOGASTER (FRUIT FLY). //P17886
 F-NT2RP2003329//HYPOTHETICAL 54.9 KD PROTEIN CD2F5.7 IN CHROMOSOME 111. //5.8e-57:186:55//CAENORHABDITIS ELEGANS. //P34284
 F-NT2RP2003339//SHORT NEUROTOXIN 1 (NEUROTOXIN ALPHA). //0.98:11:72 //DENDROASPIS POLYLEPIS POLYLEPIS (BLACK MAMBA). //P01416
 F-NT2RP2003347//60S RIBOSOMAL PROTEIN L38. //0.83:42:33//OSTERTAGIA OSTERTAGI. //Q61570
 F-NT2RP2003367//SYNERGISTIC-TYPE VENOM PROTEIN C9S3, CHAIN 1. //1.0:37:35//DENDROASPIS ANGSTICEPS (EASTERN GREEN MAMBA). //P01408
 F-NT2RP2003391//NRMA TRANSPORT REGULATOR NTR10. //3.3e-11:229:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //Q99189
 F-NT2RP2003393//PROTOCHLOROPHYLLIDE REDUCTASE CHLB SUBUNIT (EC 1.3.1.33) (NADPH- PROTOCHLOROPHYLLIDE OXIDOREDUCTASE CHLB SUBUNIT) (FRAGMENT). //0.94:29:34//ARAUCARIA HETEROPHYLLA. //P37843
 F-NT2RP2003394
 F-NT2RP2003401//60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN). //0.95:125:28//THERMUS AQUATICUS (SUBSP. THERMOPHILUS). //P45746
 F-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT. //9.8e-78:178:84//RATTUS NORVEGICUS (RAT). //P38378
 F-NT2RP2003445
 F-NT2RP2003446//HYPOTHETICAL PROTEIN E-115. //0.00030:106:33//HUMAN ADENOVIRUS TYPE 2. //P03290
 F-NT2RP2003456//PHOTOSYSTEM II REACTION CENTRE M PROTEIN. //1.0:27:51//MARCHANTIA POLYMORPHA (LIVERWORT). //P12168
 F-NT2RP2003466//LIMOLEOYL-COA DESATURASE (EC 1.14.99.25) (DELTA(6)-DESATURASE). //6.7e-06:108:32//SYNCHOCYSTIS SP. (STRAIN PCC 6803). //Q08871
 F-NT2RP2003480//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2) (CBF-2) (T-14-6). //7.2e-15:38:50//CALLUS GALLUS (CHICKEN). //Q98937
 F-NT2RP2003499//SE5 ANTIGEN. //0.090:114:32//RATTUS NORVEGICUS (RAT). //Q63003
 F-NT2RP2003506//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR). //2.0e-11:91:43//SUS SCROFA (PIG). //P04175
 F-NT2RP2003511//PARAMYOSIN, SHORT FORM (MINIPARAMYOSIN). //0.0020:108:25//DROSOPHILA MELANOGASTER (FRUIT FLY). //P35416
 F-NT2RP2003513//PTB-ASSOCIATED SPLICING FACTOR (PSF). //1.2e-05:96:36//HOMO SAPIENS (HUMAN). //P23246
 F-NT2RP2003517//HYPOTHETICAL 12.9 KD PROTEIN CY49.27. //0.0059:22:31//MYCOBACTERIUM TUBERCULOSIS. //Q10696
 F-NT2RP2003522//HYPOTHETICAL 10.0 KD PROTEIN. //1.0:65:30//THERMOPLOTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1). //P19283
 F-NT2RP2003533//LINE-1 REVERSE TRANSCRIPTASE HOMOLOGY. //8.7e-18:94:54//HOMO SAPIENS (HUMAN). //P08547
 F-NT2RP2003543//SYNAPSINS IA AND IB. //0.045:101:35//RATTUS NORVEGICUS (RAT). //P09951
 F-NT2RP2003559//ITBA2 PROTEIN (DXS9879E). //0.98:37:37//HOMO SAPIENS (HUMAN). //Q14657
 F-NT2RP2003564//52 KD RD PROTEIN (SJOEGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)). //6.4e-35:175:44//HOMO SAPIENS (HUMAN). //P19474
 F-NT2RP2003567//HYPOTHETICAL 11.2 KD PROTEIN T18D3.7 IN CHROMOSOME X. //0.72:82:34//CAENORHABDITIS ELEGANS. //Q22544
 F-NT2RP2003581//HOMEOBOX PROTEIN OTX1. //0.90:61:37//MUS MUSCULUS (MOUSE). //P80205
 F-NT2RP2003596//ELONGATION FACTOR P (EF-P). //0.83:61:32//MYOPLASMA GENITALIUM. //P47272
 F-NT2RP2003604//ALPHA-CATENIN. //1.5e-11:152:33//DROSOPHILA MELANOGASTER (FRUIT FLY). //P35220
 F-NT2RP2003629//PHOSPHOLIPASE A2 ALPHA (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE 2-ACYLHYDROLASE). //0.97:85:27//CROTALUS ADAMANTEUS (EASTERN DIAMONDBACK RATTLESNAKE). //P00623
 F-NT2RP2003643//ACYLNEURAMINATE CYTIDYLTRANSFERASE (EC 2.7.7.43) (CMP-N- ACETYLNEURAMINIC ACID SYNTHETASE) (CMP-NEURON SYNTHETASE) (CMP-SIALIC ACID SYNTHETASE). //3.9e-12:84:40//NEISSERIA MENINGITIS DIS. //Q57385
 F-NT2RP2003668//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//5.0e-33:74:81//HOMO SAPIENS (HUMAN). //P39195
 F-NT2RP2003687//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//5.7e-05:40:67//HOMO SAPIENS (HUMAN). //P39188
 F-NT2RP2003691//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.5e-37:56:67//HOMO SAPIENS (HUMAN). //P39194
 F-NT2RP2003702//HYPOTHETICAL OXIDOREDUCTASE IN INLA 5' REGION (EC 1.-.-) (ORFA). //1.3e-07:98:37//LISTERIA MONOCYTOGENES. //P25145
 F-NT2RP2003704//GAMMA-GLUTAMYLTRANSFERASE 5 PRECURSOR (EC 2.3.2.2) (GAMMA- GLUTAMYLTRANSFERASE 5) (GGT-REL). //0.66:23:52//HOMO SAPIENS (HUMAN). //P36269
 F-NT2RP2003706//GLUTAMYL AMINOPEPTIDASE (EC 3.4.11.7) (EAP) (AMINOPEPTIDASE A) (APA) (DIFFERENTIATION ANTIGEN GP160). //1.2e-22:187:35//HOMO SAPIENS (HUMAN). //Q07075
 F-NT2RP2003713//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 6 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 6) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 6) (DEUBIQUITINATING ENZYME 6) (PROTO-ONCOGENE TRE-2). //2.7e-06:119:34//HOMO SAPIENS (HUMAN). //P35125
 F-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7). //6.7e-27:68:75//HOMO SAPIENS (HUMAN). //Q05481
 F-NT2RP2003727//HYPOTHETICAL PROTEIN MG007 HOMOLOGY. //0.64:110:30//MYOPLASMA PNEUMONIAE. //P75105
 F-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN- PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2). //1.2e-72:147:90//HOMO SAPIENS (HUMAN), MUS MUSCULUS (MOUSE), RATTUS NORVEGICUS (RAT), AND XENOPUS LAEVIS (AFRICAN CLAWED FROG). //P51669
 F-NT2RP2003751//EXTRACELLULAR GLOBIN PRECURSOR. //0.67:68:30//PSEUDOTERRANOVA DECIPiens (COD WORM). //P26914
 F-NT2RP2003760//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-COP). //1.0e-98:235:82//BOS TAURUS (BOVINE). //P53620
 F-NT2RP2003764//HYPOTHETICAL 29.3 KD PROTEIN (ORF92). //0.011:69:34//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEMORRHOIS VIRUS (OPNPV). //0.10341
 F-NT2RP2003769//ATP SYNTHASE PROTEIN B (EC 3.6.1.34) (A6L). //1.0:33:36//EQUUS CABALLUS (HORSE). //P48663
 F-NT2RP2003770//PHOSPHATE REGULON SENSOR PROTEIN PHOR (EC 2.7.3.-) (FRAGMENT). //0.029:35:42//PSEUDOMONAS AERUGINOSA. //P23621
 F-NT2RP2003777//HYPOTHETICAL 82 KD AVIRULENCE PROTEIN IN AVRBS3 REGION. //0.041:67:34//XANTHOMONAS CAMPESTRIS (PV. VESICATORIA). //P14728
 F-NT2RP2003781//HYPOTHETICAL 36.7 KD PROTEIN AH6.2 IN CHROMOSOME 1. //4.7e-54:204:47//CAENORHABDITIS ELEGANS. //Q09201
 F-NT2RP2003793//PSEUDO-HEVEIN (MINOR HEVEIN). //0.61:30:36//HEVEA BRASILIENSIS (PARA RUBBER TREE). //P80359
 F-NT2RP2003825//ENDOTHELIN-1 PRECURSOR (ET-1) (FRAGMENT). //1.0:35:37//CANIS FAMILIARIS (DOG). //P13206
 F-NT2RP2003840//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X. //2.5e-05:80:38//CAENORHABDITIS ELEGANS. //Q11076
 F-NT2RP2003857//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17). //0.54:28:50//ESCHERICHIA COLI. //P05834
 F-NT2RP2003859//DROSOCIN PRECURSOR. //1.0:37:35//DROSOPHILA MELANOGASTER (FRUIT FLY). //P36193
 F-NT2RP2003871
 F-NT2RP2003885//CUTICLE PROTEIN 32 (LW-32) (LW-ACP 32) (FRAGMENT). //1.0:28:50//LOCUSTA MIGRATORIA (MIGRATORY LOCUST). //P11736
 F-NT2RP2003912//SERINE/THREONINE-PROTEIN KINASE NEK1 (EC 2.7.1.-) (NIMA-RELATED PROTEIN KINASE 1). //4.8e-110:268:80//MUS MUSCULUS (MOUSE). //P51954
 F-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B). //0.00024:92:31//RATTUS NORVEGICUS (RAT). //Q09175
 F-NT2RP2003968//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN). //9.2e-05:101:36//XENOPUS LAEVIS (AFRICAN CLAWED FROG). //P17437
 F-NT2RP2003976//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.7e-21:62:62//HOMO SAPIENS (HUMAN). //P39188
 F-NT2RP2003981//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS8. //2.7e-08:165:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P39702
 F-NT2RP2003984//UNC-87 PROTEIN. //0.75:71:28//CAENORHABDITIS ELEGANS. //P17806
 F-NT2RP2003986//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//5.3e-19:47:70//HOMO SAPIENS (HUMAN). //P39193
 F-NT2RP2003988//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//2.2e-18:80:58//HOMO SAPIENS (HUMAN). //P39195
 F-NT2RP2004013//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE B TRANSCRIPTION FACTOR 3). //1.0e-52:141:77//HOMO SAPIENS (HUMAN). //P20290
 F-NT2RP2004014//MACROPHAGE INFLAMMATORY PROTEIN-2-ALPHA (MIP2-ALPHA) (CINC-2-ALPHA). //0.99:45:26//RATTUS NORVEGICUS (RAT). //Q10746
 F-NT2RP2004041//SYNAPSINS IA AND IB. //0.0022:51:37//BOS TAURUS (BOVINE). //P17599
 F-NT2RP2004042//CRUSTACEAN HYPERGLYCEMIC HORMONE PRECURSOR (CHH) (FRAGMENT). //1.0:49:28//PENAEUS VANNAMEI (PENAEID SHRIMP) (EUROPEAN WHITE SHRIMP). //Q26181
 F-NT2RP2004066//CALDESMON (CDM). //2.9e-05:175:21//GALLUS GALLUS (CHICKEN). //P12957
 F-NT2RP2004081//CADMIUM-METALLOTHIONEIN (CD-MT). //0.93:59:23//HELI X POMATIA (ROMAN SNAIL) (EDIBLE SNAIL). //P33187
 F-NT2RP2004098//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1). //4.6e-09:121:30//HOMO SAPIENS (HUMAN). //Q15404
 F-NT2RP2004124//NONHISTONE CHROMOSOMAL PROTEIN HMG-17. //0.068:63:31//GALLUS GALLUS (CHICKEN). //P02314
 F-NT2RP2004142//HYPOTHETICAL 59.1 KD PROTEIN IN VPS15-YMC2 INTERGENIC REGION. //7.9e-05:94:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P38262
 F-NT2RP2004152//LAMIN L(1). //0.25:167:19//XENOPUS LAEVIS (AFRICAN CLAWED FROG). //P09010

【0663】

【表365】

F-NT2RP2004165//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERG
ENIC REGION.//0.0014:124:31//SACCHAROMYCES CEREVISIAE (BAKER'S YE
ST).//P53214
F-NT2RP2004170//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.012:125:3
0//MUS MUSCULUS (MOUSE).//P05143
F-NT2RP2004172//HYPOTHETICAL 105.7 KD PROTEIN IN TP3-K-PIR1 INTERGE
NIC REGION.//4.1e-26:214:35//SACCHAROMYCES CEREVISIAE (BAKER'S YE
ST).//P36051
F-NT2RP2004187//ZINC FINGER PROTEIN 174.//3.7e-12:76:47//HOMO SAPI
ENS (HUMAN).//Q15697
F-NT2RP2004194//HYPOTHETICAL 10.5 KD PROTEIN C31A2.13C IN CHROMOSO
ME 1.//0.0013:92:23//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q
09730
F-NT2RP2004196//METALLOTHIONEIN 10-11 (MT-10-11).//0.92:36:36//MYT
ILUS EDULIS (BLUE MUSSEL).//P80247
F-NT2RP2004207//MALE ACCESSORY GLAND SECRETORY PROTEIN 355A PRECUR
SOR.//0.92:62:35//DROSOPHILA SIMULANS (FRUIT FLY).//P33737
F-NT2RP2004226//66 KD STRESS PROTEIN (P66).//0.030:113:26//PHYSARU
M POLYCEPHALUM (SLIME MOLD).//P90587
F-NT2RP2004232//PROTEIN KINASE C, MU TYPE (EC 2.7.1.-) (NPKC-MU).//
2.0e-48:211:51//HOMO SAPIENS (HUMAN).//Q15139
F-NT2RP2004239//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PREC
URSOR.//0.00038:111:36//TRITICUM AESTIVUM (WHEAT).//P08489
F-NT2RP2004240//METALLOTHIONEIN-11 (MT-11) (METALLOTHIONEIN-LIKE P
ROTEIN) (MT-CE).//1.0:39:28//CAENORHABDITIS ELEGANS.//P17512
F-NT2RP2004242//RAS-RELATED PROTEIN RGP1 (GTP-BINDING REGULATORY P
ROTEIN RGP1).//0.0036:64:28//ORYZA SATIVA (RICE).//P25766
F-NT2RP2004245//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:2
1:42//POMBO PYCMAEUS PYCMAEUS (BORNEAN ORANGUTAN).//P92896
F-NT2RP2004270//SPIDROIN 2 (ORAGLINE SILK FIBROIN 2) (FRAGMENT).//
0.00023:118:33//MEPHILA CLAVIPES (ORB SPIDER).//P46804
F-NT2RP2004300//PROBABLE E4 PROTEIN.//0.18:77:40//HUMAN PAPILLOMAV
IRUS TYPE 8.//P06425
F-NT2RP2004316
F-NT2RP2004321//HYPOTHETICAL 10.8 KD PROTEIN SSR2439.//1.0:50:28//
SYNECHOCYSTIS SP. (STRAIN PCC 6803).//Q01904
F-NT2RP2004339//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//5.0e-33:
84:77//HOMO SAPIENS (HUMAN).//P39195
F-NT2RP2004347//HYPOTHETICAL 40.9 KD PROTEIN F33H1.3 FROM CHROMOSO
ME 11.//0.78:96:30//CAENORHABDITIS ELEGANS.//Q09556
F-NT2RP2004364//MINOR OUTER CAPSID PROTEIN (NS26) (NONSTRUCTURAL P
ROTEIN VP9).//0.059:143:30//BOVINE ROTAVIRUS (STRAIN UK).//P04515
F-NT2RP2004365//EAMZP30-47 PROTEIN (FRAGMENT).//0.27:38:39//EIMERI
A ACERVULINA.//P21959
F-NT2RP2004366//GLYCOPROTEIN L PRECURSOR.//0.64:71:28//MAREK'S DIS
EASE HERPESVIRUS (STRAIN GA) (MDHV).//P52510
F-NT2RP2004373//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR (HISTIDINE-P
ROLINE RICH GLYCOPROTEIN) (HPRG) (FRAGMENT).//0.59:50:40//ORYZOLA
GUS CUMICULUS (RABBIT).//Q28640
F-NT2RP2004389//HYPOTHETICAL 70.7 KD PROTEIN F09C8.3 IN CHROMOSOME
111.//4.0e-16:89:43//CAENORHABDITIS ELEGANS.//P34388
F-NT2RP2004392
F-NT2RP2004396//SINGLE-STRANDED NUCLEIC ACID-BINDING PROTEIN.//0.4
2:89:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P10080
F-NT2RP2004399//SOMATOTROPIN PRECURSOR (GROWTH HORMONE).//1.0:72:3
4//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//P37886
F-NT2RP2004400
F-NT2RP2004412//SPERM PROTAMINE P1.//0.24:38:31//NOTORYCTES TYPHLO
PS (MARSUPIAL MOLE).//P42143
F-NT2RP2004425//SUPPRESSOR PROTEIN SRP40.//0.0087:197:22//SACCHARO
MYCES CEREVISIAE (BAKER'S YEAST).//P32583
F-NT2RP2004463//ALPHA-2A ADRENERGIC RECEPTOR (ALPHA-2A ADRENOCEPTO
R) (ALPHA-2AAR).//1.3e-05:121:37//MUS MUSCULUS (MOUSE).//Q01338
F-NT2RP2004476//NICKEL-SENSITIVE T-TYPE CALCIUM CHANNEL ALPHA-1 SU
BUNIT (RBE-11).//0.20:68:36//RATTUS NORVEGICUS (RAT).//Q07652
F-NT2RP2004490//F05-RELATED ANTIGEN 1.//0.94:59:33//HOMO SAPIENS
(HUMAN).//P15407
F-NT2RP2004512//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 (EC 1.6.5.
3) (FRAGMENTS).//1.0:37:32//PISASTER OCHRACEUS (SEA STAR).//P24998
F-NT2RP2004523//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.1e-15:
57:71//HOMO SAPIENS (HUMAN).//P39194
F-NT2RP2004538//KINESIN-LIKE PROTEIN KIFIA (AXONAL TRANSPORTER OF
SYNAPTIC VESICLES).//1.2e-48:121:60//HOMO SAPIENS (HUMAN).//Q12756
F-NT2RP2004551//HYPOTHETICAL 7.6 KD PROTEIN (ORF 65).//1.0:20:50//
EUGLENA GRACILIS.//P32095
F-NT2RP2004568//PUTATIVE ATP-DEPENDENT RNA HELICASE C30D11.03.//5.
2e-07:150:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09903
F-NT2RP2004580//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//3.7e-37:
100:78//HOMO SAPIENS (HUMAN).//P39192
F-NT2RP2004587//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERG
ENIC REGION.//8.2e-06:150:32//SACCHAROMYCES CEREVISIAE (BAKER'S YE
AST).//P53214
F-NT2RP2004594//HYPOTHETICAL 45.3 KD PROTEIN C09F5.7 IN CHROMOSOME
11.//0.84:105:24//CAENORHABDITIS ELEGANS.//Q09458
F-NT2RP2004600//MYRISTOYLATED ALANINE-RICH C-KINASE SUBSTRATE (MAR
CKS).//0.17:127:29//RATTUS NORVEGICUS (RAT).//P30009
F-NT2RP2004602//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-05:5
0:58//HOMO SAPIENS (HUMAN).//P39188
F-NT2RP2004614//HYPOTHETICAL 11.6 KD PROTEIN.//1.0:68:33//VACCINIA
VIRUS (STRAIN COPENHAGEN).//P20561
F-NT2RP2004655//GLYCINE-RICH RNA-BINDING PROTEIN 7.//7.0e-05:70:42
//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q03250
F-NT2RP2004664//HYPOTHETICAL 104.0 KD PROTEIN C32A11.03C IN CHROMO
SOME 1.//0.30:78:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q
10328
F-NT2RP2004675
F-NT2RP2004681
F-NT2RP2004689//HYPOTHETICAL 78.3 KD PROTEIN IN RAM2-ATP7 INTERGEN
IC REGION.//0.021:179:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST
).//P34243
F-NT2RP2004709//HYPOTHETICAL PROTEIN MJ0647.//0.90:39:43//METHANOC
CCUS JANNASCHII.//Q58063
F-NT2RP2004710//GAR2 PROTEIN.//0.085:60:30//SCHIZOSACCHAROMYCES PO
MBE (FISSION YEAST).//P41891
F-NT2RP2004736//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.4e-15:9
7:49//HOMO SAPIENS (HUMAN).//P39188
F-NT2RP2004743//MALE SPECIFIC SPERM PROTEIN MST8F.//0.43:24:41//D
ROSOPHILA MELANOGASTER (FRUIT FLY).//P08175
F-NT2RP2004767//36.4 KD PROLINE-RICH PROTEIN.//0.0051:88:27//LYCOP
ERSICOM ESCULENTUM (TOMATO).//Q08451
F-NT2RP2004768//SERINE/THREONINE-PROTEIN KINASE NRK1 (EC 2.7.1.-)
(N-RICH KINASE 1).//9.0e-29:166:43//SACCHAROMYCES CEREVISIAE (BAKE
R'S YEAST).//P38692
F-NT2RP2004775
F-NT2RP2004791//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUC
INE-TRNA LIGASE) (LEURS).//7.4e-60:226:53//CAENORHABDITIS ELEGAN
S.//Q09996
F-NT2RP2004799//SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PREC
URSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BET
A).//2.2e-42:133:57//NEOCALLIMASTIX FRONTALIS (RUMEN FUNGUS).//P53
587
F-NT2RP2004802//HYPOTHETICAL 17.1 KD PROTEIN IN PURS 3' REGION.//0.
018:86:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38898
F-NT2RP2004816//HK(BETA)58 PROTEIN.//1.0e-68:145:93//MUS MUSCULUS
(MOUSE).//P40336
F-NT2RP2004841//DSRD PROTEIN.//0.83:33:39//ARCHAEOGLOBUS FULGIDUS.
//P70742
F-NT2RP2004861//KERATIN, HIGH-SULFUR MATRIX PROTEIN, IIIA3A.//0.00
72:41:39//OVIS ARIES (SHEEP).//P02443
F-NT2RP2004897//METALLOTHIONEIN-LIKE PROTEIN 1.//0.99:41:41//CASUA
RINA GLAUCA (SWAMP OAK).//Q39511
F-NT2RP2004933//DEATH-ASSOCIATED PROTEIN KINASE 1 (EC 2.7.1.-) (OA
P KINASE 1).//8.4e-34:102:67//HOMO SAPIENS (HUMAN).//P53355
F-NT2RP2004936//HIGH POTENTIAL IRON-SULFUR PROTEIN, ISOZYME 2 (HIP
IP 2).//0.87:36:33//ECTOTHORHODOSPIRA VACUOLATA.//P38524
F-NT2RP2004959//STEM CELL FACTOR PRECURSOR (SCF) (MAST CELL GROWTH
FACTOR) (MCF) (C-KIT LIGAND).//1.0:69:28//CANIS FAMILIARIS (DOG).
//Q06220
F-NT2RP2004961//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN K0X3
1) (K1AA0065) (H0A946) (FRAGMENT).//2.1e-21:73:58//HOMO SAPIENS (H
UMAN).//Q06730
F-NT2RP2004962//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//0.17:28:
57//HOMO SAPIENS (HUMAN).//P39189
F-NT2RP2004967//HYPOTHETICAL 7.3 KD PROTEIN.//0.76:41:31//THERMOPH
OTEX TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19301
F-NT2RP2004978//SPERMATID-SPECIFIC PROTEIN T2 [CONTAINS: SPERM PRO
TAMINE SP2].//0.44:40:45//SEPIA OFFICINALIS (COMMON CUTTLEFISH).//
P80002
F-NT2RP2004982
F-NT2RP2004985//HYPOTHETICAL PROTEIN KIAA0144.//1.2e-51:204:57//HO
MO SAPIENS (HUMAN).//Q14157
F-NT2RP2004999//LONG NEUROTOXIN 1 (ALPHA-BUNGAROTOXIN) (BGTX).//0.
23:73:26//BUNGARUS MULTICINCTUS (MANY-BANDED KRAIT).//P01378
F-NT2RP2005000//ATPASE STABILIZING FACTOR 15 KD PROTEIN.//0.12:37:
32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P16965
F-NT2RP2005001//SMALL PROLINE RICH PROTEIN 11 (SPR-11) (CLONE 930
).//0.90:54:31//HOMO SAPIENS (HUMAN).//P22531
F-NT2RP2005003//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.
//1.6e-30:78:56//MUS MUSCULUS (MOUSE).//P15533
F-NT2RP2005012//NPL1 PROTEIN (SEC63 PROTEIN).//0.00024:94:35//SACC

【0664】

【表366】

HARMONYCES CEREVISIAE (BAKER'S YEAST). //P14906
 F-NT2RP2005018//GAG POLYPROTEIN (CORE POLYPROTEIN) [CONTAINS: CORE
 PROTEINS P19, P10] (FRAGMENT). //1.0:91:28//AVIAN ENDOGENOUS ROUS-
 ASSOCIATED VIRUS-0 (EV-2) (AVIAN RETROVIRUS RAV-0). //P06937
 F-NT2RP2005020
 F-NT2RP2005022//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1. //4.9
 e-11:106:35//PODOSPORA ANSERINA. //Q00808
 F-NT2RP2005031
 F-NT2RP2005037//ANTI-SILENCING PROTEIN 1. //2.2e-32:117:55//SACCHAR
 OMYCES CEREVISIAE (BAKER'S YEAST). //P32447
 F-NT2RP2005038//DNA NUCLEOTIDYLEXOTRANSFERASE (EC 2.7.7.31) (TERMI
 NAL ADDITION ENZYME) (TERMINAL DEOXYNUCLEOTIDYLTRANSFERASE) (TERMI
 NAL TRANSFERASE). //9.3e-28:187:40//AMBYSTOMA MEXICANUM (AXOLOTL). //
 /O57486
 F-NT2RP2005108//CUTICLE COLLAGEN 2. //0.33:62:38//CAENORHABDITIS EL
 EGANS. //P17656
 F-NT2RP2005116//PUTATIVE EUKARYOTIC TRANSLATION INITIATION FACTOR
 3 ALPHA SUBUNIT (EIF-3 ALPHA). //4.0e-54:161:63//CAENORHABDITIS ELE
 GANS. //P34466
 F-NT2RP2005126//CHLOROPLAST 50S RIBOSOMAL PROTEIN L27 (FRAGMENT). //
 /0.23:46:39//PLEUROCHYSIS HAPTONOMERA. //P41552
 F-NT2RP2005139//COLLAGEN ALPHA 1 (II) CHAIN (FRAGMENTS). //0.016:4
 3:37//BOS TAURUS (BOVINE). //P25508
 F-NT2RP2005140//HYPOTHETICAL 7.4 KD PROTEIN YCF33. //0.96:51:39//GU
 ILLARDIA THETA (CRYPTOMONAS PHI). //O78517
 F-NT2RP2005144//TUBBY PROTEIN. //5.6e-08:66:45//MUS MUSCULUS (MOUS
 E). //P50586
 F-NT2RP2005147
 F-NT2RP2005159//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECUR
 SOR. //0.94:57:29//NICOTIANA TABACUM (COMMON TOBACCO), AND SPINACIA
 OLERACEA (SPINACH). //P12164
 F-NT2RP2005162//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGEN
 IC REGION. //1.2e-33:139:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
 T). //P38821
 F-NT2RP2005168//HETEROGENOUS NUCLEAR RIBONUCLEOPROTEIN U (HNRNP U
). //2.8e-33:102:61//HOMO SAPIENS (HUMAN). //Q00839
 F-NT2RP2005204//DNA DAMAGE TOLERANCE PROTEIN RHC31 (RAD31 HOMOLOG
). //3.9e-28:141:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //Q06
 624
 F-NT2RP2005227
 F-NT2RP2005239//TRNA SPLICING PROTEIN SPL1. //2.0e-38:117:64//CANDI
 DA ALBICANS (YEAST). //P87185
 F-NT2RP2005254//OMEGA-AGATOXIN 1B (OMEGA-AGA-1B) (FRAGMENT). //0.2
 6:29:48//AGELENOPTIS APERTA (FUNNEL-WEB SPIDER). //P15970
 F-NT2RP2005270//HOMEOBOX PROTEIN HOX-A4 (HOX-1.4). //0.037:82:34//
 GALLUS GALLUS (CHICKEN). //P17277
 F-NT2RP2005276//LONG-CHAIN-FATTY-ACID-COA LIGASE 4 (EC 6.2.1.3)
 (LONG-CHAIN ACYL-COA SYNTHETASE 4) (LACS 4). //2.0e-59:174:61//RATT
 US NORVEGICUS (RAT). //O35547
 F-NT2RP2005287//ZINC FINGER PROTEIN 26 (ZINC FINGER PROTEIN KOX20)
 (FRAGMENT). //1.5e-05:27:70//HOMO SAPIENS (HUMAN). //P17031
 F-NT2RP2005288//PROBABLE RUBREDOXIN MUPI. //1.0:42:28//RHIZOBIUM LE
 GUMINOSARUM (BIOVAR VICIAE). //P28151
 F-NT2RP2005289//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!! //1.1e-21:
 75:70//HOMO SAPIENS (HUMAN). //P39193
 F-NT2RP2005293//TRANSLATION INITIATION FACTOR IF-2. //0.58:170:24//
 HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI). //P55972
 F-NT2RP2005315//CUTICLE COLLAGEN 7 (FRAGMENT). //0.091:65:38//CAENO
 RHABDITIS ELEGANS. //P18832
 F-NT2RP2005325//CHROMOGRAMIN A PRECURSOR (CGA) (PITUITARY SECRETOR
 Y PROTEIN 1) (SP-1) [CONTAINS: PANCREASTATIN: WE-14]. //9.5e-09:98:
 39//HOMO SAPIENS (HUMAN). //P10645
 F-NT2RP2005336//HYPOTHETICAL 68.7 KD PROTEIN IN STBI-MCK1 INTERGEN
 IC REGION. //0.0001:124:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
 T). //P42846
 F-NT2RP2005344//PROBABLE CALCIUM-TRANSPORTING ATPASE 4 (EC 3.6.1.3
 8). //4.7e-21:92:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //Q12
 675
 F-NT2RP2005354
 F-NT2RP2005358//MYOSIN IC HEAVY CHAIN. //0.012:91:39//ACANTHAMOEBA
 CASTELLANI (AMOEBA). //P10569
 F-NT2RP2005360//ACROSIN PRECURSOR (EC 3.4.21.10). //0.0022:73:36//O
 RYCTOLAGUS CULICULUS (RABBIT). //P48038
 F-NT2RP2005393//HYPOTHETICAL 25.9 KD PROTEIN AH6.3 IN CHROMOSOME 1
 1. //0.0086:135:28//CAENORHABDITIS ELEGANS. //Q09202
 F-NT2RP2005407//SQUALENE MONOOXYGENASE (EC 1.14.99.7) (SQUALENE EP
 OXIDASE) (SE). //0.96:109:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEA
 ST). //P32476
 F-NT2RP2005436//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN). //
 0.0011:54:42//ZEA MAYS (MAIZE). //P14918
 F-NT2RP2005441//PROLINE-RICH PROTEIN MP-2 PRECURSOR. //0.039:182:29
 //MUS MUSCULUS (MOUSE). //P05142
 F-NT2RP2005453
 F-NT2RP2005457//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B (EC
 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B14.5B) (CI-B14.5B). //4.0e-10:12
 4:37//BOS TAURUS (BOVINE). //Q02827
 F-NT2RP2005464//HYPOTHETICAL 9.5 KD PROTEIN. //0.96:42:33//VACCINIA
 VIRUS (STRAIN COPENHAGEN). //P20553
 F-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2. //4.6e-09:92:42
 //SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P38127
 F-NT2RP2005472//HYPOTHETICAL PROTEIN B80129. //0.76:80:32//BORRELIA
 BURGDORFERI (LYME DISEASE SPIROCHETE). //O51155
 F-NT2RP2005476//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!! //1.0e-31:
 39:89//HOMO SAPIENS (HUMAN). //P39193
 F-NT2RP2005490//METALLOTHIONEIN-II (MT-II). //0.14:27:33//SCYLLA SE
 RRATA (MUD CRAB). //P02806
 F-NT2RP2005491//DNA-DIRECTED RNA POLYMERASE SUBUNIT I (EC 2.7.7.6
). //0.95:45:31//METHANOCOCCUS JANNASCHII. //Q58785
 F-NT2RP2005495//HYPOTHETICAL 10.8 KD PROTEIN IN GP30-R111 INTERGEN
 IC REGION. //0.99:68:30//BACTERIOPHAGE T4. //Q02407
 F-NT2RP2005496//ZINC FINGER PROTEIN 135. //1.4e-54:120:59//HOMO SAP
 IENS (HUMAN). //P52742
 F-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNI
 T, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFOR
 M) (ALPHA-PR55). //9.5e-76:146:86//RATTUS NORVEGICUS (RAT). //P36876
 F-NT2RP2005501//GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 AN
 TIGEN) (ICE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING
 PROTEIN 35) (CBP 35) (LAMININ-BINDING PROTEIN) (LECTIN L-29) (L-3
 1) (GALACTOSIDE-BINDING PROTEIN) (GALBP). //0.025:70:40//HOMO SAPIE
 NS (HUMAN). //P17931
 F-NT2RP2005509//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR. //1.0:166:2
 7//GALLUS GALLUS (CHICKEN). //P02457
 F-NT2RP2005520//CHROMOSOME ASSEMBLY PROTEIN XCAP-E. //7.9e-45:118:7
 9//XENOPUS LAEVIS (AFRICAN CLAWED FROG). //P50533
 F-NT2RP2005525//50S RIBOSOMAL PROTEIN L11. //1.0:47:27//BORRELIA BU
 RGDORFERI (LYME DISEASE SPIROCHETE). //O51354
 F-NT2RP2005531//PROTEIN-TYROSINE PHOSPHATASE MEG1 (EC 3.1.3.48) (P
 TPASE-MEG1) (MEG). //9.8e-13:84:45//HOMO SAPIENS (HUMAN). //P29074
 F-NT2RP2005539//RING CANAL PROTEIN (KELCH PROTEIN). //4.9e-10:90:33
 //DROSOPHILA MELANOGASTER (FRUIT FLY). //Q04652
 F-NT2RP2005540//NUCLEOTIDE BINDING PROTEIN EXP2. //0.36:119:21//BAC
 ILLUS SUBTILIS. //P39115
 F-NT2RP2005549//HYPOTHETICAL 32.0 KD PROTEIN C16C10.10 IN CHROMOSO
 ME 11. //6.0e-39:179:46//CAENORHABDITIS ELEGANS. //Q09253
 F-NT2RP2005555
 F-NT2RP2005557//HYPOTHETICAL 23.7 KD PROTEIN C13G6.14 IN CHROMOSOM
 E 1. //4.9e-06:90:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //Q
 09790
 F-NT2RP2005581
 F-NT2RP2005600//BASIC PROLINE-RICH PEPTIDE P-E (18-9). //0.014:37:4
 0//HOMO SAPIENS (HUMAN). //P02811
 F-NT2RP2005605//GONADOLIBERIN I PRECURSOR (LHRH I) (LUTEINIZING HO
 RMONE RELEASING HORMONE I) (GONADOTROPIN RELEASING HORMONE I) (GHR
 H I) (LULIBERIN I) (FRAGMENT). //0.64:26:42//MACACA MULATTA (RHESUS
 MACAQUE). //P55247
 F-NT2RP2005620//HYPOTHETICAL 45.1 KD PROTEIN IN RP55-ZMS1 INTERGEN
 IC REGION. //8.7e-31:138:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
 T). //P47160
 F-NT2RP2005622//NEUROTOXIN-LIKE PROTEIN STRI (AMATOXIN AAH STRI). //
 /0.39:22:40//ANDROCTONUS AUSTRALIS HECTOR (SAHARA SCORPION). //P809
 50
 F-NT2RP2005635//HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-HMD2 INTERGEN
 IC REGION. //5.8e-43:144:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
 T). //P38795
 F-NT2RP2005637//VPU PROTEIN (U ORF PROTEIN). //0.91:33:45//CHIMPANZ
 EE IMMUNODEFICIENCY VIRUS (SIV(CP2)) (CIV). //P17286
 F-NT2RP2005640//METALLOTHIONEIN-LIKE PROTEIN LSC54. //0.63:41:31//B
 RASSICA NAPUS (RAPE). //P43402
 F-NT2RP2005645
 F-NT2RP2005651//OCTAMER-BINDING TRANSCRIPTION FACTOR 3A (OCT-3A)
 (OCT-4). //0.0023:50:42//HOMO SAPIENS (HUMAN). //Q01860
 F-NT2RP2005654//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGEN
 IC REGION. //6.1e-16:76:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
 T). //P40564
 F-NT2RP2005669//METALLOTHIONEIN-II (MT-II). //0.76:16:50//SCYLLA SE
 RRATA (MUD CRAB). //P02806
 F-NT2RP2005675//PUTATIVE ORAL CANCER SUPPRESSOR (DELETED IN ORAL C
 ANCER-1). //6.5e-26:116:54//MESOCRICETUS AURATUS (GOLDEN HAMSTER). //
 /P49119
 F-NT2RP2005683//HYPOTHETICAL PROTEIN H10275. //0.17:50:40//HAEMOPHI

【0665】

【表367】

LUS INFLUENZAE.//P43975
 F-NT2RP2005690//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5 CR) (PSC REDUCTASE).//1.3e-16:75:30//PISUM SATIVUM (GARDEN PEA).//Q04708
 F-NT2RP2005694//HYPOTHETICAL PROTEIN KIAA0032.//9.6e-11:135:34//HOMO SAPIENS (HUMAN).//Q15034
 F-NT2RP2005701//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.084:158:32//HOMO SAPIENS (HUMAN).//P10161
 F-NT2RP2005712//METALLOTHIONEIN-11 (MT-11).//0.19:14:50//STENELLA COERULEALBA (STRIPED DOLPHIN).//P14425
 F-NT2RP2005719//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).//1.0:36:41//ORYCTOLAGUS CUNICULUS (RABBIT).//P02456
 F-NT2RP2005722//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//7.8e-37:131:62//HOMO SAPIENS (HUMAN).//P16415
 F-NT2RP2005723//ALU SUBFAMILY SC WARNING ENTRY !!!!!//0.98:23:60//HOMO SAPIENS (HUMAN).//P39192
 F-NT2RP2005726//HYPOTHETICAL PROTEIN TP0375.//0.98:30:43//TREPONEMA PALLIDUM.//Q083390
 F-NT2RP2005732//PERIOD CLOCK PROTEIN (FRAGMENT).//0.41:20:55//DROSOPHILA ROBUSTA (FRUIT FLY).//Q03296
 F-NT2RP2005741//SMR1 PROTEIN PRECURSOR (VCS-ALPHA 1).//0.38:58:36//RATTUS NORVEGICUS (RAT).//P13432
 F-NT2RP2005748//ZINC FINGER PROTEIN KOX23 (FRAGMENT).//0.026:19:68//HOMO SAPIENS (HUMAN).//P17034
 F-NT2RP2005752//PROCOLLAGEN ALPHA 1(III) CHAIN PRECURSOR.//0.90:10:31//HOMO SAPIENS (HUMAN).//P02461
 F-NT2RP2005753//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.50:22:59//HOMO SAPIENS (HUMAN).//P30808
 F-NT2RP2005763//PUTATIVE ATP-DEPENDENT RNA HELICASE STE13.//4.7e-14:108:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09181
 F-NT2RP2005767//NORMHISTONE CHROMOSOMAL PROTEIN 6B.//4.1e-08:65:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P11633
 F-NT2RP2005773//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5 CR) (PSC REDUCTASE).//1.2e-14:65:61//HOMO SAPIENS (HUMAN).//P32322
 F-NT2RP2005775//NEUROTENSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP).//1.3e-103:199:90//ORYCTOLAGUS CUNICULUS (RABBIT).//P42675
 F-NT2RP2005781//SALIVARY ACIDIC PROLINE-RICH PHOSPHOPROTEIN 1/2 PRECURSOR (PRP-1 / PRP-3) (PRP-2 / PRP-4) (PIF-F / PIF-S) (PROTEIN A / PROTEIN C) [CONTAINS: PEPTIDE P-C].//0.090:73:36//HOMO SAPIENS (HUMAN).//P02810
 F-NT2RP2005784//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (IMMEDIATE-EARLY PROTEIN IE110) (VIR110) (ALPHA-0 PROTEIN).//3.5e-06:79:37//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN 17).//P08393
 F-NT2RP2005804//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//1.8e-07:43:55//ONCHOSOMA FUSIFORMIS.//P12260
 F-NT2RP2005812//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//6.3e-14:143:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40004
 F-NT2RP2005815//FERROCHELATASE (EC 4.99.1.1) (PROTOME FERRO-LYASE) (HEME SYNTHETASE).//0.0017:123:37//MYCOBACTERIUM AVIUM.//Q07401
 F-NT2RP2005835//SHP1 PROTEIN.//1.2e-08:135:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P34223
 F-NT2RP2005841//SMALL PROLINE-RICH PROTEIN II (SPR-11) (CLONE 174 N).//0.23:28:53//HOMO SAPIENS (HUMAN).//P22532
 F-NT2RP2005853//HYPOTHETICAL 8.5 KD PROTEIN IN ASIA-MOTA INTERGENIC REGION.//0.99:33:48//BACTERIOPHAGE T4.//P22917
 F-NT2RP2005857//CHROMOSOME ASSEMBLY PROTEIN XCAP-C.//8.6e-84:235:66//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P50532
 F-NT2RP2005859//MALE SPECIFIC SPERM PROTEIN MST8408.//0.017:60:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643
 F-NT2RP2005868//ATP SYNTHASE B' CHAIN PRECURSOR (EC 3.6.1.34) (SUBUNIT 11).//0.28:121:28//SPINACIA OLERACEA (SPINACH).//P31853
 F-NT2RP2005886//MICRONUCLEAR LINKER HISTONE POLYPROTEIN (MIC LH) [CONTAINS: LINKER HISTONE PROTEINS ALPHA, BETA, DELTA AND GAMMA].//0.80:130:28//TETRAHYMENA THERMOPHILA.//P40631
 F-NT2RP2005890
 F-NT2RP2005901//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.35:18:44//DROSOPHILA YAKUBA (FRUIT FLY).//P03933
 F-NT2RP2005908//ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.0e-28:61:65//HOMO SAPIENS (HUMAN).//P39194
 F-NT2RP2005933//PERIOD CLOCK PROTEIN (P230) (FRAGMENT).//1.7e-11:85:49//ACETABULARIA MEDITERRANEA (MERMAID'S WINE GLASS).//P12347
 F-NT2RP2005942//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEOTIDE ADENYLTRANSFERASE).//7.2e-59:216:58//BOS TAURUS (BOVINE).//P25500
 F-NT2RP2005980//HYPOTHETICAL 11.5 KD PROTEIN IN RSPBA-AST1 INTERGENIC REGION.//1.0:49:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38185
 F-NT2RP2006023//DNA REPAIR PROTEIN RECN (RECOMBINATION PROTEIN N) (FRAGMENT).//1.0:40:45//VIBRIO CHOLERAE.//P52118
 F-NT2RP2006038//HYPOTHETICAL 30.2 KD PROTEIN CO2FS.4 IN CHROMOSOME 111.//4.0e-11:90:34//CAENORHABDITIS ELEGANS.//P34281
 F-NT2RP2006043//LAMININ BETA-1 CHAIN VARIANT (LAMININ BETA-1-2 CHAIN) (FRAGMENT).//0.00067:73:38//GALLUS GALLUS (CHICKEN).//Q01636
 F-NT2RP2006052//METALLOTHIONEIN-1 (MT-1).//0.19:31:38//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET).//P02797
 F-NT2RP2006069//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENTS).//1.0:66:34//RATTUS NORVEGICUS (RAT).//P02466
 F-NT2RP2006071//RESTIN.//0.40:156:29//GALLUS GALLUS (CHICKEN).//Q42184
 F-NT2RP2006098//HYPOTHETICAL 21.7 KD PROTEIN IN TUP1-ABP1 INTERGENIC REGION.//0.99:95:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25651
 F-NT2RP2006100//LONG NEUROTOXIN 4 (ALPHA-NEUROTOXIN).//0.94:43:34//OPHIOPHAGUS HANNAH (KING COBRA) (NAJA HANNAH).//P08156
 F-NT2RP2006103//50S RIBOSOMAL PROTEIN L32.//0.40:36:38//SYNECHOCYSTIS SP. (STRAIN PCC 6803).//P73014
 F-NT2RP2006106//CUTICLE COLLAGEN 1.//0.28:85:29//CAENORHABDITIS ELEGANS.//P08124
 F-NT2RP2006141//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME 1.//1.9e-08:57:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09701
 F-NT2RP2006166
 F-NT2RP2006184//HYPOTHETICAL 11.2 KD PROTEIN IN CSGC-MDOC INTERGENIC REGION PRECURSOR.//0.95:87:26//ESCHERICHIA COLI.//P75917
 F-NT2RP2006186//MICROTUBULE-ASSOCIATED PROTEIN 2.//0.088:124:33//MUS MUSCULUS (MOUSE).//P20357
 F-NT2RP2006196//ALU SUBFAMILY SP WARNING ENTRY !!!!!//4.0e-05:49:61//HOMO SAPIENS (HUMAN).//P39193
 F-NT2RP2006200//PROCOLLAGEN ALPHA 2(V) CHAIN PRECURSOR.//0.0013:205:32//HOMO SAPIENS (HUMAN).//P05997
 F-NT2RP2006219//GONADAL PROTEIN GDL.//3.5e-18:158:37//DROSOPHILA MELANOGASTER (FRUIT FLY).//P22468
 F-NT2RP2006237//FIBRINOGEN- AND IGF-BINDING PROTEIN PRECURSOR (MRP PROTEIN).//0.79:103:28//STREPTOCOCCUS PYOGENES.//P30141
 F-NT2RP2006238//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//4.7e-07:127:39//MUS MUSCULUS (MOUSE).//P05143
 F-NT2RP2006258//PROBABLE E5 PROTEIN.//0.78:47:34//RHESUS PAPILLOMA VIRUS TYPE 1 (RHPV 1).//P24834
 F-NT2RP2006261//PENAEIDIN-3A PRECURSOR (P3-A).//0.61:35:40//PENAEUS VANNAMEI (PENOEID SHRIMP) (EUROPEAN WHITE SHRIMP).//P81058
 F-NT2RP2006275//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 2 (FRAGMENT).//1.2e-28:59:57//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P14401
 F-NT2RP2006312//HIGH-MOBILITY-GROUP PROTEIN (NORMHISTONE CHROMOSOMAL PROTEIN).//1.6e-06:53:35//TETRAHYMENA PYRIFORMIS.//P40625
 F-NT2RP2006320//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).//0.90:24:41//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (HIV-1) (HIV-1).//P04612
 F-NT2RP2006321//ALU SUBFAMILY SP WARNING ENTRY !!!!!//0.0051:25:76//HOMO SAPIENS (HUMAN).//P39193
 F-NT2RP2006323//WISKOTT-ALDRICH SYNDROME PROTEIN (WASP).//0.84:33:39//HOMO SAPIENS (HUMAN).//P42768
 F-NT2RP2006333//MYOTOXIN 3 PRECURSOR (CROTAMINE 3).//0.56:37:40//CROTALUS DURISSUS TERRIFICUS (SOUTH AMERICAN RATTLESNAKE).//P24333
 F-NT2RP2006334//SUCCINYL-COA LIGASE [GDP-FORMING], ALPHA-CHAIN 3 PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, ALPHA CHAIN 3).//0.00097:46:41//TRICHOMONAS VAGINALIS.//P53401
 F-NT2RP2006365//NONSPECIFIC LIPID-TRANSFER PROTEIN 4.3 PRECURSOR (LTP 4.3).//0.18:75:29//HORDEUM VULGARE (BARLEY).//Q42842
 F-NT2RP2006393//OMEGA-CONOTOXIN MVIIC PRECURSOR (FRAGMENT).//0.82:15:66//CONUS MAGUS (MAGUS CONE).//P37300
 F-NT2RP2006436//ANTERIOR-RESTRICTED HOMEOBOX PROTEIN (RATHKE POUCH HOMEO BOX).//1.4e-08:50:50//MUS MUSCULUS (MOUSE).//Q01658
 F-NT2RP2006441//METALLOTHIONEIN-LIKE PROTEIN 1.//0.99:22:54//MIMULUS GUTTATUS (SPOTTED MONKEY FLOWER) (YELLOW MONKEY FLOWER).//P20238
 F-NT2RP2006454//SPERM PROTAMINE P1.//0.60:47:36//TACHYGLOSSUS ACULEATUS ACULEATUS (AUSTRALIAN ECHIDNA).//P35311
 F-NT2RP2006456
 F-NT2RP2006464//PHOTOSYSTEM I IRON-SULFUR CENTER (PHOTOSYSTEM I SUBUNIT VII) (9 KD POLYPEPTIDE) (PSI-C).//0.91:79:30//SYNECHOCOCCUS SP. (STRAIN PCC 7002) (AGMENELLUM QUADRUPLICATUM).//P31087
 F-NT2RP2006467//PUTATIVE CUTICLE COLLAGEN F55C10.3.//0.15:53:35//CAENORHABDITIS ELEGANS.//Q21184
 F-NT2RP2006472//HYPOTHETICAL 19 KD PROTEIN (ORF 167).//0.33:98:26//MARCHANTIA POLYMORPHA (LIVERWORT).//P12202

【0666】

【表368】

F-NT2RP2006534
F-NT2RP2006554//ANTI-SIGMA F FACTOR ANTAGONIST (STAGE II SPORULATION PROTEIN AA).//0.91:50:34//BACILLUS SPHAERICUS.//032723
F-NT2RP2006565//SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 1 (S CAMP 37).//6.0e-66:93:96//RATTUS NORVEGICUS (RAT).//P56603
F-NT2RP2006571//CYTOCHROME P450 2B10 (EC 1.14.14.1) (CYP1B10) (TE STOSTERONE 16-ALPHA HYDROXYLASE) (P450-16-ALPHA) (CLONE PF3/46).//4.5e-40:138:57//MUS MUSCULUS (MOUSE).//P12791
F-NT2RP2006573//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//0.53:46:39//BOS TAURUS (BOVINE).//P02318
F-NT2RP2006598//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.3e-12:44:77//HOMO SAPIENS (HUMAN).//P39195
F-NT2RP3000002//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.4e-19:60:63//HOMO SAPIENS (HUMAN).//P39192
F-NT2RP3000031//HYPOTHETICAL 89.8 KD PROTEIN F41H10.6 IN CHROMOSOM E IV.//2.1e-39:210:42//CAENORHABDITIS ELEGANS.//Q20296
F-NT2RP3000046//POSSIBLE THIOPHENE AND FURAN OXIDATION PROTEIN THD F.//1.4e-25:149:44//PSEUDOMONAS PUTIDA.//P25755
F-NT2RP3000047//NPLA PROTEIN.//4.7e-48:275:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33755
F-NT2RP3000050//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//3.2e-72:232:59//HOMO SAPIENS (HUMAN).//P51522
F-NT2RP3000055//MALE SPECIFIC SPERM PROTEIN MSTR40B.//0.26:57:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643
F-NT2RP3000068//HYPOTHETICAL 182.0 KD PROTEIN IN NMDS-HOM6 INTERGENIC REGION.//0.0014:66:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47170
F-NT2RP3000072//HYPOTHETICAL 6.7 KD PROTEIN IN MOHA-CSPI INTERGENIC REGION.//0.95:49:30//ESCHERICHIA COLI.//P77695
F-NT2RP3000080//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.1e-17:64:68//HOMO SAPIENS (HUMAN).//P39188
F-NT2RP3000085//BIOTIN CARBOXYLASE (EC 6.3.4.14) (A SUBUNIT OF ACETYL-COA CARBOXYLASE (EC 6.4.1.2)) (ACC).//4.4e-43:169:51//BACILLUS SUBTILIS.//P49787
F-NT2RP3000092//CELL DIVISION CONTROL PROTEIN 1.//0.00016:103:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40986
F-NT2RP3000109//ACTYL CARRIER PROTEIN HOMOLOG (ACP).//0.76:83:28//MYCOPLASMA GENITALIUM.//P47529
F-NT2RP3000134
F-NT2RP3000142//GAR2 PROTEIN.//0.00098:241:20//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891
F-NT2RP3000149//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.0014:33:36//POMCO PYGMAEUS ABELII (SUMATRAN ORANGUTAN).//P92694
F-NT2RP3000186//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//8.3e-15:36:83//HOMO SAPIENS (HUMAN).//P39188
F-NT2RP3000197//HYPOTHETICAL 6.0 KD PROTEIN IN TH112 5' REGION.//0.91:21:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53820
F-NT2RP3000207//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//0.026:209:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640
F-NT2RP3000220//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//1.0:26:42//HOMO SAPIENS (HUMAN).//P30808
F-NT2RP3000233//RING CANAL PROTEIN (KELCH PROTEIN).//2.1e-42:249:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
F-NT2RP3000235//HOMEBOX PROTEIN H40 (FRAGMENT).//0.55:45:40//APIS MELLIFERA (HONEYBEE).//P15858
F-NT2RP3000247//HYPOTHETICAL PROTEIN KIAA0218.//1.7e-82:123:69//HOMO SAPIENS (HUMAN).//Q93075
F-NT2RP3000251//SERINE PROTEINASE STUBBLE (EC 3.4.21.-) (STUBBLE-S TUBBLOID PROTEIN).//1.0:53:33//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q05319
F-NT2RP3000252//HYPOTHETICAL 40 KD GTP-BINDING PROTEIN IN RIBOSOMAL PROTEIN GENE CLUSTER 5' REGION.//2.2e-06:96:32//HALOBACTERIUM CUTIRUBRUM.//P17103
F-NT2RP3000255//HISTONE H1.1 (FRAGMENT).//0.95:71:33//BOS TAURUS (BOVINE).//P02253
F-NT2RP3000267//HYPOTHETICAL 21.1 KD PROTEIN IN SSR-SERA INTERGENIC REGION (O182).//0.38:77:33//ESCHERICHIA COLI.//P09160
F-NT2RP3000299//MYOSIN IC HEAVY CHAIN.//1.2e-11:147:34//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569
F-NT2RP3000312//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.64:216:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214
F-NT2RP3000320//TRANSLATION INITIATION FACTOR IF-2.//5.2e-05:184:22//AQUIFEX AEOLICUS.//Q08785
F-NT2RP3000324//HYPOTHETICAL PROTEIN HI1036.//0.69:64:35//HAEMOPHILUS INFLUENZAE.//P44097
F-NT2RP3000333//WIRIA PROTEIN.//0.35:51:41//TRITICUM AESTIVUM (WHEAT).//Q01482
F-NT2RP3000341//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.1e-30:57:80//HOMO SAPIENS (HUMAN).//P39189
F-NT2RP3000348
F-NT2RP3000350//HYPOTHETICAL 40 KD GTP-BINDING PROTEIN IN RIBOSOMAL PROTEIN GENE CLUSTER 5' REGION.//0.0011:77:35//HALOBACTERIUM CUTIRUBRUM.//P17103
F-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//1.2e-97:222:84//BOS TAURUS (BOVINE).//P08760
F-NT2RP3000361//PRE-MRNA SPLICING FACTOR PRP5.//2.2e-08:128:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P19735
F-NT2RP3000366//RAS-RELATED PROTEIN RAB-18.//2.1e-107:206:99//MUS MUSCULUS (MOUSE).//P35293
F-NT2RP3000393//HOMEBOX PROTEIN HOX-C4 (HOX-3E) (CP19).//0.0023:6:52//HOMO SAPIENS (HUMAN).//P09017
F-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13).//5.5e-27:116:44//MUS MUSCULUS (MOUSE).//Q35286
F-NT2RP3000403//PRE-MRNA PROCESSING PROTEIN PRP40.//0.00044:67:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33203
F-NT2RP3000418//RETROVIRUS-RELATED POLYPROTEIN (CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE).//2.2e-16:228:34//MUS MUSCULUS (MOUSE).//P11369
F-NT2RP3000433//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.7e-17:79:55//HOMO SAPIENS (HUMAN).//P39188
F-NT2RP3000439//HYPOTHETICAL 46.4 KD PROTEIN IN FFH-CRPE INTERGENIC REGION.//9.8e-10:201:26//ESCHERICHIA COLI.//P37908
F-NT2RP3000441//PROTEIN-EXPORT MEMBRANE PROTEIN SECC HOMOLOG.//0.91:48:35//MYCOBACTERIUM LEPAE.//P38388
F-NT2RP3000449//HOMEBOX PROTEIN HOX-B8 (CHOX-2.4) (FRAGMENT).//1.0:42:33//GALLUS GALLUS (CHICKEN).//P23681
F-NT2RP3000451
F-NT2RP3000456//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.00018:178:36//RATTUS NORVEGICUS (RAT).//P02454
F-NT2RP3000484//METALLOTHIONEIN-111 (MT-111) (GROWTH INHIBITORY FACTOR) (GIF).//0.098:40:27//BOS TAURUS (BOVINE).//P37359
F-NT2RP3000487//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//0.0037:16:81//VOLVOX CARTERI.//P21997
F-NT2RP3000512
F-NT2RP3000526//HYPOTHETICAL NIN REGION PROTEIN ORF56.//0.51:37:43//BACTERIOPHAGE LAMBDA.//P03769
F-NT2RP3000527//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//1.0e-16:234:30//HOMO SAPIENS (HUMAN).//P51522
F-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//3.4e-15:192:30//HOMO SAPIENS (HUMAN).//P15151
F-NT2RP3000542//CYTOCHROME C OXIDASE POLYPEPTIDE II (EC 1.9.3.1) (FRAGMENT).//0.60:51:39//ASTERINA PECTINIFERA (STARFISH).//P11958
F-NT2RP3000561//HYPOTHETICAL ATP-BINDING PROTEIN MJ0423.//0.79:53:32//METHANOCOCCUS JANNASCHII.//Q57866
F-NT2RP3000562//ACCESSORY GLAND PEPTIDE PRECURSOR (PARAGONIAL PEPTIDE B).//0.99:26:34//DROSOPHILA MAURITIANA (FRUIT FLY), AND DROSOPHILA SIMULANS (FRUIT FLY).//Q18666
F-NT2RP3000578//HYPOTHETICAL 49.8 KD PROTEIN IN RPL148-GPA1 INTERGENIC REGION.//1.5e-26:127:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38755
F-NT2RP3000582
F-NT2RP3000584//METALLOTHIONEIN-11 (MT-11).//0.28:27:29//MUS MUSCULUS (MOUSE).//P02798
F-NT2RP3000590//UVS-2 PROTEIN.//4.8e-10:113:33//NEUROSPORA CRASSA.//P33288
F-NT2RP3000592//TRANSCRIPTION INITIATION FACTOR TF110 135 KD SUBUNIT (TAF11-135) (TAF11135) (TAF11-130) (TAF11130).//0.00087:178:31//HOMO SAPIENS (HUMAN).//Q00268
F-NT2RP3000596//YEMANUCLEIN-ALPHA.//1.8e-05:98:34//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25992
F-NT2RP3000599//SPLICOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A6).//0.00095:90:37//HOMO SAPIENS (HUMAN).//Q15428
F-NT2RP3000603//SE5 ANTIGEN.//1.0e-09:181:34//RATTUS NORVEGICUS (RAT).//Q63003
F-NT2RP3000605//STEROL REGULATORY ELEMENT BINDING PROTEIN-1 (SREB-1) (STEROL REGULATORY ELEMENT-BINDING TRANSCRIPTION FACTOR 1).//0.00098:76:34//HOMO SAPIENS (HUMAN).//P36956
F-NT2RP3000622//HYPOTHETICAL PROTEIN MG096 HOMOLOG 5 (P02_ORF427).//0.15:52:36//MYCOPLASMA PNEUMONIAE.//P75277
F-NT2RP3000624//HYPOTHETICAL PROTEIN KIAA0256.//5.4e-16:222:31//HOMO SAPIENS (HUMAN).//Q93073
F-NT2RP3000628
F-NT2RP3000632//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10).//2.0e-16:52:63//MUS MUSCULUS (MOUSE).//Q61967
F-NT2RP3000644//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//6.7e-40:102:79//HOMO SAPIENS (HUMAN).//P39194
F-NT2RP3000661//HYPOTHETICAL 139.1 KD PROTEIN C08B11.3 IN CHROMOSOME 11.//6.0e-08:83:36//CAENORHABDITIS ELEGANS.//Q09441

【0667】

【表369】

F-NT2RP3000665//HOMEBOX PROTEIN PROPHET OF PIT-1 (PROP-1) (PITUITARY SPECIFIC HOMEODOMAIN FACTOR).//0.13:48:35//HOMO SAPIENS (HUMAN).//075360
 F-NT2RP3000685//HYPOTHETICAL 33.5 KD PROTEIN IN CAT1 5' REGION (ORF Y).//0.26:202:23//CLOSTRIDIUM KLUYVERI.//P38943
 F-NT2RP3000690//INORGANIC PYROPHOSPHATASE (EC 3.6.1.1) (PYROPHOSPHATE PHOSPHO- HYDROLASE) (PPASE).//0.99:131:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P00817
 F-NT2RP3000736//HYPOTHETICAL 28.7 KD PROTEIN IN RNR3-ARC15 INTERGENIC REGION.//3.5e-27:211:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40516
 F-NT2RP3000739//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME 1.//6.0e-23:114:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10149
 F-NT2RP3000742//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA-1) (PLC-111).//6.7e-12:85:36//RATTUS NORVEGICUS (RAT).//P10688
 F-NT2RP3000753//CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1).//0.00011:208:28//CLOSTRIDIUM THERMOCELLUM.//Q06852
 F-NT2RP3000759//ADP-RIBOSYLATION FACTOR 6.//8.1e-28:141:38//GALLUS GALLUS (CHICKEN).//P26990
 F-NT2RP3000815//CYTOCHROME C-551 (C551) (CYTOCHROME CB).//0.24:45:37//PSEUDOMONAS DENITRIFICANS.//P00103
 F-NT2RP3000825//ALPHA-LACTALBUMIN (LACTOSE SYNTHASE B PROTEIN (EC 2.4.1.22)).//0.82:51:39//MACROPUS RUFUGRISUS (RED-NECKED WALLABY).//P07458
 F-NT2RP3000826//COLLAGEN ALPHA 1(XI) CHAIN (FRAGMENTS).//0.025:79:37//BOS TAURUS (BOVINE).//P25508
 F-NT2RP3000836//HYPOTHETICAL PROTEIN IN KSGA 3' REGION (ORF L5) (FRAGMENT).//0.85:36:47//MYCOPLASMA CAPRICOLUM.//P43040
 F-NT2RP3000841//UDP-GLUCURONOSYLTRANSFERASE 1-7 PRECURSOR. MICROSO MAL (EC 2.4.1.17) (UDPGT) (UGT1*7) (UGT1-07) (UGT1.7) (UGT1A7) (UGTP4) (FRAGMENT).//1.0:70:34//MUS MUSCULUS (MOUSE).//Q62452
 F-NT2RP3000845//PUTATIVE SERINE/THREONINE-PROTEIN KINASE P78 (EC 2.7.1.1).//5.2e-72:247:61//HOMO SAPIENS (HUMAN).//P27448
 F-NT2RP3000847//HYPOTHETICAL PROTEIN KIAA0161.//0.037:55:30//HOMO SAPIENS (HUMAN).//P50876
 F-NT2RP3000850//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//7.4e-31:90:75//HOMO SAPIENS (HUMAN).//P39194
 F-NT2RP3000852//HYDROPHOBIC SEED PROTEIN (HPS).//0.33:23:69//GLYCIME MAX (SOYBEAN).//P24337
 F-NT2RP3000859//IMMEDIATE-EARLY PROTEIN.//3.6e-07:189:25//HERPESVIRUS SAIMIRI (STRAIN 11).//Q10142
 F-NT2RP3000865
 F-NT2RP3000868//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE ISOFORM (FRAGMENT).//1.4e-09:232:28//GALLUS GALLUS (CHICKEN).//P29616
 F-NT2RP3000869//CUTICLE COLLAGEN 2.//4.5e-08:58:46//CAENORHABDITIS ELEGANS.//P17656
 F-NT2RP3000875//HOMEBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEBOX PROTEIN 2).//0.90:62:37//MUS MUSCULUS (MOUSE).//P43241
 F-NT2RP3000901//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.99:124:33//BOS TAURUS (BOVINE).//P02453
 F-NT2RP3000904
 F-NT2RP3000917//DHP1 PROTEIN.//8.5e-60:229:55//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P40848
 F-NT2RP3000919//HYPOTHETICAL 33.5 KD PROTEIN C1D4.02C IN CHROMOSOME 1.//2.4e-19:159:34//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10149
 F-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A.//3.7e-48:73:98//HOMO SAPIENS (HUMAN), AND RATTUS NORVEGICUS (RAT).//P39027
 F-NT2RP3000980//COPA/INCA PROTEIN (REPA3 PROTEIN).//0.24:19:47//ESCHERICHIA COLI.//P13946
 F-NT2RP3000994//MATERNAL EFFECT PROTEIN STAUFEN.//1.4e-10:78:48//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25159
 F-NT2RP3001004//HYPOTHETICAL 7.6 KD PROTEIN B0563.8 IN CHROMOSOME X.//0.70:50:32//CAENORHABDITIS ELEGANS.//Q11084
 F-NT2RP3001007
 F-NT2RP3001055//N-TERMINAL ACETYLTRANSFERASE COMPLEX ARD1 SUBUNIT HOMOLOG.//1.3e-05:138:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P36416
 F-NT2RP3001057//ZINC FINGER PROTEIN 45 (BRC1744).//4.0e-28:141:51//HOMO SAPIENS (HUMAN).//Q02386
 F-NT2RP3001081//HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMOSOME 111.//3.8e-08:144:29//CAENORHABDITIS ELEGANS.//P34568
 F-NT2RP3001084//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//3.4e-06:217:32//NEPHILA CLAVIPES (ORB SPIDER).//P46804
 F-NT2RP3001096//SYNAPTONEMAL COMPLEX PROTEIN SC65.//1.1e-30:244:33//RATTUS NORVEGICUS (RAT).//Q64375
 F-NT2RP3001107//ARYLSULFATASE F (EC 3.1.6.-) (ASF) (FRAGMENT).//0.041:47:44//HOMO SAPIENS (HUMAN).//P54793
 F-NT2RP3001109
 F-NT2RP3001111//MALE SPECIFIC SPERM PROTEIN MST84DC.//0.17:28:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01644
 F-NT2RP3001113//INVOLUCRIN.//0.00036:192:23//MUS MUSCULUS (MOUSE).//P48997
 F-NT2RP3001115
 F-NT2RP3001116//AMINOPEPTIDASE G (EC 3.4.11.-) (FRAGMENT).//0.99:29:51//STREPTOMYCES LIVIDANS.//Q54340
 F-NT2RP3001119//COLLAGEN ALPHA 4(IV) CHAIN (FRAGMENT).//0.0015:73:39//BOS TAURUS (BOVINE).//Q29442
 F-NT2RP3001120//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//1.3e-57:229:52//HOMO SAPIENS (HUMAN).//P16415
 F-NT2RP3001126//HYPOTHETICAL 91.2 KD PROTEIN IN RPS4B-SC9 INTERGENIC REGION.//2.8e-07:83:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38888
 F-NT2RP3001133//CALCIUM BINDING PROTEIN.//2.0e-08:171:32//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P35085
 F-NT2RP3001140//F-SPONDIN PRECURSOR.//2.0e-147:244:97//RATTUS NORVEGICUS (RAT).//P35446
 F-NT2RP3001147//TROPOMYOSIN 2 (TM1).//0.11:159:23//SCHISTOSOMA MANSONI (BLOOD FLUKE).//P42638
 F-NT2RP3001150//OCTAPEPTIDE-REPEAT PROTEIN T2.//6.2e-09:163:25//MUS MUSCULUS (MOUSE).//Q06666
 F-NT2RP3001155//DNA POLYMERASE ALPHA-BINDING PROTEIN (POB1/CTF4 PROTEIN) (CHROMOSOME REPLICATION PROTEIN CHL15).//4.1e-05:244:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q01454
 F-NT2RP3001176//LEUKOSIALIN PRECURSOR (LEUCOCYTE SIALOGLYCOPROTEIN) (SIALOPHORIN) (CD43) (LY 48) (B CELL DIFFERENTIATION ANTIGEN L P-3).//0.21:136:26//MUS MUSCULUS (MOUSE).//P15702
 F-NT2RP3001214//SAP1 PROTEIN.//0.058:133:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39955
 F-NT2RP3001216//CYCLICIN 1 (MULTIPLE-BAND POLYPEPTIDE 1) (FRAGMENT).//2.1e-08:137:33//HOMO SAPIENS (HUMAN).//P35663
 F-NT2RP3001221//GAMMA-BUTYROBETAIN, 2-OXOGLUTARATE DIOXYGENASE (EC 1.14.11.1) (GAMMA-BUTYROBETAIN HYDROXYLASE).//4.2e-05:131:26//PSEUDOMONAS SP. (STRAIN AK-1).//P80193
 F-NT2RP3001232//HYPOTHETICAL PROTEIN PRECURSOR IN CS5 3' REGION (FRAGMENT).//0.75:57:31//ESCHERICHIA COLI.//P33792
 F-NT2RP3001236//TRANSFORMING PROTEIN MAF.//0.017:136:30//AVIAN MUSCULOPONEUROTIC FIBROSARCOMA VIRUS AS42.//P23091
 F-NT2RP3001239//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 1 (FRAGMENT).//4.2e-55:221:49//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P14400
 F-NT2RP3001245
 F-NT2RP3001253//TROPOMYOSIN 2, MUSCLE THORACIC ISOFORM (TROPOMYOSIN 1).//0.0042:142:24//DROSOPHILA MELANOGASTER (FRUIT FLY).//P09491
 F-NT2RP3001260//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR.//0.0011:89:43//HOMO SAPIENS (HUMAN).//P53420
 F-NT2RP3001268//ZINC FINGER PROTEIN 45 (BRC1744).//9.0e-29:194:44//HOMO SAPIENS (HUMAN).//Q02386
 F-NT2RP3001272//HYPOTHETICAL 75.2 KD PROTEIN C13F4.08C IN CHROMOSOME 1.//8.2e-17:183:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10199
 F-NT2RP3001274//SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.1) (PP5) (PROTEIN PHOSPHATASE T) (PPT) (FRAGMENT).//1.7e-09:78:39//MUS MUSCULUS (MOUSE).//Q60676
 F-NT2RP3001281//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//7.7e-08:38:71//HOMO SAPIENS (HUMAN).//P39188
 F-NT2RP3001297//HYPOTHETICAL PROTEIN KIAA0281 (HA6725).//2.2e-57:159:70//HOMO SAPIENS (HUMAN).//Q92556
 F-NT2RP3001307//SPERM PROTAMINE P1.//0.21:46:39//ORNITHORHYNCHUS A NATIVUS (DUCKBILL PLATYPUS).//P35307
 F-NT2RP3001318
 F-NT2RP3001325//ENHANCER OF RUDIMENTARY HOMOLOG.//1.0:73:24//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//Q98874
 F-NT2RP3001338//ZINC FINGER PROTEIN 29 (ZINC FINGER PROTEIN KOX26) (FRAGMENT).//0.0021:56:35//HOMO SAPIENS (HUMAN).//P17037
 F-NT2RP3001339//CITRON PROTEIN.//3.6e-06:90:33//MUS MUSCULUS (MOUSE).//P49025
 F-NT2RP3001340//HYPOTHETICAL PROTEIN UL61.//7.2e-11:202:34//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818
 F-NT2RP3001355//TRICARBOXYLATE TRANSPORT PROTEIN PRECURSOR (CITRATE TRANSPORT PROTEIN) (CTP) (TRICARBOXYLATE CARRIER PROTEIN).//7.7e-16:129:33//HOMO SAPIENS (HUMAN).//P53007
 F-NT2RP3001356//RAS-RELATED PROTEIN RABA (FRAGMENT).//0.00041:66:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P34141
 F-NT2RP3001374
 F-NT2RP3001383//PTB-ASSOCIATED SPLICING FACTOR (PSF).//2.5e-06:190:32//HOMO SAPIENS (HUMAN).//P23246

【0668】

【表370】

F-NT2RP3001384//CHORION PROTEIN S15.//0.00079:94:37//DROSOPHILA VIRILIS (FRUIT FLY).//P13424
 F-NT2RP3001392//VPU PROTEIN (ORF-X PROTEIN) (UPX PROTEIN).//1.0:2:45//CAPRINE ARTHRITIS ENCEPHALITIS VIRUS (CAEV).//P31834
 F-NT2RP3001396//HYPOTHETICAL 8.1 KD PROTEIN (ORF4).//1.0:37:32//ST RANBERRY WILD YELLOW EDGE-ASSOCIATED VIRUS (SMYEV).//Q00848
 F-NT2RP3001398//KRUPEL-RELATED ZINC FINGER PROTEIN 2 (HKR2 PROTEIN) (FRAGMENT).//1.9e-08:45:37//HOMO SAPIENS (HUMAN).//P10073
 F-NT2RP3001398//SSU72 PROTEIN.//7.3e-18:84:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53538
 F-NT2RP3001407//SCY1 PROTEIN.//1.5e-08:143:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53009
 F-NT2RP3001420//HYPOTHETICAL 7.9 KD PROTEIN.//0.25:41:26//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20542
 F-NT2RP3001426//DNAJ PROTEIN.//7.5e-15:78:43//HAEMOPHILUS INFLUENZAE.//P43735
 F-NT2RP3001427//WERNER SYNDROME HELICASE.//3.6e-13:159:33//HOMO SAPIENS (HUMAN).//Q14191
 F-NT2RP3001428//NUCLEOPROTEIN TPR.//1.8e-53:117:99//HOMO SAPIENS (HUMAN).//P12270
 F-NT2RP3001432//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 (EC 1.6.5.3) (FRAGMENT).//0.96:52:21//TARSISUS SYRICHIA (TARSIER).//Q36151
 F-NT2RP3001447//HYPOTHETICAL 5.5 KD PROTEIN IN REPLICATION ORIGIN REGION (ORF1).//0.96:45:35//ESCHERICHIA COLI.//P14505
 F-NT2RP3001449//HOMEBOX PROTEIN SAX-1 (CHX-3) (FRAGMENT).//0.004:3:53:43//GALLUS GALLUS (CHICKEN).//P19601
 F-NT2RP3001453//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.0048:65:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643
 F-NT2RP3001457//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS28.//0.55:121:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q02767
 F-NT2RP3001459//MYOSIN IC HEAVY CHAIN.//0.10:126:34//ACANTHAMEBA CASTELLANI (AMOEBA).//P10569
 F-NT2RP3001472//HOMHISTONE CHROMOSOMAL PROTEIN 6A.//3.0e-14:87:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P11632
 F-NT2RP3001490//METALLOTHIONEIN-LIKE PROTEIN LSC54.//1.0:39:35//BRASSICA NAPUS (RAPE).//P43402
 F-NT2RP3001495//UBIQUITIN-PROTEIN LIGASE RSP5 (EC 6.3.2.-).//3.3e-14:148:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39940
 F-NT2RP3001497//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.13:44:38//BOS TAURUS (BOVINE).//P25508
 F-NT2RP3001527//SPERM PROTAMINE P1.//0.35:29:37//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM), AND MONDELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM).//P53305
 F-NT2RP3001529//HYPOTHETICAL 43.3 KD GTP-BINDING PROTEIN IN DABC-R PMA INTERGENIC REGION.//3.3e-21:125:37//ESCHERICHIA COLI.//P42641
 F-NT2RP3001538//HNF3/PH TRANSCRIPTION FACTOR GENESIS (WINGED HELIX PROTEIN CHX-3).//0.13:53:39//GALLUS GALLUS (CHICKEN).//P79772
 F-NT2RP3001554//ELECTROMOTOR NEURON-ASSOCIATED PROTEIN 2 (FRAGMENT).//2.3e-48:137:52//TORPEDO CALIFORNICA (PACIFIC ELECTRIC RAY).//P14401
 F-NT2RP3001580//GERM CELL-LESS PROTEIN.//8.2e-18:100:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01820
 F-NT2RP3001587//UBIQUITIN-ACTIVATING ENZYME E1-LIKE (POLYMERASE-IN TERACTING PROTEIN 2).//2.0e-47:188:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P52488
 F-NT2RP3001589//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//7.4e-41:87:80//HOMO SAPIENS (HUMAN).//P39193
 F-NT2RP3001607//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:4:9:32//DICENTRARCHUS LABRAX (EUROPEAN SEA BASS).//Q36362
 F-NT2RP3001608//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.0013:177:25//ZEA MAYS (MAIZE).//P14918
 F-NT2RP3001621//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.84:29:37//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645
 F-NT2RP3001629//RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 1 (P21-RAC1) (FRAGMENTS).//0.91:57:24//CAVIA PORCELLUS (GUINEA PIG).//P80236
 F-NT2RP3001634//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//8.9e-11:73:54//HOMO SAPIENS (HUMAN).//P39189
 F-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210.//1.1e-12:117:29//HOMO SAPIENS (HUMAN).//Q92609
 F-NT2RP3001646//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//0.0092:69:3:4//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMV).//Q10341
 F-NT2RP3001671//RING CANAL PROTEIN (KELCH PROTEIN).//0.0042:55:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
 F-NT2RP3001672
 F-NT2RP3001676//GTP-BINDING PROTEIN LEPA (FRAGMENT).//1.2e-15:56:6:2//PSEUDOMONAS FLUORESCENS.//P26843
 F-NT2RP3001678//SPIDROIN 2 (DRAGLINE SILK FIBROIN 2) (FRAGMENT).//0.054:187:31//NEMPHILA CLAVIPES (ORB SPIDER).//P46804
 F-NT2RP3001679//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME 111.//1.5e-07:63:44//CAENORHABDITIS ELEGANS.//P34679
 F-NT2RP3001688//GLUCANAMYLASE S1 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE) (GA1).//1.0:83:28//SACCHAROMYCES DIASTATICUS (YEAST).//P04065
 F-NT2RP3001690//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//0.021:247:24//HOMO SAPIENS (HUMAN).//P12883
 F-NT2RP3001698
 F-NT2RP3001708//TWISTED GASTRULATION PROTEIN PRECURSOR.//7.7e-12:7:3:43//DROSOPHILA MELANOGASTER (FRUIT FLY).//P54356
 F-NT2RP3001712//CEC-1 PROTEIN.//1.9e-07:121:29//CAENORHABDITIS ELEGANS.//P34618
 F-NT2RP3001716//SALIVARY GLUE PROTEIN SGS-3 PRECURSOR.//0.89:54:40//DROSOPHILA SIMULANS (FRUIT FLY).//P13729
 F-NT2RP3001724//CHROMODOMAIN-HELICASE-DNA-BINDING PROTEIN 1 (CHD-1).//7.7e-41:164:48//HOMO SAPIENS (HUMAN).//Q14646
 F-NT2RP3001727//HYPOTHETICAL 37.7 KD PROTEIN ZK686.3 IN CHROMOSOME 111.//1.5e-51:240:41//CAENORHABDITIS ELEGANS.//P34669
 F-NT2RP3001730//SEPTIN 2 HOMOLOG (FRAGMENT).//2.4e-122:267:86//HOMO SAPIENS (HUMAN).//Q14141
 F-NT2RP3001739//INTESTINAL SODIUM/DICARBOXYLATE COTRANSPORTER (NA (+)/DICARBOXYLATE COTRANSPORTER).//0.99:63:34//RATTUS NORVEGICUS (RAT).//P70545
 F-NT2RP3001752//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//4.0e-21:60:85//HOMO SAPIENS (HUMAN).//P39193
 F-NT2RP3001753//HYPOTHETICAL PROTEIN KIAA0127.//7.9e-12:83:44//HOMO SAPIENS (HUMAN).//Q14140
 F-NT2RP3001764//DUAL SPECIFICITY PROTEIN PHOSPHATASE 6 (EC 3.1.3.4) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE PYST1).//7.7e-25:146:36//HOMO SAPIENS (HUMAN).//Q16828
 F-NT2RP3001777//SERINE/THREONINE-PROTEIN KINASE STE20 HOMOLOG (EC 2.7.1.-).//0.0096:204:25//CANDIDA ALBICANS (YEAST).//Q92212
 F-NT2RP3001782//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.91:34:44//PONGO PYGMAEUS ABELII (SUMATRAN ORANGUTAN).//P92694
 F-NT2RP3001792//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRPM).//1.8e-33:159:53//HOMO SAPIENS (HUMAN).//P52272
 F-NT2RP3001799//LIGHT-HARVESTING PROTEIN B800/830/1020, ALPHA-2 CHAIN (EHS-ALPHA-2) (ANTENNA PIGMENT PROTEIN, ALPHA-2 CHAIN).//0.14:46:28//ECTOTHORHODOSPIRA HALOCHLORIS.//P80103
 F-NT2RP3001819//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR.//0.00030:7:7:36//HOMO SAPIENS (HUMAN).//P08123
 F-NT2RP3001844//OCTAMER-BINDING TRANSCRIPTION FACTOR 1 (OTF-1) (N F-A1) (FRAGMENT).//0.99:43:34//MACROPUS EUGENII (TAMMAR WALLABY).//Q48466
 F-NT2RP3001854//FIBRINOGEN- AND IGF-BINDING PROTEIN PRECURSOR (NRP PROTEIN).//9.3e-10:213:24//STREPTOCOCCUS PYOGENES.//P30141
 F-NT2RP3001855//HOMEBOX PROTEIN PKNOX1 (HOMEBOX PROTEIN PREP-1).//2.6e-61:220:60//HOMO SAPIENS (HUMAN).//P55347
 F-NT2RP3001857//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1.//1.0e-13:213:24//PODOSPORA ANSERINA.//Q00808
 F-NT2RP3001896//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A6).//0.074:124:34//HOMO SAPIENS (HUMAN).//Q15428
 F-NT2RP3001898//REGULATORY PROTEIN E2.//0.36:131:29//CANINE ORAL PAPILLOMAVIRUS (CPV).//Q89420
 F-NT2RP3001915//CHITIN BIOSYNTHESIS PROTEIN CHS5 (CAL3 PROTEIN).//0.0021:237:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12114
 F-NT2RP3001926//HYPOTHETICAL 14.0 KD PROTEIN IN RPL15B-CCR3 INTERGENIC REGION.//1.0:63:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03880
 F-NT2RP3001929//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.4e-14:35:60//HOMO SAPIENS (HUMAN).//P39195
 F-NT2RP3001931//HYPOTHETICAL 59.3 KD PROTEIN IN TAP42-ARF9 INTERGENIC REGION.//0.86:162:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q05040
 F-NT2RP3001938//GLYCOPROTEIN GP50.//0.0036:54:40//PSEUDORABIES VIRUS (STRAIN RICE) (PRV).//P07645
 F-NT2RP3001943//33.2 KD PROTEIN IN DIND-RPH INTERGENIC REGION (ORF X).//1.0:113:27//ESCHERICHIA COLI.//P23839
 F-NT2RP3001944//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME E 111.//4.1e-56:208:47//CAENORHABDITIS ELEGANS.//Q09251
 F-NT2RP3001969//PUFF 11/8-2 PROTEIN PRECURSOR.//0.0078:149:26//SCIAEOPHILA (FUNGUS GNAT).//P22312
 F-NT2RP3001989//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE).//1.0:41:31//MUS MUSCULUS (MOUSE).//P02319
 F-NT2RP3002002//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.2e-44:69:79//HOMO SAPIENS (HUMAN).//P39195
 F-NT2RP3002004//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2).//0.00024:45:40//MUS MUSCULUS (MOUSE).//Q61345
 F-NT2RP3002007//TENASCIN PRECURSOR (TN) (HEXABRACHION) (CYTOTACTIN) (NEURONECTIN) (CNEP) (J1) (MOTENDINOUS ANTIGEN) (GLIOMA-ASSOCI

【0669】

【表371】

ATED-EXTRACELLULAR MATRIX ANTIGEN) (GP 150-225) (TENASCIN-C). //0.2
1:115:28//HOMO SAPIENS (HUMAN). //P24821
F-NT2RP3002014//HYPOTHETICAL 32.0 KD PROTEIN C9F5.2 IN CHROMOSOME
111. //1.7e-25:139:48//CAENORHABDITIS ELEGANS. //Q09232
F-NT2RP3002033//ACTIVATOR OF APOPTOSIS HARAKIRI (NEURONAL DEATH PR
OTEIN DPS). //0.14:65:41//HOMO SAPIENS (HUMAN). //000198
F-NT2RP3002045//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX
2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA
MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT). //0.1e-108:192:9
8//MUS MUSCULUS (MOUSE). //P17427
F-NT2RP3002054//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.
//0.046:176:31//STREPTOMYCES FRADIAE. //P20186
F-NT2RP3002056//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140). //1.4e-0
7:245:25//RATTUS NORVEGICUS (RAT). //P41777
F-NT2RP3002057//SMALL HYDROPHOBIC PROTEIN. //1.0:12:66//SIMIAN VIRU
S 5 (STRAIN W3) (SVS). //P07577
F-NT2RP3002062//PROTEASE A INHIBITOR 3 (PROTEINASE INHIBITOR 1(A)
3). //1.0:49:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P01094
F-NT2RP3002063//ACYL CARRIER PROTEIN (ACP). //0.99:38:31//HAEMOPHIL
US INFLUENZAE. //P43709
F-NT2RP3002081//HYPOTHETICAL 100.5 KD PROTEIN C189.04 IN CHROMOSOM
E 1. //5.8e-35:253:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //Q10429
F-NT2RP3002097//HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-GCR2 INTERGE
NIC REGION. //6.2e-06:99:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
T). //P40164
F-NT2RP3002102//HYPOTHETICAL 7.4 KD PROTEIN. //0.68:34:47//THERMOPR
OTUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1). //P19302
F-NT2RP3002108//HYPOTHETICAL 105.5 KD PROTEIN R13F6.10 IN CHROMOSO
ME 111. //7.9e-19:179:34//CAENORHABDITIS ELEGANS. //Q21986
F-NT2RP3002142//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.6e-17:3
7:75//HOMO SAPIENS (HUMAN). //P39188
F-NT2RP3002146//CUTICLE COLLAGEN 40. //0.00034:90:37//CAENORHABDITI
S ELEGANS. //P34804
F-NT2RP3002147//SALIVARY PROLINE-RICH PROTEIN PO PRECURSOR (ALLELE
S). //0.011:166:28//HOMO SAPIENS (HUMAN). //P10163
F-NT2RP3002151//G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (GTP-BI
NDING PROTEIN GST1-HS). //4.8e-11:60:53//HOMO SAPIENS (HUMAN). //P15
170
F-NT2RP3002163//TRANSCRIPTION INITIATION FACTOR TF1D 135 KD SUBUN
IT (TAF11-135) (TAF11135) (TAF11-130) (TAF11130). //0.028:191:29//H
OMO SAPIENS (HUMAN). //000268
F-NT2RP3002165//TRANSCRIPTIONAL REGULATOR PROTEIN HCNPG. //2.3e-13.
1:223:91//MUS MUSCULUS (MOUSE). //Q02614
F-NT2RP3002166//D-ALANYL CARRIER PROTEIN (DCP). //1.0:65:33//LACTOB
ACILLUS CASEI. //P55153
F-NT2RP3002173//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.4e-26:
114:62//HOMO SAPIENS (HUMAN). //P39194
F-NT2RP3002181//MALE SPECIFIC SPERM PROTEIN MSTR4DD. //0.25:31:38//
DROSOPHILA MELANOGASTER (FRUIT FLY). //Q01645
F-NT2RP3002244//SPERM PROTAMINE P1 (CYSTEINE-RICH PROTAMINE). //0.0
69:16:62//OVIS ARIES (SHEEP), AND CAPRA HIRCUS (GOAT). //P04102
F-NT2RP3002248//MICROFIBRILLAR-ASSOCIATED PROTEIN 1 (ASSOCIATED MI
CROFIBRIL PROTEIN) (AMP). //0.0079:187:24//GALLUS GALLUS (CHICKEN).
//P55080
F-NT2RP3002255//PROLINE-RICH PROTEIN NP-3 (FRAGMENT). //4.6e-10:16
8:34//MUS MUSCULUS (MOUSE). //P05143
F-NT2RP3002273//SCD6 PROTEIN. //1.5e-11:160:33//SACCHAROMYCES CEREV
ISIAE (BAKER'S YEAST). //P45978
F-NT2RP3002276//PROBABLE E4 PROTEIN. //0.91:54:29//HUMAN PAPILLOMAV
IRUS TYPE 16. //P06922
F-NT2RP3002303//HYPOTHETICAL 30.2 KD PROTEIN C407.04C IN CHROMOSOM
E 1. //1.7e-42:191:43//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //Q14171
F-NT2RP3002304
F-NT2RP3002330//NRP-1 PROTEIN. //0.52:140:18//MUS MUSCULUS (MOUSE).
//P56183
F-NT2RP3002343//SE5 ANTIGEN. //0.0056:189:30//RATTUS NORVEGICUS (RA
T). //Q63003
F-NT2RP3002351//NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGEN
ASE (EC 1.5.1.15) / METHENYLTETRAHYDROFOLATE CYCLOHYDROLASE (EC 3.
5.4.9) MITOCHONDRIAL PRECURSOR. //1.0e-66:196:68//HOMO SAPIENS (HUM
AN). //P13995
F-NT2RP3002352//PRESYNAPTIC PROTEIN SAPI02 (SYNAPSE-ASSOCIATED PRO
TEIN 102) (NEUROENDOCRINE-DLG) (NE-DLG). //0.79:173:27//HOMO SAPIEN
S (HUMAN). //Q92796
F-NT2RP3002377//PUTATIVE HELICASE YGR271W. //1.0e-56:216:44//SACCHA
ROMYCES CEREVISIAE (BAKER'S YEAST). //P53327
F-NT2RP3002399//MINICHROMOSOME MAINTENANCE PROTEIN 6. //1.4e-19:13
6:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P53091
F-NT2RP3002402//EBNA-6 NUCLEAR PROTEIN (EBNA-3C) (EBNA-4B). //0.74:
107:36//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4). //P03204
F-NT2RP3002455//DNAJ PROTEIN (FRAGMENT). //5.6e-06:57:42//AGROBACTE
RIUM TUMEFACIENS. //P50018
F-NT2RP3002484//HYPOTHETICAL 46.5 KD PROTEIN C12B10.04 IN CHROMOSO
ME 1. //0.00032:52:48//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //Q10438
F-NT2RP3002501//HYPOTHETICAL 34.9 KD PROTEIN IN FRE2-JEN1 INTERGEN
IC REGION. //9.4e-42:209:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
T). //P36007
F-NT2RP3002512//HYPOTHETICAL 37.4 KD PROTEIN IN GPM1-MCR1 INTERGEN
IC REGION. //7.7e-32:162:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
T). //P36059
F-NT2RP3002529//PUTATIVE VACUOLAR PROTEIN SORTING-ASSOCIATED PROTE
IN C2G11.03C. //2.1e-45:241:43//SCHIZOSACCHAROMYCES POMBE (FISSION
YEAST). //Q09805
F-NT2RP3002545
F-NT2RP3002549//HYPOTHETICAL 26.6 KD PROTEIN T19C3.4 IN CHROMOSOME
111. //2.8e-41:161:52//CAENORHABDITIS ELEGANS. //Q10010
F-NT2RP3002566//IMMEDIATE-EARLY PROTEIN IE180. //0.56:130:24//PSEUD
ORABIES VIRUS (STRAIN KAPLAN) (PRV). //P33479
F-NT2RP3002587
F-NT2RP3002590
F-NT2RP3002602//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.
3.4.1) (THIOREDOXIN-RELATED GLYCOPROTEIN 1). //0.00091:111:28//SAC
CHAROMYCES CEREVISIAE (BAKER'S YEAST). //P17967
F-NT2RP3002603//HYPOTHETICAL 14.2 KD PROTEIN IN BLAB 3' REGION. //1.
0:65:40//STREPTOMYCES CACAO1. //P33654
F-NT2RP3002628//DNAJ-LIKE PROTEIN SLR0093. //2.4e-17:101:44//SYNECH
OCYSTIS SP. (STRAIN PCC 6803). //P50027
F-NT2RP3002631//METALLOTHIONEIN-1B (MT-1B). //0.092:36:33//HOMO SAP
IENS (HUMAN). //P07438
F-NT2RP3002650//DUALIN. //3.0e-21:184:37//GALLUS GALLUS (CHICKEN). //Q90830
F-NT2RP3002659//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR. //0.00016:2
23:33//HOMO SAPIENS (HUMAN). //P08123
F-NT2RP3002660//40S RIBOSOMAL PROTEIN S27A. //0.16:72:31//CAENORHAB
DITIS ELEGANS. //P37165
F-NT2RP3002663//OXYSTEROL-BINDING PROTEIN. //5.4e-23:168:41//HOMO S
APIENS (HUMAN). //P22059
F-NT2RP3002671//HYPOTHETICAL 124.5 KD PROTEIN IN SKO1-RPL44A INTER
GENIC REGION. //6.0e-38:203:43//SACCHAROMYCES CEREVISIAE (BAKER'S Y
EAST). //P53893
F-NT2RP3002682//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.
3). //0.25:63:31//ARTEMIA SALINA (BRINE SHRIMP). //P19049
F-NT2RP3002687//HYPOTHETICAL 30.4 KD PROTEIN IN LEF3-IAP2 INTERGEN
IC REGION. //0.029:60:36//AUTOPHAGIA CALIFORNICA NUCLEAR POLYHEDROS
IS VIRUS (ACMPV). //P41469
F-NT2RP3002688//KINESIN-LIKE PROTEIN KIF18. //5.3e-61:130:88//MUS M
USCULUS (MOUSE). //Q60575
F-NT2RP3002701//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS). //7.
4e-05:109:33//MUS MUSCULUS (MOUSE). //P15265
F-NT2RP3002713//PROBABLE ATP-DEPENDENT RNA HELICASE DDX10 (DEAH BO
X PROTEIN 10). //0.77:70:32//HOMO SAPIENS (HUMAN). //Q13206
F-NT2RP3002763//HYPOTHETICAL 11.3 KD PROTEIN C2C6.07 IN CHROMOSOME
1. //6.7e-11:66:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //Q1
4056
F-NT2RP3002770//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT). //0.33:87:34
//MUS MUSCULUS (MOUSE). //Q05722
F-NT2RP3002785//LETHAL(2) DENTICLELESS PROTEIN (DTL83 PROTEIN). //9.
7e-36:187:39//DROSOPHILA MELANOGASTER (FRUIT FLY). //Q24371
F-NT2RP3002799//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//5.6e-08:4
1:73//HOMO SAPIENS (HUMAN). //P39188
F-NT2RP3002810//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//0.0034:3
5:65//HOMO SAPIENS (HUMAN). //P39193
F-NT2RP3002818//MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN
B) (CENP-B). //3.2e-17:148:37//MUS MUSCULUS (MOUSE). //P27790
F-NT2RP3002861//HYPOTHETICAL 70.2 KD PROTEIN IN GSH1-CHS6 INTERGEN
IC REGION. //1.7e-05:95:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
T). //P42951
F-NT2RP3002869//TRYPSIN INHIBITOR 11 (BOT1-11). //0.97:23:39//BRYON
IA DIOICA (RED BRYONY). //P11968
F-NT2RP3002876//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP3
3). //0.00017:140:31//RATTUS NORVEGICUS (RAT). //P04474
F-NT2RP3002877//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.5e-06:
55:60//HOMO SAPIENS (HUMAN). //P39194
F-NT2RP3002909//P53-BINDING PROTEIN 53BP2 (BCL2-BINDING PROTEIN)
(BBP). //4.6e-08:129:38//HOMO SAPIENS (HUMAN). //Q13625
F-NT2RP3002911//HYPOTHETICAL PROTEIN C18. //0.99:26:50//SWINEPOX VI

【0670】

【表372】

RUS (STRAIN KASZA) (SPV).//P32217
 F-NT2RP3002948//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-23:113:47//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
 F-NT2RP3002953//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT P ROTIN).//0.55:115:27//DROSOPHILA MELANOGASTER (FRUIT FLY).//P33450
 F-NT2RP3002955//HYPOTHETICAL 16.5 KD PROTEIN IN BLTR-SPO11IC INTERGENIC REGION.//0.87:67:37//BACILLUS SUBTILIS.//P54445
 F-NT2RP3002969//LONG-CHAIN-FATTY-ACID-COA LIGASE 4 (EC 6.2.1.3) (LONG-CHAIN ACYL-COA SYNTHETASE 4) (LACS 4).//6.7e-56:189:59//HOMO SAPIENS (HUMAN).//Q06488
 F-NT2RP3002974//HYPOTHETICAL 73.0 KD PROTEIN IN CLAA-MID1 INTERGENIC REGION.//0.0028:147:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS T).//P48566
 F-NT2RP3002978//PROBABLE E5 PROTEIN.//0.15:55:36//HUMAN PAPILLOMAVIRUS TYPE 51.//P26553
 F-NT2RP3002985//METALLOTHIONEIN (MT).//0.0031:49:42//PLEURONECTES PLATESSA (PLAICE).//P07216
 F-NT2RP3002988//NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR (NOTCH PROTEIN).//1.1:0:111:29//MUS MUSCULUS (MOUSE).//Q01705
 F-NT2RP3003008//HYPOTHETICAL 54.7 KD PROTEIN F37A4.1 IN CHROMOSOME 111.//0.96:112:25//CAENORHABDITIS ELEGANS.//P41879
 F-NT2RP3003032
 F-NT2RP3003059//HYPOTHETICAL 52.3 KD PROTEIN C56F8.06C IN CHROMOSOME 1 PRECURSOR.//9.7e-27:216:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10254
 F-NT2RP3003061//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//3.7e-25:167:34//HOMO SAPIENS (HUMAN).//P16157
 F-NT2RP3003068//SERYL-TRNA SYNTHETASE (EC 6.1.1.11) (SERINE--TRNA LIGASE) (SERRS) (FRAGMENT).//0.074:82:39//SULFOLOBUS SOLFATARICUS.//Q033780
 F-NT2RP3003071//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//0.085:128:30//HOMO SAPIENS (HUMAN).//P50552
 F-NT2RP3003078//SPERM ACROSOMAL PROTEIN FSA-ACR.1 PRECURSOR (FRAGMENT).//0.028:165:31//VULPES VULPES (RED FOX).//P53353
 F-NT2RP3003101//TETRACYCLINE RESISTANCE PROTEIN, CLASS C (TETA(C)).//1.0e-14:243:25//ESCHERICHIA COLI.//P02981
 F-NT2RP3003121//SUPPRESSOR PROTEIN SRP40.//7.4e-05:143:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
 F-NT2RP3003133//65 KD YES-ASSOCIATED PROTEIN (YAP65).//0.024:61:42//GALLUS GALLUS (CHICKEN).//P46936
 F-NT2RP3003138//KINESIN-LIKE PROTEIN K1F4.//1.1e-118:151:93//MUS MUSCULUS (MOUSE).//P33174
 F-NT2RP3003139//ATP-BINDING CASSETTE TRANSPORTER ABC1.//1.0:70:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q92337
 F-NT2RP3003145//MILK FAT GLOBULE-EGF FACTOR 8 PRECURSOR (MFG-E8) (MFG) (BREAST EPITHELIAL ANTIGEN BA46) (MFGN).//2.0e-12:121:37//HOMO SAPIENS (HUMAN).//Q08431
 F-NT2RP3003150
 F-NT2RP3003151//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//4.0e-79:260:54//HOMO SAPIENS (HUMAN).//P51522
 F-NT2RP3003185//TROPOMYOSIN.//0.077:122:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q02088
 F-NT2RP3003193//ZINC FINGER PROTEIN 135.//7.2e-91:239:65//HOMO SAPIENS (HUMAN).//P52742
 F-NT2RP3003197//HYPOTHETICAL 28.1 KD PROTEIN IN SIPU-PBPC INTERGENIC REGION.//1.3e-07:117:34//BACILLUS SUBTILIS.//P42966
 F-NT2RP3003203//HYPOTHETICAL 33.5 KD PROTEIN CID4.02C IN CHROMOSOME 1.//9.9e-23:132:39//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10149
 F-NT2RP3003204//RAS-LIKE PROTEIN RASB.//0.92:103:27//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P32252
 F-NT2RP3003210//VERY HYPOTHETICAL 13.2 KD PROTEIN IN PTC3-SAS3 INTERGENIC REGION.//0.23:106:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38190
 F-NT2RP3003212//SUPPRESSOR PROTEIN SRP40.//0.019:171:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
 F-NT2RP3003230//CORONIN-LIKE PROTEIN P57.//8.3e-74:183:73//BOS TAURUS (BOVINE).//Q92176
 F-NT2RP3003242//STANNICALCIN PRECURSOR.//1.4e-21:127:37//HOMO SAPIENS (HUMAN).//P52823
 F-NT2RP3003251//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//3.1e-51:198:52//MUS MUSCULUS (MOUSE).//P15533
 F-NT2RP3003264//E6 PROTEIN.//1.0:31:41//HUMAN PAPILLOMAVIRUS TYPE 48.//Q08920
 F-NT2RP3003278//45.8 KD PROTEIN IN SHM1-MRPL37 INTERGENIC REGION.//8.6e-07:80:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38344
 F-NT2RP3003282//DYNAMIN 2 (DYNAMIN UDMN).//8.0e-108:226:88//MUS MUSCULUS (MOUSE).//P39054
 F-NT2RP3003290//BIOM PROTEIN.//0.0055:107:30//ESCHERICHIA COLI.//P13001
 F-NT2RP3003301//MITOCHONDRIAL LOW PROTEASE HOMOLOG 1 PRECURSOR (EC 3.4.21.-).//1.3e-69:200:55//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q064948
 F-NT2RP3003302//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.4e-69:102:66//HOMO SAPIENS (HUMAN).//P08547
 F-NT2RP3003311//MYOSIN II HEAVY CHAIN, NON MUSCLE.//0.18:225:26//A CANTHAMEBA CASTELLANI (AMOEBA).//P05659
 F-NT2RP3003313//SALIVARY PROLINE-RICH PROTEIN PD (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.0014:142:33//HOMO SAPIENS (HUMAN).//P10162
 F-NT2RP3003327//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) (RO52).//8.8e-18:94:43//MUS MUSCULUS (MOUSE).//Q62191
 F-NT2RP3003330//HYPOTHETICAL PROTEIN KIAAD176 (FRAGMENT).//1.3e-20:123:44//HOMO SAPIENS (HUMAN).//Q14681
 F-NT2RP3003344//HYPOTHETICAL 8.8 KD PROTEIN IN ICDC-MINE INTERGENIC REGION.//1.0:28:42//ESCHERICHIA COLI.//P75991
 F-NT2RP3003346//!!!! ALU SUBFAMILY S82 WARNING ENTRY !!!!//6.9e-26:74:78//HOMO SAPIENS (HUMAN).//P39191
 F-NT2RP3003353//HYPOTHETICAL 52.4 KD PROTEIN R08D7.2 IN CHROMOSOME 111.//3.7e-10:118:33//CAENORHABDITIS ELEGANS.//P30641
 F-NT2RP3003377//PUTATIVE CUTICLE COLLAGEN F09G8.6.//1.5e-05:102:37//CAENORHABDITIS ELEGANS.//P34391
 F-NT2RP3003384
 F-NT2RP3003385//SKD3 PROTEIN.//5.1e-83:210:69//MUS MUSCULUS (MOUSE).//Q06049
 F-NT2RP3003403
 F-NT2RP3003409//SOX-22 PROTEIN.//0.042:173:28//HOMO SAPIENS (HUMAN).//Q15370
 F-NT2RP3003411//PROBABLE E3 PROTEIN.//0.17:91:31//BOVINE PAPILLOMAVIRUS TYPE 2.//P11300
 F-NT2RP3003427//MOLOTICIN 3 PRECURSOR.//0.012:36:41//MOLOTICIN 3 DIOMPHALIA.//Q25055
 F-NT2RP3003433
 F-NT2RP3003464//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION.//0.0042:110:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53214
 F-NT2RP3003490
 F-NT2RP3003491//10 KD CHAPERONIN (PROTEIN CPN10) (PROTEIN GROES) (HEAT SHOCK 10 KD PROTEIN).//0.99:49:34//LEPTOSPIRA INTERROGANS.//P35472
 F-NT2RP3003500//SCY1 PROTEIN.//6.8e-14:192:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53009
 F-NT2RP3003543//COLLAGEN ALPHA 5(IV) CHAIN PRECURSOR.//0.0026:175:30//HOMO SAPIENS (HUMAN).//P29400
 F-NT2RP3003552//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.19:21:47//BOS TAURUS (BOVINE).//P20072
 F-NT2RP3003555//HYPOTHETICAL 32.6 KD PROTEIN IN MET30-PIG2 INTERGENIC REGION.//7.3e-27:159:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40529
 F-NT2RP3003564//RNA REPLICASE POLYPROTEIN (EC 2.7.7.48).//1.0:99:30//TURNIP YELLOW MOSAIC VIRUS.//P10358
 F-NT2RP3003572//PUTATIVE CUTICLE COLLAGEN F09G8.6.//0.33:128:32//CAENORHABDITIS ELEGANS.//P34391
 F-NT2RP3003576//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//7.1e-28:58:77//HOMO SAPIENS (HUMAN).//P39195
 F-NT2RP3003589//RAS-RELATED PROTEIN RAB-10.//5.4e-54:114:94//CANIS FAMILIARIS (DOG).//P24409
 F-NT2RP3003621//COAGULATION FACTOR XI PRECURSOR (EC 3.4.21.38) (HAGEMAN FACTOR) (HAF).//2.0e-15:89:40//HOMO SAPIENS (HUMAN).//P00748
 F-NT2RP3003625//MALE SPECIFIC SPERM PROTEIN MST84DD.//0.99:22:50//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645
 F-NT2RP3003656//HOMEBOX PROTEIN OTX3 (ZOTX3).//0.30:111:25//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO).//Q90267
 F-NT2RP3003659//HYPOTHETICAL 49.8 KD PROTEIN IN RPL14B-GPA1 INTERGENIC REGION.//1.1e-20:127:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38755
 F-NT2RP3003665//PENAEIDIN-3C PRECURSOR (P3-C).//0.34:52:34//PENAEUS VANNAMEI (PENAEID SHRIMP) (EUROPEAN WHITE SHRIMP).//P81060
 F-NT2RP3003672//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (M1C2 PROTEIN) (I2E7).//8.7e-15:146:42//HOMO SAPIENS (HUMAN).//P14209
 F-NT2RP3003680//HYPOTHETICAL 55.1 KD PROTEIN IN FABI-PES4 INTERGENIC REGION.//4.3e-25:159:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43601
 F-NT2RP3003686//NONHISTONE CHROMOSOMAL PROTEIN HMG-17.//0.067:63:31//GALLUS GALLUS (CHICKEN).//P02314
 F-NT2RP3003701//F-SPONDIN PRECURSOR.//1.8e-13:193:27//RATTUS NORVE

【0671】

【表3.73】

GICUS (RAT). //P35446
 F-NT2RP3003716//SLIT PROTEIN PRECURSOR. //1.3e-12:150:34//DROSOPHILA A MELANOGASTER (FRUIT FLY). //P24014
 F-NT2RP3003726//INSERTION ELEMENT IS136 HYPOTHETICAL 16.9 KD PROTEIN. //0.47:109:28//AGROBACTERIUM TUMEFACIENS. //P05680
 F-NT2RP3003746//HYPOTHETICAL 7.7 KD PROTEIN IN FIXX 3' REGION (ORF 1). //0.57:34:38//AZORHIZOBIIUM CAULINODANS. //P26486
 F-NT2RP3003795//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//4.3e-10:40:90//HOMO SAPIENS (HUMAN). //P39195
 F-NT2RP3003799//MATING-TYPE PHEROMONE BBP1(3) PRECURSOR. //0.75:60:36//SCHIZOPHYLLUM COMMUNE (BRACKET FUNGUS). //P78744
 F-NT2RP3003800//PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC (EC 2.7.1.12) (P60-SRC). //4.2e-51:72:95//GALLUS GALLUS (CHICKEN). //P00523
 F-NT2RP3003805//HYPOTHETICAL 32.1 KD PROTEIN IN DBP7-GCN3 INTERGENIC REGION. //0.00069:160:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P36121
 F-NT2RP3003809//COLLAGEN ALPHA 1(I1) CHAIN (FRAGMENTS). //0.028:13:5:35//GALLUS GALLUS (CHICKEN). //P12105
 F-NT2RP3003819//C-HORDEIN (PCP387) (FRAGMENT). //0.0026:90:33//HORD ELM VULGARE (BARLEY). //P06472
 F-NT2RP3003825//PHOSPHATIDYLCHOLINE TRANSFER PROTEIN (PC-TP). //5.6e-20:174:31//BOS TAURUS (BOVINE). //P02720
 F-NT2RP3003828//ADENYLATE CYCLASE, TYPE V (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (CA(2+)-INHIBITABLE ADENYL CYCLASE). //0.0017:111:38//CANIS FAMILIARIS (DOG). //P30803
 F-NT2RP3003831//ENDONUCLEASE C PRECURSOR (EC 3.1.30.-) (ENDO G). //1.1e-37:187:42//MUS MUSCULUS (MOUSE). //P008600
 F-NT2RP3003833//HYPOTHETICAL 6.4 KD PROTEIN IN INTE-PIN INTERGENIC REGION. //1.0:38:39//ESCHERICHIA COLI. //P75979
 F-NT2RP3003842
 F-NT2RP3003846//RETINAL DEGENERATION B PROTEIN (PROBABLE CALCIUM TRANSPORTER RDBG). //0.61:54:35//DROSOPHILA MELANOGASTER (FRUIT FLY). //P43125
 F-NT2RP3003870//MALE SPECIFIC SPERM PROTEIN MST840B. //0.83:51:37//DROSOPHILA MELANOGASTER (FRUIT FLY). //Q01643
 F-NT2RP3003876//PROTEIN TRANSPORT PROTEIN SEC2. //0.0017:151:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P17065
 F-NT2RP3003914//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT). //3.3e-23:76:64//DROSOPHILA MELANOGASTER (FRUIT FLY). //Q09332
 F-NT2RP3003918//VESICLE-ASSOCIATED MEMBRANE PROTEIN/SYNAPOBREVIN BINDING PROTEIN (VAP-33). //5.5e-45:127:69//APLYSIA CALIFORNICA (CALIFORNIA SEA HARE). //Q16943
 F-NT2RP3003932
 F-NT2RP3003989//PREPROTEIN TRANSLOCASE SECE SUBUNIT. //0.96:46:32//THERMOTOGA MARITIMA. //P35874
 F-NT2RP3003992//NUCLEAR LOCALIZATION SEQUENCE BINDING PROTEIN (P67). //0.0011:170:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P27476
 F-NT2RP3004013//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1). //3.6e-21:13:4:45//RATTUS NORVEGICUS (RAT). //P51400
 F-NT2RP3004016//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION. //0.00021:64:40//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACNPV). //P41479
 F-NT2RP3004041//SPERM PROTEIN P1. //0.0028:43:46//ORNITHORHYNCHUS ANATINUS (DUCKBILL PLATYPUS). //P35307
 F-NT2RP3004051//MICROBIAL COLLAGENASE PRECURSOR (EC 3.4.24.3) (120 KD COLLAGENASE). //0.0079:194:24//CLOSTRIDIUM PERFRINGENS. //P43153
 F-NT2RP3004070//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.4e-11:5:1:72//HOMO SAPIENS (HUMAN). //P39188
 F-NT2RP3004078//DNA BINDING PROTEIN RFX2. //2.7e-114:243:87//MUS MUSCULUS (MOUSE). //P48379
 F-NT2RP3004093//HYPOTHETICAL 32.3 KD PROTEIN IN RHSE-MARV INTERGENIC REGION (ORF8). //0.0e-13:111:41//ESCHERICHIA COLI. //P37757
 F-NT2RP3004095//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-17:7:2:65//HOMO SAPIENS (HUMAN). //P39188
 F-NT2RP3004110//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.6e-10:51:72//HOMO SAPIENS (HUMAN). //P39195
 F-NT2RP3004125//ZINC FINGER PROTEIN 75. //1.1e-28:118:47//HOMO SAPIENS (HUMAN). //P51815
 F-NT2RP3004145//AEROLYSIN REGULATORY PROTEIN. //0.012:45:33//AEROMONAS SOBRIA. //P09165
 F-NT2RP3004148//METALLOTHIONEIN-1 (MT-1). //0.055:18:50//COLUMBA LIVIA (DOMESTIC PIGEON). //P15786
 F-NT2RP3004155//UBIQUINONE BIOSYNTHESIS PROTEIN COQ7 HOMOLOG. //1.7e-82:178:89//RATTUS NORVEGICUS (RAT). //Q63619
 F-NT2RP3004189//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1. //1.7e-11:215:24//PODOSPORA ANSERINA. //Q00808
 F-NT2RP3004206//CROOKED NECK PROTEIN. //3.8e-101:241:73//DROSOPHILA MELANOGASTER (FRUIT FLY). //P17886
 F-NT2RP3004207//CUTICLE COLLAGEN 12 PRECURSOR. //0.13:130:33//CAENORHABDITIS ELEGANS. //P20630
 F-NT2RP3004209//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG). //6.5e-16:207:29//HOMO SAPIENS (HUMAN). //Q13107
 F-NT2RP3004215//PROTEIN TRANSPORT PROTEIN SEC61 GAMMA SUBUNIT. //1.0:69:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P35179
 F-NT2RP3004242//HYPOTHETICAL 30.2 KD PROTEIN ZK632.12 IN CHROMOSOME 111. //1.1e-64:191:63//CAENORHABDITIS ELEGANS. //P34657
 F-NT2RP3004246//RING3 PROTEIN (KIAA9001). //0.060:101:28//HOMO SAPIENS (HUMAN). //P25440
 F-NT2RP3004253//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS). //1.1e-07:18:4:35//BOS TAURUS (BOVINE). //P02453
 F-NT2RP3004258//SUPPRESSOR PROTEIN SRP40. //4.9e-08:98:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P32583
 F-NT2RP3004262//DNAJ PROTEIN HOMOLOG 1 (HDJ-1) (HEAT SHOCK PROTEIN 40) (HSP40). //1.6e-63:210:61//HOMO SAPIENS (HUMAN). //P25685
 F-NT2RP3004282//HYPOTHETICAL PROTEIN F44G.1 IN CHROMOSOME 11 (FRAGMENT). //1.6e-29:177:38//CAENORHABDITIS ELEGANS. //P54073
 F-NT2RP3004332//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT). //0.030:118:36//CRICETULUS GRISEUS (CHINESE HAMSTER). //P11414
 F-NT2RP3004334
 F-NT2RP3004341//ALPHA-INTERNEKIN (ALPHA-INK). //0.91:110:26//MUS MUSCULUS (MOUSE). //P46660
 F-NT2RP3004348//HYPOTHETICAL 105.3 KD PROTEIN C01G6.5 IN CHROMOSOME 111. //0.60:198:24//CAENORHABDITIS ELEGANS. //P46012
 F-NT2RP3004349//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.0e-37:60:76//HOMO SAPIENS (HUMAN). //P39193
 F-NT2RP3004378//HYPOTHETICAL 18.8 KD PROTEIN IN CNTR-CGT INTERGENIC REGION (O162). //0.0026:76:28//ESCHERICHIA COLI. //P46854
 F-NT2RP3004399//LEUCINE-RICH PRIMARY RESPONSE PROTEIN 1 (FOLLICLE-STIMULATING HORMONE PRIMARY RESPONSE PROTEIN). //4.4e-109:212:96//HOMO SAPIENS (HUMAN). //Q92674
 F-NT2RP3004424//JTV-1 PROTEIN. //4.5e-18:60:70//HOMO SAPIENS (HUMAN). //Q13155
 F-NT2RP3004428//METALLOTHIONEIN-A (MTA). //0.0010:36:47//STROMBYLOC ENTROTUS PURPURATUS (PURPLE SEA URCHIN). //P04734
 F-NT2RP3004451//MYOSIN IC HEAVY CHAIN. //0.00072:113:34//ACANTHAMOEBA CASTELLANII (AMOEBA). //P10569
 F-NT2RP3004454//VERPROLIN. //3.3e-07:156:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P37370
 F-NT2RP3004466//HYPOTHETICAL PROTEIN F-215. //0.0013:125:32//HUMAN ADENOVIRUS TYPE 2. //P03291
 F-NT2RP3004470//HYPOTHETICAL 15.4 KD PROTEIN C16C10.11 IN CHROMOSOME 111. //1.0:33:51//CAENORHABDITIS ELEGANS. //Q09254
 F-NT2RP3004472//GERM CELL-LESS PROTEIN. //7.3e-33:170:40//DROSOPHILA MELANOGASTER (FRUIT FLY). //Q01820
 F-NT2RP3004475//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (KIAA0131). //8.4e-54:214:46//HOMO SAPIENS (HUMAN). //P98171
 F-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35. //3.9e-47:199:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P34110
 F-NT2RP3004490//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN N). //0.0013:121:33//XENOPUS LAEVIS (AFRICAN CLAWED FROG). //P17437
 F-NT2RP3004498//HYPOTHETICAL 43.5 KD PROTEIN IN COTD-KOUD INTERGENIC REGION PRECURSOR. //0.066:87:35//BACILLUS SUBTILIS. //P50840
 F-NT2RP3004503//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//2.0e-34:102:69//HOMO SAPIENS (HUMAN). //P39194
 F-NT2RP3004504//SUPPRESSOR PROTEIN SRP40. //0.64:93:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P32583
 F-NT2RP3004507//WOB1 PROTEIN (MPS1 BINDER 1). //2.2e-16:90:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P40484
 F-NT2RP3004527
 F-NT2RP3004534//S-PHASE ENTRY CYCLIN 6. //0.38:148:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P32943
 F-NT2RP3004539//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN 1 PRECURSOR (IGFBP-1) (IGF-1) (IGF-BINDING PROTEIN 1). //0.38:89:38//RATTUS NORVEGICUS (RAT). //P21743
 F-NT2RP3004544//CYTADHERENCE HIGH MOLECULAR WEIGHT PROTEIN 2 (CYTADHERENCE ACCESSORY PROTEIN 2). //0.0024:200:24//MYCOPLASMA PNEUMONIAE. //P75471
 F-NT2RP3004566//GASTRULA ZINC FINGER PROTEIN XLGCF1.1 (FRAGMENT). //4.6e-25:126:43//XENOPUS LAEVIS (AFRICAN CLAWED FROG). //P18713
 F-NT2RP3004569//ANKYRIN. //8.3e-07:150:28//MUS MUSCULUS (MOUSE). //Q02357
 F-NT2RP3004572//TRANSCRIPTION INITIATION FACTOR TFIID 150 KD SUBUNIT

【0672】

【表374】

IT (TAF11-150) (TAF1150).//1.6e-70:247:54//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24325
 F-NT2RP3004578//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//1.5e-10:210:26//HOMO SAPIENS (HUMAN).//Q22224
 F-NT2RP3004594//PS4 PROTEIN PRECURSOR.//0.0044:230:24//ENTEROCOCCUS FAECIUM (STREPTOCOCCUS FAECIUM).//P13692
 F-NT2RP3004617//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//1.5e-14:113:34//MUS MUSCULUS (MOUSE).//P15533
 F-NT2RP3004618//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME 111.//4.5e-08:149:30//CAENORHABDITIS ELEGANS.//P34681
 F-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN).//1.0e-24:75:48//DROSOPHILA MELANOGASTER (FRUIT FLY).//P54352
 F-NT2RP3004670//CUTICLE COLLAGEN 2.//0.00090:159:29//CAENORHABDITIS ELEGANS.//P17656
 F-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64.//4.0e-79:243:62//BOS TAURUS (BOVINE).//P35526
 F-NT2RP4000023
 F-NT2RP4000035//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.6e-06:46:67//HOMO SAPIENS (HUMAN).//P39194
 F-NT2RP4000049//CALDESMON (CDM).//0.41:63:34//GALLUS GALLUS (CHICKEN).//P12957
 F-NT2RP4000051//DUALIN.//2.3e-23:195:37//GALLUS GALLUS (CHICKEN).//Q90830
 F-NT2RP4000078//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-24:182:31//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
 F-NT2RP4000102//XPART PROTEIN.//1.0:54:33//BACILLUS LICHENIFORMIS.//Q99166
 F-NT2RP4000109//SLIT PROTEIN PRECURSOR.//1.9e-60:230:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//P24014
 F-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//1.4e-91:157:100//BOS TAURUS (BOVINE).//Q10568
 F-NT2RP4000129//SES ANTIGEN.//0.00072:124:37//RATTUS NORVEGICUS (RAT).//Q63003
 F-NT2RP4000147//ZINC FINGER PROTEIN GCS1.//1.5e-26:119:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P35197
 F-NT2RP4000150
 F-NT2RP4000151//HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME 111.//4.2e-31:180:47//CAENORHABDITIS ELEGANS.//P32740
 F-NT2RP4000159//SPORE COAT PROTEIN SP96.//0.84:107:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P14328
 F-NT2RP4000167//HYPOTHETICAL 98.1 KD PROTEIN IN SPX19-CCR2 INTERGENIC REGION.//2.4e-08:133:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40164
 F-NT2RP4000185//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (YMW118 PROTEIN).//5.4e-05:143:32//HERPES SIMPLEX VIRUS (TYPE 2 / STRAIN H G52).//P28284
 F-NT2RP4000210//PAIRED AMPHIPATHIC HELIX PROTEIN.//1.8e-40:258:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P22579
 F-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//1.4e-20:104:40//APLYSIA CALIFORNICA (CALIFORNIA SEA HARE).//P15287
 F-NT2RP4000214//FERREDOXIN.//1.0:19:42//MOORELLA THERMOACETICA (CLOSTRIDIUM THERMOACETICUM).//P00203
 F-NT2RP4000218//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.7e-15:48:60//HOMO SAPIENS (HUMAN).//P39188
 F-NT2RP4000243//DUALIN.//5.8e-78:192:70//GALLUS GALLUS (CHICKEN).//Q90830
 F-NT2RP4000246//WPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//3.1e-83:207:76//MUS MUSCULUS (MOUSE).//Q03173
 F-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9).//5.5e-29:153:43//HELIANTHUS ANNUUS (COMMON SUNFLOWER).//Q23968
 F-NT2RP4000263//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.98:42:40//BOS TAURUS (BOVINE).//P20072
 F-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G8.09C IN CHROMOSOME 1.//3.5e-71:209:66//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87115
 F-NT2RP4000312//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//8.9e-22:166:37//HOMO SAPIENS (HUMAN).//Q15404
 F-NT2RP4000321//VERPROLIN.//0.00018:260:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P37370
 F-NT2RP4000323//ANTHOPLEURIN B (TOXIN AP-B).//0.42:15:46//ANTHOPLEURA XANTHOGRAMMICA (GIANT GREEN SEA ANEMONE).//P01531
 F-NT2RP4000355//HYPOTHETICAL 90.9 KD PROTEIN IN GCN20-CHK1 INTERGENIC REGION.//0.75:125:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43596
 F-NT2RP4000360//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.27:92:33//RATTUS NORVEGICUS (RAT).//P10164
 F-NT2RP4000367//HYPOTHETICAL 7.3 KD PROTEIN IN 100 KD PROTEIN REGION.//0.99:52:32//HUMAN ADENOVIRUS TYPE 41.//P23691
 F-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1).//4.1e-40:163:52//HOMO SAPIENS (HUMAN).//Q75570
 F-NT2RP4000376//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//4.2e-59:125:80//RATTUS NORVEGICUS (RAT).//P54319
 F-NT2RP4000381//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//0.00058:194:30//MUS MUSCULUS (MOUSE).//P19246
 F-NT2RP4000398//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.2e-45:153:39//HOMO SAPIENS (HUMAN).//Q99676
 F-NT2RP4000415//HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DALS INTERGENIC REGION PRECURSOR.//0.00066:201:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47179
 F-NT2RP4000417//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B).//1.8e-25:186:40//MUS MUSCULUS (MOUSE).//P39098
 F-NT2RP4000424//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//1.0e-15:72:61//HOMO SAPIENS (HUMAN).//P39195
 F-NT2RP4000448//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//7.0e-23:63:82//HOMO SAPIENS (HUMAN).//P39192
 F-NT2RP4000449//REGULATORY PROTEIN SIR2 (SILENT INFORMATION REGULATOR 2).//1.3e-41:102:45//KLUYVEROMYCES LACTIS (YEAST).//P33294
 F-NT2RP4000455//HOMEBOX PROTEIN SAX-1 (CHX-3) (FRAGMENT).//0.00014:92:30//GALLUS GALLUS (CHICKEN).//P19601
 F-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 7 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 7) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 7) (DEUBIQUITINATING ENZYME 7) (HERPESVIRUS ASSOCIATED UBIQUITIN-SPECIFIC PROTEASE).//1.0e-29:218:38//HOMO SAPIENS (HUMAN).//Q93009
 F-NT2RP4000480//TRANSCRIPTIONAL REGULATORY PROTEIN ALGP (ALGINATE REGULATORY PROTEIN ALGR3).//0.049:117:29//PSEUDOMONAS AERUGINOSA.//P15276
 F-NT2RP4000481//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME 111.//2.3e-05:152:23//CAENORHABDITIS ELEGANS.//Q09475
 F-NT2RP4000498//MOBI PROTEIN (MPS1 BINDER 1).//2.3e-48:172:52//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40484
 F-NT2RP4000500//HYPOTHETICAL 83.6 KD PROTEIN R05D3.2 IN CHROMOSOME 111.//1.3e-23:165:35//CAENORHABDITIS ELEGANS.//P34535
 F-NT2RP4000515//PHOSPHODIESTERASE 1 (EC 3.1.4.1) (5'-EXONUCLEASE) (5'-NUCLEOTIDE PHOSPHODIESTERASE) (FRAGMENT).//1.0:48:37//BOS TAURUS (BOVINE).//P15396
 F-NT2RP4000517//METALLOTHIONEIN-LIKE PROTEIN TYPE 2.//1.0:41:36//VICIA FABA (BROAD BEAN).//Q41657
 F-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.1e-11:93:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P45818
 F-NT2RP4000519//COLLAGEN ALPHA 1(XI) CHAIN (FRAGMENTS).//0.68:55:40//BOS TAURUS (BOVINE).//P25508
 F-NT2RP4000524//ICA FC RECEPTOR PRECURSOR (BETA ANTIGEN) (B ANTIGEN).//0.37:187:24//STREPTOCOCCUS AGALACTIAE.//P27951
 F-NT2RP4000528//NPL4 PROTEIN.//2.1e-45:305:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33755
 F-NT2RP4000541//HOMEBOX PROTEIN CHOX-1 (FRAGMENT).//0.23:28:50//GALLUS GALLUS (CHICKEN).//P13544
 F-NT2RP4000556//HYPOTHETICAL 34.1 KD PROTEIN C40H1.4 IN CHROMOSOME 111.//4.3e-14:174:34//CAENORHABDITIS ELEGANS.//Q03574
 F-NT2RP4000560//HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME 111.//2.1e-19:155:36//CAENORHABDITIS ELEGANS.//P34679
 F-NT2RP4000588//HYPOTHETICAL PROTEIN E-115.//0.014:64:35//HUMAN ADENOVIRUS TYPE 2.//P03290
 F-NT2RP4000614//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//2.7e-27:188:44//GALLUS GALLUS (CHICKEN).//P30352
 F-NT2RP4000638//EARLY MODULIN 55-1 PRECURSOR (N-55-1) (FRAGMENT).//0.55:40:40//GLYCINE MAX (SOYBEAN).//Q05544
 F-NT2RP4000648//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.4e-06:31:74//HOMO SAPIENS (HUMAN).//P39188
 F-NT2RP4000657//HYPOTHETICAL PROTEIN MJ1065.//2.5e-40:237:40//METHANOCOCCUS JANNA SCHII.//Q58465
 F-NT2RP4000704
 F-NT2RP4000713//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//4.0e-07:134:40//STREPTOMYCES FRADIAE.//P20186
 F-NT2RP4000724//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//1.1e-62:109:88//HOMO SAPIENS (HUMAN).//P10266
 F-NT2RP4000728//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//0.0033:190:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33232
 F-NT2RP4000737//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.0e-05:114:34//HOMO SAPIENS (HUMAN).//P23246
 F-NT2RP4000739//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:20:50//ANAS PLATYRHYNCHOS (DOMESTIC DUCK).//P50655
 F-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION

【0673】

【表375】

NIC REGION.//0.0013:67:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS T).//P53915
 F-NT2RP4000787//POLLEN SPECIFIC PROTEIN SF3.//1.3e-13:79:39//MELIA NTHUS ANHUIS (COMMON SUNKFLOWER).//P29675
 F-NT2RP4000817//SUPPRESSOR PROTEIN SRP40.//1.3e-05:255:21//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
 F-NT2RP4000833
 F-NT2RP4000837//MALE SPECIFIC SPERM PROTEIN MST840B.//0.18:38:44//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643
 F-NT2RP4000839//TRANSCRIPTION INITIATION FACTOR TF11D 90 KD SUBUNIT (TAF11-90).//0.026:38:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS T).//P38129
 F-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//2.8e-64:229:53//RATTUS NORVEGICUS (RAT).//Q09175
 F-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//3.6e-84:174:54//HOMO SAPIENS (HUMAN).//P16415
 F-NT2RP4000878//MYELOID UPREGULATED PROTEIN.//8.2e-88:227:74//MUS MUSCULUS (MOUSE).//Q35682
 F-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN).//9.1e-55:268:43//HOMO SAPIENS (HUMAN).//P22314
 F-NT2RP4000907//BONE/NT-3 GROWTH FACTORS RECEPTOR PRECURSOR (EC 2.7.1.112) (TRKB TYROSINE KINASE) (GPI45-TRKB) (TRK-B).//5.4e-10:220:25//HOMO SAPIENS (HUMAN).//Q16620
 F-NT2RP4000915//60S ACIDIC RIBOSOMAL PROTEIN P2 (FRAGMENT).//0.46:23:60//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P51407
 F-NT2RP4000918//METHYL-ACCEPTING CHEMOTAXIS PROTEIN TLPB.//0.00010:148:32//BACILLUS SUBTILIS.//P39217
 F-NT2RP4000925//FIBRINOGEN PRECURSOR (FN) (COLLAGEN-BINDING 59 K D PROTEIN).//3.5e-27:220:36//HOMO SAPIENS (HUMAN).//Q06828
 F-NT2RP4000927//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO (P135 PROTEIN) (IER 2.9/ER2.6).//0.64:75:37//BOVINE HERPESVIRUS TYPE 1 (STRAIN JURA).//P29128
 F-NT2RP4000928//PHOSPHATIDATE CYTIDYLTRANSFERASE (EC 2.7.7.41) (CDP-DIGLYCERIDE SYNTHETASE) (CDP-DIGLYCERIDE PYROPHOSPHORYLASE) (CDP-DIACYLGLYCEROL SYNTHASE) (CDS) (CTP:PHOSPHATIDATE CYTIDYLTRANSFERASE) (CDP-DAG SYNTHASE).//3.1e-104:263:66//HOMO SAPIENS (HUMAN).//Q92903
 F-NT2RP4000929//HYPOTHETICAL 22.2 KD PROTEIN IN NSR1-TIF4631 INTERGENIC REGION.//0.93:107:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS T).//P53288
 F-NT2RP4000955//PUTATIVE CUTICLE COLLAGEN F09G.6.//2.0e-05:102:37//CAENORHABDITIS ELEGANS.//P34391
 F-NT2RP4000973//HYPOTHETICAL 48.6 KD PROTEIN IN BET1-PAN1 INTERGENIC REGION.//2.3e-17:78:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS T).//P04564
 F-NT2RP4000975//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) (CONTAINS: PEPTIDE P-Q) (FRAGMENT).//0.0041:142:33//HOMO SAPIENS (HUMAN).//P10162
 F-NT2RP4000979//HYPOTHETICAL 14.5 KD PROTEIN.//0.77:106:33//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20517
 F-NT2RP4000984//HYPOTHETICAL 124.8 KD PROTEIN C29E.4 IN CHROMOSOME III.//0.90:94:25//CAENORHABDITIS ELEGANS.//P34343
 F-NT2RP4000989//ANTHOPLEURIN B (TOXIN AP-B).//0.76:41:41//ANTHOPLEURA XANTHOCRAMMICA (GIANT GREEN SEA ANEMONE).//P01531
 F-NT2RP4000996//PROTEIN Q300.//0.00024:41:53//MUS MUSCULUS (MOUSE).//Q02722
 F-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT).//8.7e-115:261:82//RATTUS NORVEGICUS (RAT).//Q054888
 F-NT2RP4001004//EC PROTEIN HOMOLOG 2 (FRAGMENT).//0.50:61:34//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q42377
 F-NT2RP4001006//HYPOTHETICAL 43.5 KD PROTEIN IN COTD-KDUD INTERGENIC REGION PRECURSOR.//0.010:152:29//BACILLUS SUBTILIS.//P50840
 F-NT2RP4001010//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//9.9e-05:247:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640
 F-NT2RP4001029//PROTEIN GRANTY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT 1-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//1.1e-14:175:31//DROSOPHILA MELANOGASTER (FRUIT FLY).//P13002
 F-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE-TRNA LIGASE) (LEURS).//1.5e-74:272:55//CAENORHABDITIS ELEGANS.//Q09996
 F-NT2RP4001057//HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME III.//0.0064:76:38//CAENORHABDITIS ELEGANS.//P34664
 F-NT2RP4001064//DUALIN.//2.5e-24:199:38//GALLUS GALLUS (CHICKEN).//Q90830
 F-NT2RP4001078//TRANSCRIPTION INITIATION FACTOR TF11D 135 KD SUBUNIT (TAF11-135) (TAF11-125) (TAF11-130) (TAF11-130).//0.11:139:38//HOMO SAPIENS (HUMAN).//Q00268
 F-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-ATPASE).//1.5e-22:242:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P13586
 F-NT2RP4001080//POLYPYRIMIDINE TRACT-BINDING PROTEIN (PTB) (HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 1) (HNRNP 1).//1.7e-82:178:69//SUSCROFA (PIG).//Q29099
 F-NT2RP4001086//LEUCINE-RICH ACIDIC NUCLEAR PROTEIN.//0.00039:141:26//RATTUS NORVEGICUS (RAT).//P49911
 F-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1).//9.9e-07:79:43//HOMO SAPIENS (HUMAN).//P78563
 F-NT2RP4001100//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGENIC REGION.//4.4e-16:207:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS T).//P40032
 F-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//8.1e-115:224:99//RATTUS NORVEGICUS (RAT).//P38378
 F-NT2RP4001122//TIPD PROTEIN.//7.5e-11:129:31//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//Q15736
 F-NT2RP4001126//TRICHOYALIN.//1.4e-19:257:28//OVIS ARIES (SHEEP).//P22793
 F-NT2RP4001138//PUTATIVE F420-DEPENDENT NADP REDUCTASE (EC 1.-.-.-).//0.00010:204:25//METHANOCOCCUS JANNASCHII.//Q58896
 F-NT2RP4001143//HYPOTHETICAL 52.9 KD PROTEIN IN SAPI55-YMR31 INTERGENIC REGION.//4.5e-34:168:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P43616
 F-NT2RP4001148//SOF1 PROTEIN.//2.4e-41:158:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33750
 F-NT2RP4001149//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//1.3e-08:106:41//VOLVOX CARTERI.//P21997
 F-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (NRCAM) (BRAVO).//3.6e-24:194:32//GALLUS GALLUS (CHICKEN).//P35331
 F-NT2RP4001159//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2).//0.0056:117:25//PLASMODIUM FALCIPARUM (ISOLATE K1 / THAILAND).//Q03643
 F-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//5.9e-24:184:34//BRASSICA OLERACEA (CAULIFLOWER).//P52178
 F-NT2RP4001206//MEROZOITE SURFACE ANTIGEN 2 PRECURSOR (MSA-2).//0.0029:117:26//PLASMODIUM FALCIPARUM (ISOLATE K1 / THAILAND).//Q03643
 F-NT2RP4001207//CHROMOSOME SEGREGATION PROTEIN CSE1.//1.0e-07:144:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P33307
 F-NT2RP4001210//DERMOPHIN 1 PRECURSOR [CONTAINS: DELTORPHIN (DERMENEKPHALIN); DERMOPHIN].//0.019:130:30//PHYLLomedusa SAUVAGEI (SAUVAGE'S LEAF FROG).//P05422
 F-NT2RP4001213//ZINC FINGER PROTEIN 177.//3.2e-28:176:39//HOMO SAPIENS (HUMAN).//Q13360
 F-NT2RP4001219//DISULFIDE ISOMERASE MPD1 PRECURSOR (EC 5.3.4.1).//2.4e-13:108:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12404
 F-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).//2.7e-56:242:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
 F-NT2RP4001235//REGULATORY PROTEIN E2.//0.0080:100:38//HUMAN PAPILLOMAVIRUS TYPE 25.//P36787
 F-NT2RP4001256//CUTICLE COLLAGEN 1.//0.014:104:31//CAENORHABDITIS ELEGANS.//P08124
 F-NT2RP4001260//BACTERIOCIN MICROBIN B17 PRECURSOR (MCB17).//0.00077:16:68//ESCHERICHIA COLI.//P05834
 F-NT2RP4001274//HISTONE H1.//0.98:65:35//TRYPANOSOMA CRUZI.//P40273
 F-NT2RP4001276//ELAV PROTEIN.//0.00054:134:33//DROSOPHILA VIRILIS (FRUIT FLY).//P23241
 F-NT2RP4001313//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.014:71:35//NICOTIANA TABACUM (COMMON TOBACCO).//P13983
 F-NT2RP4001315//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS9.//2.3e-12:190:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P54787
 F-NT2RP4001336//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.//0.0037:108:31//PODOSPORA ANSERINA.//Q00808
 F-NT2RP4001339//HYPOTHETICAL PROTEIN MJ0810.//1.2e-09:150:34//METHANOCOCCUS JANNASCHII.//Q58220
 F-NT2RP4001343//HYPOTHETICAL 85.2 KD PROTEIN F52C9.3 IN CHROMOSOME III.//1.4e-18:244:27//CAENORHABDITIS ELEGANS.//Q10123
 F-NT2RP4001345//PHOSPHATIDYLCHOLINE-STEROL ACYLTRANSFERASE PRECURSOR (EC 2.3.1.43) (LECITHIN-CHOLESTEROL ACYLTRANSFERASE) (PHOSPHOLIPID-CHOLESTEROL ACYLTRANSFERASE) (FRAGMENT).//4.0e-49:212:50//GALLUS GALLUS (CHICKEN).//P53760
 F-NT2RP4001351//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//5.7e-11:229:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25386
 F-NT2RP4001353//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN)

【0674】

【表376】

(RSP-1).//0.00088:84:28//HOMO SAPIENS (HUMAN).//Q15404
 F-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRR
 EC PROTEIN).//1.0e-22:222:30//DROSOPHILA MELANOGASTER (FRUIT FLY).
 //Q08180
 F-NT2RP4001373//OV-17 ANTIGEN PRECURSOR (IMMUNODOMINANT HYPODERMAL
 ANTIGEN).//0.51:92:26//ONCHOCERCA VOLVULUS.//P36991
 F-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.
 7.1.112) (TYROSINE- PROTEIN KINASE 1).//3.5e-13:146:35//DICTYOSTEL
 IUM DISCOIDEUM (SLIME MOLD).//P18160
 F-NT2RP4001379//HYPOTHETICAL 64.2 KD PROTEIN IN SLT2-PUT2 INTERGEN
 IC REGION.//1.2e-14:207:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
 T).//P38767
 F-NT2RP4001389//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC
 2.7.7.6) (RPB1) (FRAGMENT).//0.073:112:33//CRICETULUS GRISEUS (CH
 INESE HAMSTER).//P11414
 F-NT2RP4001407//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//0.0019:23
 3:24//HOMO SAPIENS (HUMAN).//Q02224
 F-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT).//6.2e-89:195:81//HOMO
 SAPIENS (HUMAN).//Q14141
 F-NT2RP4001433//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//1.5e-
 85:216:56//HOMO SAPIENS (HUMAN).//P28160
 F-NT2RP4001442//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC
 2.7.7.6) (VERSION 1).//0.012:107:35//ARABIDOPSIS THALIANA (MOUSE-
 EAR CRESS).//P18616
 F-NT2RP4001447//60S ACIDIC RIBOSOMAL PROTEIN P2 (EL12).//0.0046:6
 9:33//ARTEMIA SALINA (BRINE SHRIMP).//P02399
 F-NT2RP4001474//CBP3 PROTEIN PRECURSOR.//0.0011:111:29//SACCHAROMY
 CES CEREVISIAE (BAKER'S YEAST).//P21560
 F-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSO
 R (EC 1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE).//6.2e-60:146:6
 1//HOMO SAPIENS (HUMAN).//Q02218
 F-NT2RP4001498//HYPOTHETICAL 72.5 KD PROTEIN C2F7.10 IN CHROMOSOME
 1.//2.3e-24:137:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q
 09701
 F-NT2RP4001502//HYPOTHETICAL 24.7 KD PROTEIN IN POM152-REC114 INTE
 RGENIC REGION.//6.0e-22:148:34//SACCHAROMYCES CEREVISIAE (BAKER'S
 YEAST).//P40206
 F-NT2RP4001507//CUTICLE COLLAGEN 40.//0.00029:166:31//CAENORHABDIT
 IS ELEGANS.//P34804
 F-NT2RP4001524//LACTOCOCCIN A IMMUNITY PROTEIN.//0.74:96:30//LACTO
 COCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS). AND LACTOCOCC
 US LACTIS (SUBSP. CREMORIS) (STREPTOCOCCUS CREMORIS).//Q00561
 F-NT2RP4001529//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (E
 LEMENT 1-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//2.8e-06:
 79:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//P13002
 F-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INT
 ERGENIC REGION.//5.4e-34:88:46//SACCHAROMYCES CEREVISIAE (BAKER'S
 YEAST).//P25656
 F-NT2RP4001551//CELL DIVISION CONTROL PROTEIN 68.//1.5e-18:243:30/
 /SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32558
 F-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).//0.00030:
 158:24//MYCOBACTERIUM TUBERCULOSIS.//P96902
 F-NT2RP4001567//IMPORTIN ALPHA-1 SUBUNIT (KARYOPHERIN ALPHA-1 SUBU
 NIT).//0.00013:147:29//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P521
 70
 F-NT2RP4001568//HYPOTHETICAL PROTEIN KIAA0041 (FRAGMENT).//8.0e-2
 2:119:42//HOMO SAPIENS (HUMAN).//Q15057
 F-NT2RP4001571//NEURONMODULIN (AXONAL MEMBRANE PROTEIN GAP-43) (PP4
 6) (B-50) (PROTEIN F1) (CALMODULIN-BINDING PROTEIN P-57).//0.012:1
 67:28//BOS TAURUS (BOVINE).//P06836
 F-NT2RP4001574//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMM
 A-COP).//6.8e-115:208:98//BOS TAURUS (BOVINE).//P53620
 F-NT2RP4001575//M-RELATED PROTEIN PRECURSOR.//0.22:184:25//STREPTO
 COCCUS PYOGENES.//P16946
 F-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCIN
 E-TRNA LIGASE) (ILERS).//7.4e-45:229:39//SYNECHOCYSTIS SP. (STRAI
 N PCC 6803).//P73505
 F-NT2RP4001610//APOLIPOPROTEIN C-III PRECURSOR (APO-CIII).//0.41:7
 4:28//SUS SCROFA (PIG).//P27917
 F-NT2RP4001614//BASIC PROLINE-RICH PEPTIDE P-E (IB-9).//1.0:29:37/
 /HOMO SAPIENS (HUMAN).//P02811
 F-NT2RP4001634//MYOSIN HEAVY CHAIN. PERINATAL SKELETAL MUSCLE (FRA
 GMENT).//0.16:233:23//RATTUS NORVEGICUS (RAT).//P04462
 F-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/MMS19.//4.2
 e-21:249:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40469
 F-NT2RP4001644//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//
 4.5e-18:111:44//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P25323
 F-NT2RP4001656//HYPOTHETICAL 108.5 KD PROTEIN R06F6.2 IN CHROMOSOM
 E 11.//3.4e-13:175:32//CAENORHABDITIS ELEGANS.//Q09600
 F-NT2RP4001677//HYPOTHETICAL 73.6 KD PROTEIN CY49.21.//0.065:66:43
 //MYCOBACTERIUM TUBERCULOSIS.//Q10690
 F-NT2RP4001679//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.3e-36:
 103:72//HOMO SAPIENS (HUMAN).//P39194
 F-NT2RP4001696//PHOTOSYSTEM II REACTION CENTRE J PROTEIN.//0.93:3
 7:37//CHLORELLA VULGARIS.//P56338
 F-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//
 4.3e-11:128:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10282
 F-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECU
 RSOR (EC 2.4.1.-) (DUGT).//4.1e-22:201:27//DROSOPHILA MELANOGASTER
 (FRUIT FLY).//Q09332
 F-NT2RP4001739//HOMEBOX PROTEIN HOX-A10 (HOX-1H) (HOX-1.8) (PL).//
 1.0:67:34//HOMO SAPIENS (HUMAN).//P31260
 F-NT2RP4001753//ZINC FINGER PROTEIN 10 (ZINC FINGER PROTEIN KOX1)
 (FRAGMENT).//1.2e-19:72:62//HOMO SAPIENS (HUMAN).//P21506
 F-NT2RP4001760//BREAKPOINT CLUSTER REGION PROTEIN.//1.8e-13:179:28
 //HOMO SAPIENS (HUMAN).//P11274
 F-NT2RP4001790//ZINC FINGER PROTEIN 38 (ZFP-38) (CTFIN51) (TRANSCR
 IPTION FACTOR RU49).//7.9e-38:147:49//MUS MUSCULUS (MOUSE).//Q0723
 1
 F-NT2RP4001803//CUTICLE COLLAGEN 12 PRECURSOR.//0.40:48:39//CAENOR
 HABDITIS ELEGANS.//P20630
 F-NT2RP4001822//NOVEL ANTIGEN 2 (NAG-2).//2.7e-27:173:36//HOMO SAP
 IENS (HUMAN).//Q14817
 F-NT2RP4001823//PUTATIVE CUTICLE COLLAGEN F09G8.6.//3.3e-16:152:42
 //CAENORHABDITIS ELEGANS.//P34391
 F-NT2RP4001828//HOLIN.//0.99:33:36//BACTERIOPHAGE HP1.//P51727
 F-NT2RP4001838//METASTASIS-ASSOCIATED PROTEIN MTA1.//1.2e-07:95:31
 //HOMO SAPIENS (HUMAN).//Q13330
 F-NT2RP4001841//INTESTINAL MUCIN-LIKE PROTEIN (MLP) (FRAGMENT).//
 0.94:141:22//RATTUS NORVEGICUS (RAT).//P98089
 F-NT2RP4001849//SH3-BINDING PROTEIN 3BP-1.//5.6e-52:276:45//MUS MU
 SCULUS (MOUSE).//P55194
 F-NT2RP4001861//HYPOTHETICAL 10.6 KD PROTEIN IN GALE-PEPT INTERGEN
 IC REGION.//0.92:39:51//BACILLUS SUBTILIS.//P55185
 F-NT2RP4001889//HYPOTHETICAL BHLF1 PROTEIN.//0.32:97:31//EPSTEIN-B
 ARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
 F-NT2RP4001893//2-5A-DEPENDENT RIBONUCLEASE (EC 3.1.26.-) (2-5A-DE
 PENDENT RNAASE) (RNAASE L) (RIBONUCLEASE 4) (FRAGMENT).//3.6e-07:12
 4:29//MUS MUSCULUS (MOUSE).//Q05921
 F-NT2RP4001896//HYPOTHETICAL 89.4 KD TRP-ASP REPEATS CONTAINING PR
 OTEIN IN PWT6-PCT1 INTERGENIC REGION.//3.9e-10:210:28//SACCHAROMYC
 ES CEREVISIAE (BAKER'S YEAST).//P42935
 F-NT2RP4001901//ACROSIN PRECURSOR (EC 3.4.21.10).//2.4e-07:53:45/
 ORYCTOLAGUS CUNICULUS (RABBIT).//P48038
 F-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//3.1e-19:170:
 32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12024
 F-NT2RP4001938//ZINC FINGER PROTEIN MOK-2.//1.3e-28:72:50//MUS MUS
 CULUS (MOUSE).//P24399
 F-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.
 1.1.77) (PROTEIN- BETA-ASPARTATE METHYLTRANSFERASE) (PMT) (PROTEI
 N L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL
 METHYLTRANSFERASE).//4.8e-14:183:30//TRITICUM AESTIVUM (WHEAT).//
 Q43209
 F-NT2RP4001950//HYPOTHETICAL PROTEIN ORF-1137.//3.7e-07:115:29//MU
 S MUSCULUS (MOUSE).//P11260
 F-NT2RP4001953
 F-NT2RP4001966//WALL-ASSOCIATED PROTEIN PRECURSOR.//0.13:151:27//B
 ACILLUS SUBTILIS.//Q07833
 F-NT2RP4001975//FIBRIL-FORMING COLLAGEN ALPHA CHAIN.//0.00031:190:
 31//RIFTIA PACHYPTILA (TUBE WORM).//P30754
 F-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).//3.5e-18:185:2
 9//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
 F-NT2RP4002047//GTP-BINDING PROTEIN GUF1 (GTPASE GUF1).//4.0e-49:1
 58:65//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P46943
 F-NT2RP4002052//HYPOTHETICAL 54.3 KD PROTEIN C23D3.03C IN CHROMOSO
 ME 1.//0.0047:148:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//
 Q08444
 F-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RN
 A HELICASE F56D2.6.//0.057:66:30//CAENORHABDITIS ELEGANS.//Q20875
 F-NT2RP4002071//VERY HYPOTHETICAL 13.2 KD PROTEIN CY251.09.//0.94:
 45:46//MYCOBACTERIUM TUBERCULOSIS.//Q10888
 F-NT2RP4002075//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//
 0.44:36:38//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HI
 V-1).//P18804
 F-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10)
 (HPF7).//2.6e-19:46:76//HOMO SAPIENS (HUMAN).//Q05481
 F-NT2RP4002081//MHC CLASS II REGULATORY FACTOR RFX1 (RFX) (ENHANCE
 R FACTOR C) (EF-C).//2.8e-05:196:31//HOMO SAPIENS (HUMAN).//P22670
 F-NT2RP4002083//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//0.0
 064:29:55//OWENIA FUSIFORMIS.//P21260

【0675】

【表377】

F-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-).//1.1e-37:159:53/
SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P38938
F-NT2RP4002791//30S RIBOSOMAL PROTEIN S20.//1.0:73:26//MELICOBACTE
R PYLORI (CAMPYLOBACTER PYLORI).//P56027
F-NT2RP4002888//HYPOTHETICAL PROTEIN TP0352.//0.98:52:26//TREPONEM
A PALLIDUM.//Q83371
F-NT2RP4002905//G2/MITOTIC-SPECIFIC CYCLIN S13-7 (B-LIKE CYCLIN)
(FRAGMENT).//5.9e-05:138:27//GLYCINE MAX (SOYBEAN).//P25012
F-NT2RP5003459//HOMEBOX PROTEIN HOX-A3 (HOX-1.5) (MO-10).//0.027:
40:40//MUS MUSCULUS (MOUSE).//P02831
F-NT2RP5003461//HYPOTHETICAL PROTEIN C2F3.14C IN CHROMOSOME 1 (FR
AGMENT).//1.1e-12:142:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAS
T).//Q99779
F-NT2RP5003477//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1.//5.3
e-13:215:28//PODOSPORA ANSERINA.//Q00808
F-NT2RP5003492//GLUCAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN
1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//0.00
55:144:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640
F-NT2RP5003500//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//9.0e-05:103:
38//MUS MUSCULUS (MOUSE).//P05142
F-NT2RP5003506//MALE SPECIFIC SPERM PROTEIN MST87F.//0.53:21:38//D
ROSOPHILA MELANOGASTER (FRUIT FLY).//P08175
F-NT2RP5003512//HYPOTHETICAL PROTEIN IN CYC3 3' REGION PRECURSOR (O
RF2) (FRAGMENT).//0.92:49:32//PARACOCUS DENITRIFICANS.//P29969
F-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR
).//2.7e-18:165:39//PHASEOLUS AUREUS (MUNG BEAN) (VIGNA RADIATA)./
P37116
F-NT2RP5003524//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//6.0e-08:12
5:41//RATTUS NORVEGICUS (RAT).//P02454
F-NT2RP5003534//ATP SYNTHASE, SUBUNIT F (EC 3.6.1.34).//0.88:37:45
//HALOBACTERIUM VOLCANII (HALOFERAX VOLCANII).//Q48331
F-OVARC1000001//GAR22 PROTEIN.//1.9e-05:41:58//HOMO SAPIENS (HUMA
N).//Q99501
F-OVARC1000004//70 KD EXOCYST COMPLEX PROTEIN.//3.7e-08:186:25//SA
CCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P19658
F-OVARC1000006//HISTONE H2A.1.//4.7e-55:117:98//RATTUS NORVEGICUS
(RAT).//P02262
F-OVARC1000013//WD-REPEAT PROTEIN POP1.//0.00022:126:28//SCHIZOSAC
CHAROMYCES POMBE (FISSION YEAST).//P87060
F-OVARC1000014//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//2.3e-05:2
20:30//CALLUS CALLUS (CHICKEN).//P02457
F-OVARC1000017//CUTICLE COLLAGEN DPLY-13.//2.6e-05:97:30//CAENORHAB
DITIS ELEGANS.//P17657
F-OVARC1000035
F-OVARC1000058//RAS-RELATED PROTEIN RAB.//0.00015:110:24//DICTYOS
TELIUM DISCOIDEUM (SLIME MOLD).//P34143
F-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.2
7.1) (RNASE LE).//6.8e-09:60:45//LYCOPERSICON ESCULENTUM (TOMATO).
//P80022
F-OVARC1000068//CYTOTOXIN 4 (CARDIOTOXIN Y-11-4).//1.0:27:44//NAJA
MOSSAMBICA (MOZAMBIQUE COBRA).//P01452
F-OVARC1000071//NUCLEAR TRANSPORT FACTOR 2 (NTF-2) (PLACENTAL PROT
EIN 15) (PPI5).//5.2e-06:115:29//HOMO SAPIENS (HUMAN). AND RATTUS
NORVEGICUS (RAT).//P13662
F-OVARC1000085
F-OVARC1000087//HISTONE MACRO-H2A.1.//1.2e-13:174:26//RATTUS NORVE
GICUS (RAT).//Q02874
F-OVARC1000091//OCTAPEPTIDE-REPEAT PROTEIN T2.//0.0013:137:32//MUS
MUSCULUS (MOUSE).//Q06666
F-OVARC1000092//MITOCHONDRIAL RIBOSOMAL PROTEIN S7.//0.97:46:39//A
CANTHAMOEBA CASTELLANII (AMOEBA).//P46756
F-OVARC1000106//HYPOTHETICAL 141.5 KD PROTEIN IN YPT53-RHO2 INTERG
ENIC REGION.//0.0012:165:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEA
ST).//P53935
F-OVARC1000109//PROLINE RICH 33 KD EXTENSIN-RELATED PROTEIN PRECUR
SOR (FRAGMENT).//0.18:35:34//DAUCUS CAROTA (CARROT).//P06600
F-OVARC1000113//HYPOTHETICAL PROTEIN C18.//1.0:26:26//SWINEPOX VIR
US (STRAIN KASZA) (SPV).//P32217
F-OVARC1000114//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//3.6e-28:
57:63//HOMO SAPIENS (HUMAN).//P39194
F-OVARC1000133
F-OVARC1000139//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.
15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PRO
TEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN H
OMOLOG).//1.9e-09:200:29//HOMO SAPIENS (HUMAN).//Q13107
F-OVARC1000145//HOMEBOX PROTEIN DLX-3.//1.0:65:30//BRACHYDANIO RE
RIO (ZEBRAFISH) (ZEBRA DANIO).//Q07102
F-OVARC1000148//HYPMAL WALL PROTEIN 1 (CELL ELONGATION PROTEIN 2).
//0.12:175:29//CANDIDA ALBICANS (YEAST).//P46593
F-OVARC1000151//HYPOTHETICAL PROTEIN KIA0161.//5.6e-20:197:30//HO
MO SAPIENS (HUMAN).//P50876
F-OVARC1000168//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.0030:7
7:38//HOMO SAPIENS (HUMAN).//P39188
F-OVARC1000191//COLANIC ACID BIOSYNTHESIS PROTEIN WCAH.//0.95:56:3
5//ESCHERICHIA COLI.//P32056
F-OVARC1000198//HISTONE H1.C2.//0.96:70:25//TRYPANOSOMA CRUZI.//P4
0268
F-OVARC1000209//HYPOTHETICAL 20.9 KD PROTEIN IN PLB1-HXT2 INTERGEN
IC REGION.//2.5e-33:178:44//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
T).//Q03677
F-OVARC1000212//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//1.7e-05:66:4
6//MUS MUSCULUS (MOUSE).//P05142
F-OVARC1000240//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//1.8e-10:
41:78//HOMO SAPIENS (HUMAN).//P39193
F-OVARC1000241//ENDOTHELIAL PAS DOMAIN PROTEIN 1 (EPAS-1) (HIF-1 A
LPHA-LIKE FACTOR) (NHLF) (HIF-RELATED FACTOR) (HRF).//7.4e-54:177:
54//MUS MUSCULUS (MOUSE).//P97481
F-OVARC1000288//HYPOTHETICAL 54.2 KD PROTEIN IN ERP5-ORC6 INTERGEN
IC REGION.//2.9e-20:115:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
T).//P38821
F-OVARC1000302//CORTICOSTEROID-BINDING GLOBULIN PRECURSOR (CBG) (T
RANSCORTIN).//1.0:79:25//MUS MUSCULUS (MOUSE).//Q06770
F-OVARC1000304//PROTEIN MOV-10.//1.6e-79:181:83//MUS MUSCULUS (MOU
SE).//P32349
F-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//6.9e-36:156:42/
ASHBYA GOSSYPII (EREMOETHICUS GOSSYPII).//Q00063
F-OVARC1000321//HYPOTHETICAL 28.1 KD PROTEIN C4F8.03 IN CHROMOSOME
1.//5.2e-45:159:53//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//0
14179
F-OVARC1000326//BASIC PROLINE-RICH PEPTIDE 1B-1.//0.036:67:35//HOM
O SAPIENS (HUMAN).//P04281
F-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGEN
IC REGION.//1.2e-16:200:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
T).//P40004
F-OVARC1000347//HYPOTHETICAL 7.6 KD PROTEIN YCF33.//0.69:41:43//CY
ANOPHORA PARADOXA.//P48273
F-OVARC1000384//ANTIFREEZE PEPTIDE 4 PRECURSOR.//0.98:49:34//PSEUD
OPLEURONECTA AMERICANUS (WINTER FLOUNDER).//P02734
F-OVARC1000408//INTEGUMENTARY MUCIN C.1 (FIM-C.1) (FRAGMENT).//8.1
e-05:115:33//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q05049
F-OVARC1000411//DYNACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED
POLYPEPTIDE) (DP-150) (DAP-150) (P150-GLUED).//0.00076:100:29//RA
TTUS NORVEGICUS (RAT).//P28023
F-OVARC1000414//HYPOTHETICAL 7.0 KD PROTEIN IN BLTR-SPO11IC INTERG
ENIC REGION.//1.0:46:34//BACILLUS SUBTILIS.//P54431
F-OVARC1000420//COLLAGEN ALPHA 2(VIII) CHAIN (ENDOTHELIAL COLLAGE
N) (FRAGMENT).//0.0028:97:37//HOMO SAPIENS (HUMAN).//P25067
F-OVARC1000427//HYPOTHETICAL 13.9 KD PROTEIN IN PRFA-SPO11R INTERG
ENIC REGION.//0.70:21:47//BACILLUS SUBTILIS.//P39150
F-OVARC1000431
F-OVARC1000437//TENSIN.//9.2e-42:195:52//GALLUS GALLUS (CHICKEN)./
Q04205
F-OVARC1000440//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS
PROTEIN).//3.4e-31:37:97//HOMO SAPIENS (HUMAN).//P48059
F-OVARC1000442
F-OVARC1000443//CUTICLE COLLAGEN 2C (FRAGMENT).//0.0056:163:34//HA
EMONCHUS CONTORTUS.//P16252
F-OVARC1000461//FIXU PROTEIN.//0.36:36:44//RHIZOBIUM LEGUMINOSARUM
(BIOVAR TRIFOLI).//P42710
F-OVARC1000465//PROTEIN TRANSPORT PROTEIN SECT.//2.4e-14:222:26//S
ACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P11075
F-OVARC1000466//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//2.3e-08:
29:93//HOMO SAPIENS (HUMAN).//P39192
F-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 7 (EC 3.1.3.4
8) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE MKP-X) (FRA
GMENT).//2.8e-06:96:36//RATTUS NORVEGICUS (RAT).//Q63340
F-OVARC1000479//PHOTOSYSTEM I REACTION CENTRE SUBUNIT X (PSI-X).//
0.99:48:37//CYANIDIUM CALDARIUM (CALDIERIA SULPHURARIA).//P31567
F-OVARC1000486
F-OVARC1000496//HYPOTHETICAL PROTEIN MJ1213.//1.0:62:32//METHANOCO
CCUS JANNASCHII.//Q58610
F-OVARC1000520//NEOZOITE SURFACE PROTEIN CMZ-8 (FRAGMENT).//0.001
1:66:40//EIMERIA ACERVULINA.//P09125
F-OVARC1000526//PROTEIN Q300.//1.2e-05:51:43//MUS MUSCULUS (MOUSE
).//Q02722
F-OVARC1000533//NEURONAL PROTEIN 3.1 (P311 PROTEIN).//0.74:43:41//
HOMO SAPIENS (HUMAN).//Q16612
F-OVARC1000543//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC
2.4.1.41) (PROTEIN- UDP ACETYL GALACTOSAMINYLTRANSFERASE) (UDP-CALN
AC:POLYPEPTIDE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-T1).//

【0676】

【表378】

2.3e-23:192:35//HOMO SAPIENS (HUMAN).//Q10472
 F-OVARC1000556
 F-OVARC1000557//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.6e-08:8
 0:47//HOMO SAPIENS (HUMAN).//P39188
 F-OVARC1000564//VPX PROTEIN (X ORF PROTEIN) (VIRAL ACCESSORY PROTEIN).//0.45:32:50//HUMAN IMMUNODEFICIENCY VIRUS TYPE 2 (ISOLATE D194) (HIV-2).//P17760
 F-OVARC1000573
 F-OVARC1000576//BETA-DEFENSIN 1 (BDB-1).//0.47:29:41//BOS TAURUS (BOVINE).//P46159
 F-OVARC1000578//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.023:96:36//BOS TAURUS (BOVINE).//P02459
 F-OVARC1000588//MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L3.//0.75:57:29//HOMO SAPIENS (HUMAN).//P09001
 F-OVARC1000605//AUTOLYSIN PRECURSOR (EC 3.4.24.38) (GAMETE LYTIC ENZYME) (GLE).//0.91:134:28//CHLAMYDOMONAS REINHARDTII.//P31178
 F-OVARC1000622//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.6e-36:100:80//HOMO SAPIENS (HUMAN).//P39189
 F-OVARC1000640//HYPOTHETICAL 8.5 KD PROTEIN YCF40 (ORF73).//0.96:34:38//ODONTELLA SINENSIS.//P49535
 F-OVARC1000649//ANTHER-SPECIFIC PROTEIN SF18 PRECURSOR (FRAGMENT).//0.0036:64:37//HELIANTHUS ANNUUS (COMMON SUNFLOWER).//P22357
 F-OVARC1000661//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENTS).//0.21:53:47//RATTUS NORVEGICUS (RAT).//P02466
 F-OVARC1000678//BACTERIOCIN MICROCIN B17 PRECURSOR (MCB17).//1.0:17:58//ESCHERICHIA COLI.//P05834
 F-OVARC1000679//DNA-DIRECTED RNA POLYMERASE OMEGA CHAIN (EC 2.7.7.6) (TRANSCRIPTASE OMEGA CHAIN) (RNA POLYMERASE OMEGA SUBUNIT).//0.096:67:29//ESCHERICHIA COLI.//P08374
 F-OVARC1000681//PROTEIN Q300.//0.72:16:43//MUS MUSCULUS (MOUSE).//Q02722
 F-OVARC1000682//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B).//7.6e-70:102:99//MUS MUSCULUS (MOUSE).//P39098
 F-OVARC1000689//CADMIUM-METALLOTHIONEIN (CD-MT).//0.032:30:40//HELIX POMATIA (ROMAN SNAIL) (EDIBLE SNAIL).//P33187
 F-OVARC1000700//BRAIN NEURON CYTOPLASMIC PROTEIN 2.//0.17:60:40//RATTUS NORVEGICUS (RAT).//P02684
 F-OVARC1000703//BASIC PROLINE-RICH PEPTIDE P-E (18-9).//0.57:42:42//HOMO SAPIENS (HUMAN).//P02811
 F-OVARC1000722//N-ACETYLTRANSFERASE SYNTHASE (EC 2.4.1.90) (N-ACETYLGLUCOSAMINE (BETA 1-4) GALACTOSYLTRANSFERASE) (EC 2.4.1.38) (LACTOSE SYNTHASE A PROTEIN (EC 2.4.1.22)) (GALACTOSYLTRANSFERASE) (G T).//1.1e-20:44:70//BOS TAURUS (BOVINE).//P08037
 F-OVARC1000730//HYPOTHETICAL 83.8 KD PROTEIN C27F2.7 IN CHROMOSOME 111.//5.2e-29:224:36//CAENORHABDITIS ELEGANS.//Q18262
 F-OVARC1000746//MATERNAL EFFECT PROTEIN STAFEN.//6.2e-12:78:48//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25159
 F-OVARC1000769
 F-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.1e-45:121:79//HOMO SAPIENS (HUMAN), AND CANIS FAMILIARIS (DOG).//P08886
 F-OVARC1000781//HOMEBOX PROTEIN GBX-2 (GASTRULATION AND BRAIN-SPECIFIC HOMEBOX PROTEIN 2).//0.81:36:52//HOMO SAPIENS (HUMAN).//P52951
 F-OVARC1000787//40S RIBOSOMAL PROTEIN S14 (FRAGMENT).//0.96:37:48//SUS SCROFA (PIG).//Q29303
 F-OVARC1000800//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.5e-31:47:82//HOMO SAPIENS (HUMAN).//P39189
 F-OVARC1000802//HYPOTHETICAL 8.8 KD PROTEIN B0302.2 IN CHROMOSOME X.//0.16:55:40//CAENORHABDITIS ELEGANS.//Q10926
 F-OVARC1000834//SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA (EC 2.7.1.-) (P68-PAK) (P21-ACTIVATED KINASE) (ALPHA-PAK) (PROTEIN KINASE MKK2).//0.87:140:31//RATTUS NORVEGICUS (RAT).//P35465
 F-OVARC1000846//NUCLEOLIN (PROTEIN C23).//7.0e-07:109:30//MESOCRICETUS AURATUS (GOLDEN HAMSTER).//P08199
 F-OVARC1000850//HYPOTHETICAL 56.2 KD PROTEIN IN ERG8-LBP8 INTERGENIC REGION.//6.9e-09:180:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04991
 F-OVARC1000862//UBIQUITIN-CONJUGATING ENZYME E2-17.5 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN).//0.0020:74:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P52490
 F-OVARC1000876//MOB1 PROTEIN (MPS1 BINDER 1).//9.8e-39:154:55//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40484
 F-OVARC1000883//METALLOTHIONEIN-1.//0.87:38:36//CANDIDA GLABRATA (YEAST) (TORULOPSIS GLABRATA).//P15113
 F-OVARC1000885//OXIDOREDUCTASE UCPA (EC 1.-.-.-).//2.8e-18:170:34//ESCHERICHIA COLI.//P37440
 F-OVARC1000886//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//0.0033:60:45//BOS TAURUS (BOVINE).//P02465
 F-OVARC1000890//PROBABLE E5 PROTEIN.//0.92:7:71//HUMAN PAPILLOMAVIRUS TYPE 70.//P50774
 F-OVARC1000891//HYPOTHETICAL 8.3 KD PROTEIN (ORF5).//1.0:36:36//PARAMECIUM TETRAURELIA.//P15806
 F-OVARC1000897//HYPOTHETICAL 6.1 KD PROTEIN PRECURSOR (ORF87).//1.0:34:44//ORGYIA PSEUDOTUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMV).//Q10337
 F-OVARC1000912//PUTATIVE CUTICLE COLLAGEN C09G5.4.//4.0e-07:98:35//CAENORHABDITIS ELEGANS.//Q09455
 F-OVARC1000915//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//1.7e-47:15:76//HOMO SAPIENS (HUMAN).//P56524
 F-OVARC1000924//CYTOCHROME B (EC 1.10.2.2) (FRAGMENT).//0.99:54:24//BOA CONSTRICTOR (BOA).//P92848
 F-OVARC1000936//HYPOTHETICAL 7.5 KD PROTEIN IN INAA-GLPQ INTERGENIC REGION.//1.0:48:33//ESCHERICHIA COLI.//P45505
 F-OVARC1000937//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//1.0:135:31//HOMO SAPIENS (HUMAN).//P02452
 F-OVARC1000945//EARLY E1A 11 KD PROTEIN.//0.087:81:24//MOUSE ADENOVIRUS TYPE 1 (NAV-1).//P12533
 F-OVARC1000948
 F-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//0.99:67:28//METHANOCOCCLUS JANNASCHII.//Q58343
 F-OVARC1000960//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.8e-32:56:75//HOMO SAPIENS (HUMAN).//P39193
 F-OVARC1000964//MAMBIN (GLYCOPROTEIN IIB-11A ANTAGONIST) (PLATELET AGGREGATION INHIBITOR) (DENDROASPIN).//1.0:30:36//DENDROASPIS JAMESONI KAIMOSAE (EASTERN JAMESON'S MAMBA).//P28375
 F-OVARC1000971
 F-OVARC1000984//HYPOTHETICAL 52.3 KD PROTEIN IN MRPL10-ERG24 INTERGENIC REGION PRECURSOR.//0.093:36:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53832
 F-OVARC1000996//MO25 PROTEIN.//1.9e-39:80:95//MUS MUSCULUS (MOUSE).//Q06138
 F-OVARC1000999//BRAIN-SPECIFIC HOMEBOX/POU DOMAIN PROTEIN 1 (BRN-1 PROTEIN).//0.00020:50:40//HOMO SAPIENS (HUMAN).//P20264
 F-OVARC1001000//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.4e-16:43:90//HOMO SAPIENS (HUMAN).//P39195
 F-OVARC1001004//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.95:33:42//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01642
 F-OVARC1001010//HYPOTHETICAL PROTEIN MJ0926.//0.50:71:23//METHANOCOCCLUS JANNASCHII.//Q58336
 F-OVARC1001011//CORTISTATIN PRECURSOR.//0.81:45:37//RATTUS NORVEGICUS (RAT).//Q62949
 F-OVARC1001032//FERREDOXIN LIKE PROTEIN.//1.0:26:46//RHIZOBIUM LEGUMINOSARUM (BIOVAR PHASEOLII).//Q05561
 F-OVARC1001034//METALLOTHIONEIN-1G (MT-1G).//0.14:9:77//HOMO SAPIENS (HUMAN).//P13640
 F-OVARC1001038//NUCLEOLIN (PROTEIN C23).//3.2e-07:36:80//HOMO SAPIENS (HUMAN).//P19338
 F-OVARC1001040//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.5e-18:45:60//HOMO SAPIENS (HUMAN).//P39194
 F-OVARC1001044//BIS(5'-NUCLEOSYL)-TETRAPHOSPHATASE (SYMMETRICAL) (EC 3.6.1.41) (DIADENOSINE TETRAPHOSPHATASE).//0.88:43:39//ESCHERICHIA COLI.//P05637
 F-OVARC1001051//SERINE PROTEINASE STUBBLE (EC 3.4.21.-) (STUBBLE-S TUBBLOID PROTEIN).//0.34:117:25//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q05319
 F-OVARC1001055//PRE-B CELL ENHANCING FACTOR PRECURSOR.//1.6e-33:43:97//HOMO SAPIENS (HUMAN).//P43490
 F-OVARC1001062
 F-OVARC1001065//METHIONYL-TRNA SYNTHETASE (EC 6.1.1.10) (METHIONINE-TRNA LIGASE) (METRS).//0.79:76:39//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//Q44951
 F-OVARC1001068//GTP-BINDING PROTEIN ERA HOMOLOG (FRAGMENT).//5.3e-15:100:44//BRADYRHIZOBIUM JAPONICUM.//Q09162
 F-OVARC1001072//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.0076:41:56//HOMO SAPIENS (HUMAN).//P39188
 F-OVARC1001074//60S RIBOSOMAL PROTEIN L38.//1.0:32:40//LYCOPERSICON ESCULENTUM (TOMATO).//P46291
 F-OVARC1001085//HYPOTHETICAL 126.5 KD PROTEIN C13F4.06 IN CHROMOSOME 1.//0.73:135:25//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10197
 F-OVARC1001092//HYPOTHETICAL 51.2 KD PROTEIN IN PETS4-DIE2 INTERGENIC REGION.//5.6e-05:30:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P50079
 F-OVARC1001107//SHK1 KINASE-BINDING PROTEIN 1.//1.8e-08:52:51//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P78963
 F-OVARC1001113//DIAPHANOUS PROTEIN.//1.9e-33:218:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48608
 F-OVARC1001117//GENE 7 PROTEIN.//0.68:12:50//SPIROPLASMA VIRUS 4 (SPV4).//P11339

【0677】

【表379】

F-OVARC1001118
F-OVARC1001129//30S RIBOSOMAL PROTEIN S17.//0.15:57:22//AQUIFEX AE
OLICUS.//066439
F-OVARC1001154//GRANULINS PRECURSOR (ACROGRAMIN).//2.3e-95:99:77//
MUS MUSCULUS (MOUSE).//P28798
F-OVARC1001161//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//
0.17:87:34//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P49177
F-OVARC1001162
F-OVARC1001167//TRBD PROTEIN.//0.92:24:45//ESCHERICHIA COLI.//P410
70
F-OVARC1001169//FRUCTOSE-1,6-BISPHOSPHATASE (EC 3.1.3.11) (D-FRUCT
OSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE) (FRAGMENT).//0.8
2:35:40//MUS MUSCULUS (MOUSE).//P97323
F-OVARC1001170//PROLINE-RICH PEPTIDE P-B.//0.17:27:37//HOMO SAPIEN
S (HUMAN).//P02814
F-OVARC1001171//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.0023:2
8:75//HOMO SAPIENS (HUMAN).//P39188
F-OVARC1001173
F-OVARC1001176//HYPOTHETICAL BHLF1 PROTEIN.//2.7e-05:158:31//EPSTE
IN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
F-OVARC1001180//UBIQUITIN-LIKE PROTEIN DSK2.//1.4e-12:208:25//SACC
HAROMYCES CEREVISIAE (BAKER'S YEAST).//P48510
F-OVARC1001188//HYPOTHETICAL 27.8 KD PROTEIN IN YMA7-RPS25A INTERG
ENIC REGION.//3.3e-31:129:51//SACCHAROMYCES CEREVISIAE (BAKER'S YE
AST).//P53215
F-OVARC1001200//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGEN
IC REGION.//0.018:148:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST
).//P47057
F-OVARC1001232//HYPOTHETICAL PROTEIN MJ1236.//2.5e-27:141:39//METH
ANOCOCCUS JANNASCHII.//Q58633
F-OVARC1001240
F-OVARC1001243
F-OVARC1001244//RING3 PROTEIN (KIAA9001).//1.7e-13:37:91//HOMO SAP
IENS (HUMAN).//P25440
F-OVARC1001261//OCTAPEPTIDE-REPEAT PROTEIN T2.//1.3e-07:109:35//MU
S MUSCULUS (MOUSE).//Q06666
F-OVARC1001268//HYPOTHETICAL 57.4 KD PROTEIN IN PILT REGION (ORF4
).//0.71:43:41//PSEUDOMONAS AERUGINOSA.//P24563
F-OVARC1001270//HYPOTHETICAL 9.0 KD PROTEIN IN UVSW-UVSY INTERGENI
C REGION.//1.0:44:29//BACTERIOPHAGE T4.//P32281
F-OVARC1001271//HYPOTHETICAL 104.7 KD PROTEIN F23F12.8 IN CHROMOSO
ME III PRECURSOR.//0.00015:188:23//CAENORHABDITIS ELEGANS.//P46504
F-OVARC1001282
F-OVARC1001296//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//
0.022:101:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38968
F-OVARC1001306//HYPOTHETICAL 52.9 KD SERINE-RICH PROTEIN C11G7.01
IN CHROMOSOME I.//0.023:134:26//SCHIZOSACCHAROMYCES POMBE (FISSION
YEAST).//013695
F-OVARC1001329//CHLOROPLAST TRIOSE PHOSPHATE TRANSLOCATOR PRECURSO
R (CTPT).//1.3e-14:150:28//ZEA MAYS (MAIZE).//P49133
F-OVARC1001330
F-OVARC1001339//RIBONUCLEOPROTEIN RB970.//0.0013:55:38//DROSOPHILA
MELANOGASTER (FRUIT FLY).//Q02926
F-OVARC1001341//HYPOTHETICAL 74.0 KD PROTEIN IN CAJ1-HOM3 INTERGEN
IC REGION.//4.9e-17:110:43//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
T).//P40032
F-OVARC1001342
F-OVARC1001344//PREPROTEIN TRANSLOCASE SECE SUBUNIT.//0.99:39:23//
STAPHYLOCOCCUS CARNOIUS.//P36253
F-OVARC1001357//METALLOTHIONEIN.//0.99:28:42//XENOPUS LAEVIS (AFRI
CAN CLAWED FROG).//Q05890
F-OVARC1001360//LARGE PROLINE-RICH PROTEIN BAT2 (HLA-B-ASSOCIATED
TRANSCRIPT 2).//0.86:109:31//HOMO SAPIENS (HUMAN).//P48634
F-OVARC1001369//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//6.7e-05:12
4:36//BOS TAURUS (BOVINE).//P02465
F-OVARC1001372//HYPOTHETICAL 34.5 KD PROTEIN IN CLCB-CLCD INTERGEN
IC REGION PRECURSOR.//0.75:33:48//PSEUDOMONAS PUTIDA, AND PSEUDOMO
NAS SP. (STRAIN B13).//Q47100
F-OVARC1001376//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.8e-24:9
6:61//HOMO SAPIENS (HUMAN).//P39188
F-OVARC1001381//MEMBRANE-ASSOCIATED ATPASE EPSILON CHAIN (EC 3.6.
1.34) (SUL-ATPASE EPSILON).//0.96:46:39//SULFOLOBUS ACIDOCALDARIU
S.//P23039
F-OVARC1001391//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTA
INS: PEPTIDE P-0] (FRAGMENT).//0.0024:189:29//HOMO SAPIENS (HUMA
N).//P10162
F-OVARC1001399//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.062:1
8:77//HOMO SAPIENS (HUMAN).//P39188
F-OVARC1001417//HYPOTHETICAL 157.0 KD PROTEIN C38C10.5 IN CHROMOSO
ME III.//0.010:185:23//CAENORHABDITIS ELEGANS.//Q03570
F-OVARC1001419//A-TYPE INCLUSION PROTEIN (ATI).//0.50:135:28//CAME
LPOX VIRUS (STRAIN CP-1).//Q05482
F-OVARC1001425//COLLAGEN ALPHA 1(X) CHAIN PRECURSOR.//0.43:85:40//
HOMO SAPIENS (HUMAN).//Q03692
F-OVARC1001436//HYPOTHETICAL 11.4 KD PROTEIN (C4 PROTEIN).//0.031:
100:30//TOMATO YELLOW LEAF CURL VIRUS (STRAIN AUSTRALIA) (TYLCV).//
P36283
F-OVARC1001442//HOMEBOX PROTEIN HTR-A2 (FRAGMENT).//1.0:32:34//HE
LOBDELLA TRISERIALIS (LEECH).//P17138
F-OVARC1001453//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FA
CTOR) (GIF).//0.74:19:47//MUS MUSCULUS (MOUSE).//P28184
F-OVARC1001476//GTP-BINDING PROTEIN GTR2.//3.0e-12:114:34//SACCHA
ROMYCES CEREVISIAE (BAKER'S YEAST).//P53290
F-OVARC1001480//COLLAGEN ALPHA 2(VI) CHAIN PRECURSOR.//0.00019:13
4:32//MUS MUSCULUS (MOUSE).//Q02788
F-OVARC1001489//HYPOTHETICAL PROTEIN H11270.//0.98:30:43//HAEMOPHI
LUS INFLUENZAE.//P44149
F-OVARC1001496//C-TERMINAL BINDING PROTEIN 2.//4.0e-65:132:100//HO
MO SAPIENS (HUMAN).//P56545
F-OVARC1001506//POLYCYSTIN PRECURSOR (AUTOSOMAL DOMINANT POLYCYSTI
C KIDNEY DISEASE PROTEIN 1).//3.2e-70:159:94//HOMO SAPIENS (HUMAN
).//P98161
F-OVARC1001525//FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 14 (FIN
14).//1.0:36:33//MUS MUSCULUS (MOUSE).//Q61077
F-OVARC1001542//SMALL PROLINE-RICH PROTEIN 28 (SPR-28).//0.69:57:3
3//HOMO SAPIENS (HUMAN).//P35325
F-OVARC1001547
F-OVARC1001555//NCG1-INTERACTING FACTOR 3.//7.6e-16:148:34//SACCHA
ROMYCES CEREVISIAE (BAKER'S YEAST).//P53081
F-OVARC1001577//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING
FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//
/8.8e-38:94:81//GALLUS GALLUS (CHICKEN).//P30352
F-OVARC1001600//GENE 7 PROTEIN.//0.80:38:39//SPIROPLASMA VIRUS SPV
1-RBA2 B.//P15898
F-OVARC1001610//DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE (EC 2.7.
8.2) (SN-1,2- DIACYLGLYCEROL CHOLINEPHOSPHOTRANSFERASE) (CHOPT).//
1.6e-22:122:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P17898
F-OVARC1001611
F-OVARC1001615//HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME
X.//0.30:43:34//CAENORHABDITIS ELEGANS.//Q11116
F-OVARC1001668//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.0e-19:
45:82//HOMO SAPIENS (HUMAN).//P39192
F-OVARC1001702//SOX-20 PROTEIN.//2.4e-28:71:83//HOMO SAPIENS (HUMA
N).//Q06048
F-OVARC1001703//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GU
ANINE NUCLEOTIDE- BINDING PROTEIN 1) (INTERFERON-GAMMA INDUCIBLE P
ROTEIN MAG-1).//0.00018:88:36//MUS MUSCULUS (MOUSE).//Q01514
F-OVARC1001711//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR1B)
(SPR1 B).//2.7e-05:98:32//MUS MUSCULUS (MOUSE).//Q62267
F-OVARC1001713//ENDOZEPINE-RELATED PROTEIN PRECURSOR (MEMBRANE-ASS
OCIATED DIAZEPAM BINDING INHIBITOR) (MA-DB1).//4.5e-20:46:67//BOS
TAURUS (BOVINE).//P07106
F-OVARC1001726//ALPHA-AMYLASE INHIBITOR PAIN 1 (PIG PANCREATIC ALP
HA-AMYLASE INHIBITOR OF MICROBES 1).//0.59:23:56//STREPTOMYCES OLI
VACEOVIRIDIS (STREPTOMYCES CORCHORUSII).//P09921
F-OVARC1001731//TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE.//2.1e-7
5:176:87//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//Q01173
F-OVARC1001745//GENE 11 PROTEIN.//0.31:36:52//SPIROPLASMA VIRUS SP
V1-RBA2 B.//P15902
F-OVARC1001762//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMIN
O-TERMINAL, ALPHA- AMINO, ACETYLTRANSFERASE 1).//2.8e-23:197:35//S
ACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P12945
F-OVARC1001766//FK506-BINDING NUCLEAR PROTEIN (PEPTIDYL-PROLYL CI
S-TRANS ISOMERASE) (PPIASE) (EC 5.2.1.8) (PROLINE ROTAMASE) (NUCLE
OLAR PROLINE ISOMERASE) (FKBP-70).//2.2e-06:99:40//SACCHAROMYCES. C
EREVISIAE (BAKER'S YEAST).//P38911
F-OVARC1001767//33.2 KD PROTEIN IN DIND-RPH INTERGENIC REGION (ORF
X).//0.99:113:27//ESCHERICHIA COLI.//P23839
F-OVARC1001768
F-OVARC1001791//HYPOTHETICAL 63.3 KD PROTEIN IN MPT5-SAE2 INTERGEN
IC REGION.//0.090:75:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
//P46945
F-OVARC1001795//HYPOTHETICAL 7.5 KD PROTEIN IN RPBA-GP46 INTERGENI
C REGION.//0.81:21:38//BACTERIOPHAGE T4.//P07878
F-OVARC1001802//PLECTOXIN V111 (PLT-V111).//0.41:19:36//
PLECTREURYS TRISTIS (SPIDER).//P36984
F-OVARC1001805//60S RIBOSOMAL PROTEIN L40 (CEP52).//0.67:24:58//SA
CHAROMYCES CEREVISIAE (BAKER'S YEAST).//P14796
F-OVARC1001809//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.23:111:3
1//RATTUS NORVEGICUS (RAT).//P02454

【0678】

【表380】

F-OVARC1001812//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (AGL).//0.99:28:42//MALICHOERUS GRYPUS (GRAY SEAL).//P38592
 F-OVARC1001813//HYPOTHETICAL 9.9 KD PROTEIN.//0.41:36:30//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20562
 F-OVARC1001820//HYPOTHETICAL PROTEIN ORF-1137.//0.80:58:29//MUS MUSCULUS (MOUSE).//P11260
 F-OVARC1001828
 F-OVARC1001846
 F-OVARC1001861//METALLOTHIONEIN (MT).//0.18:11:54//PLEURONECTES PLATYSSA (PLAICE).//P07216
 F-OVARC1001873
 F-OVARC1001879//HYPOTHETICAL 55.9 KD PROTEIN EEDB.6 IN CHROMOSOME 11.//2.3e-05:73:31//CAENORHABDITIS ELEGANS.//Q09296
 F-OVARC1001880//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONE CP7) [CONTAINS: BASIC PEPTIDE P-F] (FRAGMENT).//2.4e-11:203:32//HOMO SAPIENS (HUMAN).//P02812
 F-OVARC1001883//!!!! ALU SUBFAMILY J WARNING ENTRY !!!//2.3e-16:6:59//HOMO SAPIENS (HUMAN).//P39188
 F-OVARC1001900//HYPOTHETICAL 105.9 KD PROTEIN F2287.5 IN CHROMOSOME 111.//0.0053:48:47//CAENORHABDITIS ELEGANS.//P34408
 F-OVARC1001901
 F-OVARC1001911//40S RIBOSOMAL PROTEIN S28.//1.0:33:36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P34789
 F-OVARC1001916//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN).//0.0082:114:27//HOMO SAPIENS (HUMAN).//P98174
 F-OVARC1001928//FERREDOXIN 111 (FD111).//1.0:64:29//ANABAENA VARIA BILIS.//P46050
 F-OVARC1001942//N-TERMINAL ACETYLTRANSFERASE 1 (EC 2.3.1.88) (AMINO-TERMINAL, ALPHA-AMINO, ACETYLTRANSFERASE 1).//3.0e-07:93:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P12945
 F-OVARC1001943//HYPOTHETICAL 62.2 KD PROTEIN ZK652.6 IN CHROMOSOME 111.//1.7e-23:147:43//CAENORHABDITIS ELEGANS.//P34664
 F-OVARC1001949//ZINC FINGER PROTEIN 177.//2.0e-23:56:66//HOMO SAPIENS (HUMAN).//Q13360
 F-OVARC1001950//!!!! ALU SUBFAMILY J WARNING ENTRY !!!//0.011:57:47//HOMO SAPIENS (HUMAN).//P39188
 F-OVARC1001981//SPERM PROTEIN P1 (CYSTEINE-RICH PROTEIN).//0.3:9:14:64//MUS MUSCULUS (MOUSE).//P02319
 F-OVARC1001989//!!!! ALU SUBFAMILY J WARNING ENTRY !!!//2.4e-13:5:72//HOMO SAPIENS (HUMAN).//P39188
 F-OVARC1002044
 F-OVARC1002050//UTROPHIN (DYSTROPHIN-RELATED PROTEIN 1) (DRP1) (DRP).//3.6e-12:221:25//HOMO SAPIENS (HUMAN).//P46939
 F-OVARC1002066
 F-OVARC1002082
 F-OVARC1002107//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.9:9:149:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25386
 F-OVARC1002112//HISTONE MACRO-H2A.1.//2.8e-64:133:98//RATTUS NORVEGICUS (RAT).//Q02874
 F-OVARC1002127//60S RIBOSOMAL PROTEIN L22.//0.0023:95:35//DROSOPHILA MELANOGASTER (FRUIT FLY).//P50887
 F-OVARC1002138//PROBABLE 26S PROTEASE SUBUNIT YTA6 (TAT-BINDING HOMOLOG 6).//6.4e-51:198:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40328
 F-OVARC1002143
 F-OVARC1002156//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC88 INTERGENIC REGION.//0.00010:64:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53915
 F-OVARC1002158//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//8.2e-07:119:35//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYOMEDUSIS VIRUS (ACMPV).//P41479
 F-OVARC1002165//EBNA-6 NUCLEAR PROTEIN (EBNA-3C) (EBNA-4B).//0.00023:90:45//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03204
 F-OVARC1002182//HYPOTHETICAL 46.2 KD TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME 11.//1.3e-34:165:35//CAENORHABDITIS ELEGANS.//Q18964
 F-PLACE1000004//HYPOTHETICAL 180.2 KD PROTEIN C31A2.05C IN CHROMOSOME 1.//8.8e-05:148:25//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09725
 F-PLACE1000005//PROTEIN Q300.//0.30:10:100//MUS MUSCULUS (MOUSE).//Q02722
 F-PLACE1000007//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE R10 E11.3 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME).//2.3e-39:134:62//CAENORHABDITIS ELEGANS.//P34547
 F-PLACE1000014//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//0.0036:63:39//HOMO SAPIENS (HUMAN).//P19474
 F-PLACE1000031
 F-PLACE1000040//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!//4.4e-12:97:41//HOMO SAPIENS (HUMAN).//P39194
 F-PLACE1000048//50S RIBOSOMAL PROTEIN L15 (FRAGMENT).//0.98:31:38//BACILLUS SP. (STRAIN C-125).//P38373
 F-PLACE1000050//COLLAGEN ALPHA 1(I1) CHAIN.//0.00062:190:33//BOS TAURUS (BOVINE).//P04258
 F-PLACE1000061//60S RIBOSOMAL PROTEIN L37A.//6.4e-19:51:86//GALLUS GALLUS (CHICKEN).//P32046
 F-PLACE1000066//SSU72 PROTEIN.//2.3e-39:165:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53538
 F-PLACE1000078//BAD PROTEIN (BCL-2 BINDING COMPONENT 6).//1.7e-06:21:95//HOMO SAPIENS (HUMAN).//Q92934
 F-PLACE1000081//HOMEBOX PROTEIN HOX-A4 (HOX-1.4) (MH-3).//0.0053:146:33//MUS MUSCULUS (MOUSE).//P06798
 F-PLACE1000094
 F-PLACE1000133//TRANSCRIPTION FACTOR BTF3 (RNA POLYMERASE 8 TRANSCRIPTION FACTOR 3).//1.8e-62:158:81//HOMO SAPIENS (HUMAN).//P20290
 F-PLACE1000142//ENOYL-COA HYDRATASE, MITOCHONDRIAL PRECURSOR (EC 4.2.1.17) (SHORT CHAIN ENOYL-COA HYDRATASE) (SCEH) (ENOYL-COA HYDRATASE 1).//9.8e-12:104:34//HOMO SAPIENS (HUMAN).//P30084
 F-PLACE1000184//AC PROTEIN.//0.44:31:29//BACTERIOPHAGE T4.//P18924
 F-PLACE1000185//HYPOTHETICAL GLYCINE-RICH 49.6 KD PROTEIN CY130.10 C PRECURSOR.//0.11:48:33//MYCOBACTERIUM TUBERCULOSIS.//Q10637
 F-PLACE1000213//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//3.4e-05:194:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640
 F-PLACE1000214
 F-PLACE1000236//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//0.027:63:34//GALLUS GALLUS (CHICKEN).//P02457
 F-PLACE1000246//TEGUMENT PROTEIN (GENE 11 PROTEIN).//0.78:100:26//EQUINE HERPESVIRUS TYPE 4 (STRAIN 1942) (EHV-4) (EQUINE HERPESVIRUS TYPE 1 SUBTYPE 2).//Q00039
 F-PLACE1000292
 F-PLACE1000308//EARLY NODULIN 75 (N-75) (NEM-75) (FRAGMENT).//0.04:9:28:42//MEDICAGO SATIVA (ALFALFA).//P11728
 F-PLACE1000332
 F-PLACE1000347//HYPOTHETICAL PROTEIN TP0420.//0.15:24:54//TREPONEMA PALLIDUM.//Q83435
 F-PLACE1000374//LYSOZYME C (EC 3.2.1.17) (1,4-BETA-N-ACETYLURAMIDASE C).//1.0:63:25//ORYZOLAGUS CUNICULUS (RABBIT).//P16973
 F-PLACE1000380//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN S MS1) (PROTEIN KINASE A INTERFERENCE PROTEIN).//0.018:169:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36027
 F-PLACE1000383//MYOTUBULARIN.//1.2e-65:215:57//HOMO SAPIENS (HUMAN).//Q13496
 F-PLACE1000401//ELASTIN PRECURSOR (TROPOLASTIN).//0.00023:145:30//MUS MUSCULUS (MOUSE).//P54320
 F-PLACE1000406//54 KD NUCLEAR RNA-BINDING PROTEIN (P54(NRB)).//3.4e-27:90:63//HOMO SAPIENS (HUMAN).//Q15233
 F-PLACE1000420//7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE).//4.7e-07:134:29//MUS MUSCULUS (MOUSE).//P53368
 F-PLACE1000421//HYPOTHETICAL 8.8 KD PROTEIN C1103.01C IN CHROMOSOME 1.//0.48:72:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10080
 F-PLACE1000424
 F-PLACE1000435
 F-PLACE1000444//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!//2.0e-31:129:63//HOMO SAPIENS (HUMAN).//P39195
 F-PLACE1000453//PROTEIN Q300.//0.013:16:68//MUS MUSCULUS (MOUSE).//Q02722
 F-PLACE1000481//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//0.14:63:36//HOMO SAPIENS (HUMAN).//P08547
 F-PLACE1000492//BASP1 PROTEIN.//0.17:114:28//HOMO SAPIENS (HUMAN).//P80723
 F-PLACE1000540
 F-PLACE1000547//MANNOSYL-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSYL-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE).//1.8e-21:87:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P41940
 F-PLACE1000562//HYPOTHETICAL PROTEIN MJ0562.//1.0:35:34//METHANOCOCCUS JANNASCHII.//Q57982
 F-PLACE1000564//ADRENAL SPECIFIC 30 KD PROTEIN (CLONE PG2).//0.13:66:37//HOMO SAPIENS (HUMAN).//P15803
 F-PLACE1000583//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//7.0e-45:192:47//HOMO SAPIENS (HUMAN).//P51522
 F-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GUANINE NUCLEOTIDE-BINDING PROTEIN 1).//5.3e-63:122:88//HOMO SAPIENS (HUMAN).//P32455
 F-PLACE1000596//RING CANAL PROTEIN (KELCH PROTEIN).//2.6e-12:120:38//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652

【0679】

【表381】

F-PLACE1000599//EARLY E3B 12.7 KD PROTEIN PRECURSOR.//0.83:53:32//
HUMAN ADENOVIRUS TYPE 12.//P36707
F-PLACE1000610
F-PLACE1000611//HYPOTHETICAL 33.6 KD PROTEIN IN MCK1-RPS19B INTERG
ENIC REGION.//9.4e-07:64:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
T).//P48558
F-PLACE1000636//MALE STERILITY PROTEIN 2.//3.7e-09:83:43//ARABIDOP
SIS THALIANA (MOUSE-EAR CRESS).//Q08891
F-PLACE1000653//PUTATIVE PHOSPHOACETYLGLUCOSAMINE MUTASE (EC 5.4.
2.3) (ACETYLGLUCOSAMINE PHOSPHOMUTASE) (N-ACETYLGLUCOSAMINE-PHOSPH
ATE MUTASE).//1.9e-30:203:41//SCHIZOSACCHAROMYCES POMBE (FISSION Y
EAST).//Q09687
F-PLACE1000656//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH
GLYCOPROTEIN).//0.0029:75:33//NICOTIANA TABACUM (COMMON TOBACCO)./
P13983
F-PLACE1000706//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (NUCLEAR
COREPRESSOR KAP-1) (KRAB-ASSOCIATED PROTEIN 1).//1.1e-38:180:42//H
OMO SAPIENS (HUMAN).//Q13263
F-PLACE1000712//VERY HYPOTHETICAL 8.9 KD PROTEIN CY441.05 PRECURSO
R.//0.93:49:34//MYCOBACTERIUM TUBERCULOSIS.//P71934
F-PLACE1000716
F-PLACE1000748//HYPOTHETICAL 10.4 KD PROTEIN IN SPAT 3' REGION (OR
F-11).//0.90:53:37//SHIGELLA FLEXNERI.//P55794
F-PLACE1000749//HYPOTHETICAL PROTEIN MG148.//0.0014:142:27//MYCOPL
ASMA GENITALIUM.//P47394
F-PLACE1000755//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME III.//
1.1e-15:98:48//CAENORHABDITIS ELEGANS.//P34529
F-PLACE1000769//VIGILIN.//0.51:60:33//GALLUS GALLUS (CHICKEN).//P8
1021
F-PLACE1000785//PROBABLE COLD SHOCK PROTEIN CY15C10.04.//1.0:22:45
//MYCOBACTERIUM TUBERCULOSIS.//Q06360
F-PLACE1000786//HYPOTHETICAL 30.2 KD PROTEIN ZK632.12 IN CHROMOSOM
E III.//2.6e-38:159:51//CAENORHABDITIS ELEGANS.//P34657
F-PLACE1000793//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP).//0.0
097:128:30//HOMO SAPIENS (HUMAN).//P50552
F-PLACE1000798//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.4e-07:4
7:61//HOMO SAPIENS (HUMAN).//P39188
F-PLACE1000841
F-PLACE1000849//ELAV PROTEIN.//3.5e-05:140:35//DROSOPHILA VIRILIS
(FRUIT FLY).//P23241
F-PLACE1000856//HYPOTHETICAL PROTEIN MJ0008.//0.95:100:23//METHANO
COCCUS JANNASCHII.//Q00319
F-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN YHR14
8W.//2.3e-46:172:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P3
2899
F-PLACE1000909//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKY
RIN).//0.0022:105:35//HOMO SAPIENS (HUMAN).//P16157
F-PLACE1000931//KILLER TOXIN HB-1.//0.95:24:33//WILLIOPSIS MRK11
(YEAST) (HANSENULEA MRK11).//P10410
F-PLACE1000948//SL CYTOKINE PRECURSOR (FLT3 LIGAND).//0.97:52:40//
HOMO SAPIENS (HUMAN).//P49771
F-PLACE1000972//MYOSIN 1D HEAVY CHAIN.//1.9e-06:79:43//DICTYOSTELI
UM DISCOIDEUM (SLIME MOLD).//P34109
F-PLACE1000977//HYPOTHETICAL 94.2 KD PROTEIN C38D4.5 IN CHROMOSOME
III.//2.5e-23:105:41//CAENORHABDITIS ELEGANS.//P46941
F-PLACE1000979//ZINC FINGER PROTEIN 7 (ZINC FINGER PROTEIN KOX4)
(ZINC FINGER PROTEIN HF.16).//0.91:83:30//HOMO SAPIENS (HUMAN).//P
17097
F-PLACE1000987//HYPOTHETICAL 111.5 KD PROTEIN C22G7.02 IN CHROMOSO
ME I.//0.10:128:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q0
9796
F-PLACE1001000
F-PLACE1001007//ZYXIN.//2.2e-05:135:30//GALLUS GALLUS (CHICKEN).//
Q04584
F-PLACE1001010//BETA-1 BUNGAROTOXIN B CHAIN, MAJOR COMPONENT PRECU
RSOR (BUNGAROTOXIN, B1 CHAIN).//1.0:30:40//BUNGARUS MULTICINCTUS
(MANY-BANDED KRAIT).//P00987
F-PLACE1001015
F-PLACE1001024
F-PLACE1001036
F-PLACE1001054//HOLOTRICIN 3 PRECURSOR.//0.0044:56:39//HOLOTRICHIA
DIOMPHALIA.//Q25055
F-PLACE1001062//SACCHAROPINE DEHYDROGENASE [NADP+, L-GLUTAMATE FOR
MING] (EC 1.5.1.10).//0.0013:38:52//SACCHAROMYCES CEREVISIAE (BAKE
R'S YEAST).//P38999
F-PLACE1001076
F-PLACE1001088//EARLY NODULIN 75 (N-75) (NCH-75) (FRAGMENT).//0.9
5:32:50//MEDICAGO SATIVA (ALFALFA).//P11728
F-PLACE1001092//HYPOTHETICAL 49.0 KD PROTEIN IN NSP1-KAR2 INTERGEN
IC REGION.//0.0026:81:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST
).//P47057
F-PLACE1001104//HYPOTHETICAL 131.5 KD PROTEIN C02F12.7 IN CHROMOSO
ME X.//0.0063:125:32//CAENORHABDITIS ELEGANS.//Q11102
F-PLACE1001118//ZINC FINGER PROTEIN ML2-4 (ZINC FINGER PROTEIN 46
).//2.6e-77:209:63//MUS MUSCULUS (MOUSE).//Q03309
F-PLACE1001136//ALPHA-N-ACETYLGLACTOSAMINIDASE PRECURSOR (EC 3.2.
1.49) (ALPHA- GALACTOSIDASE B).//0.99:107:30//HOMO SAPIENS (HUMAN
).//P17050
F-PLACE1001168
F-PLACE1001171//RETROVIRUS-RELATED POL POLYPROTEIN (FRAGMENT).//0.
00012:37:59//HOMO SAPIENS (HUMAN).//P12895
F-PLACE1001185//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGE
NIC REGION.//3.6e-12:88:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
T).//P53867
F-PLACE1001238
F-PLACE1001241//METALLOTHIONEIN B (MTB) (FRAGMENT).//0.13:30:53//C
OLINUS VIRGINIANUS (BOBWHITE QUAIL) (COMMON BOBWHITE).//P27087
F-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN).//4.1e-24:125:4
6//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
F-PLACE1001272//HYPOTHETICAL PROTEIN IN KSCA 3' REGION (ORF L5) (FR
AGMENT).//1.0:24:45//MYCOPLASMA CAPRICOLUM.//P43040
F-PLACE1001279//CYTOTOXIN 3 (CYTOTOXIN V-11-3).//0.98:31:41//NAJA
MOSSAMBICA (MOZAMBIQUE COBRA).//P01470
F-PLACE1001280//PROCOLLAGEN ALPHA 1(I1) CHAIN PRECURSOR [CONTAINS:
CHONDROCALCIN].//0.0051:156:32//MUS MUSCULUS (MOUSE).//P28481
F-PLACE1001294//GAMETOGENESIS EXPRESSED PROTEIN GEG-154.//3.7e-56:
109:93//MUS MUSCULUS (MOUSE).//P50636
F-PLACE1001304//ZINC FINGER PROTEIN 35 (ZFP-35).//3.2e-30:75:57//M
US MUSCULUS (MOUSE).//P15620
F-PLACE1001311//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//2.7e-31:
66:66//HOMO SAPIENS (HUMAN).//P39189
F-PLACE1001323
F-PLACE1001351//REV PROTEIN (ANTI-REPRESSION TRANSACTIVATOR PROTEI
N) (ART/TRS).//0.11:66:27//SIMIAN IMMUNODEFICIENCY VIRUS (AGM155 I
SOLATE) (SIV-AGM).//P27971
F-PLACE1001366//SHORT NEUROTOXIN 2 (TOXIN CM-14) (TOXIN V-N-12).//
0.070:18:33//NAJA HAJE ANNULIFERA (BANDS EGYPTIAN COBRA).//P01422
F-PLACE1001377//DISINTEGRIN TRIGRAMIN BETA (PLATELET AGGREGATION A
CTIVATION INHIBITOR).//4.9e-06:50:46//TRIMERESURUS GRAMINEUS (INDI
AN GREEN TREE VIPER) (GREEN HABU SNAKE).//P17495
F-PLACE1001383//W PROTEIN, SEROTYPE 49 PRECURSOR.//0.080:136:24//S
TREPTOCOCCUS PYOGENES.//P16947
F-PLACE1001384
F-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE
EPSB.//1.9e-22:142:39//HOMO SAPIENS (HUMAN).//Q12929
F-PLACE1001395//HYPOTHETICAL 8.5 KD PROTEIN IN ASIA-MOTA INTERGENI
C REGION.//0.98:67:34//BACTERIOPHAGE T4.//P22917
F-PLACE1001399//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.1e-32:
47:74//HOMO SAPIENS (HUMAN).//P39194
F-PLACE1001412//GLYCOPHORIN C (PAS-2') (GLYCOPROTEIN BETA) (GLPC)
(GLYCOCONECTIN) (SIALOGLYCOPROTEIN D) (GLYCOPHORIN D) (GPD).//0.0
0021:125:36//HOMO SAPIENS (HUMAN).//P04921
F-PLACE1001414//CHYMOTRYPSIN/ELASTASE ISOINHIBITORS 2 TO 5.//0.99:
37:35//ASCARIS SUUM (PIG ROUNDWORM) (ASCARIS LUMBRICOIDES).//P0785
2
F-PLACE1001440//PROLINE-RICH PEPTIDE P-B.//0.35:16:50//HOMO SAPIEN
S (HUMAN).//P02814
F-PLACE1001456//RELAXIN.//0.48:38:36//BALAENOPTERA ACUTOROSTRATA
(MINKE WHALE) (LESSER RORQUAL).//P11184
F-PLACE1001468//HYPOTHETICAL PROTEIN MJ0602.//0.10:86:32//METHANOC
COCCUS JANNASCHII.//Q58019
F-PLACE1001484//HYPOTHETICAL 7.5 KD PROTEIN IN DNAC-RPL1 INTERGENI
C REGION.//1.0:47:34//BACILLUS SUBTILIS.//P37480
F-PLACE1001502//COLLAGEN 1(X) CHAIN PRECURSOR.//0.00029:118:34//BO
S TAURUS (BOVINE).//P23206
F-PLACE1001503//HYPOTHETICAL 77.3 KD PROTEIN T05G5.8 IN CHROMOSOME
III.//2.2e-07:107:30//CAENORHABDITIS ELEGANS.//P34561
F-PLACE1001517//SMALL PROTEIN INHIBITOR OF INSECT ALPHA-AMYLASES 2
(SI ALPHA-2).//0.56:22:45//SORGHUM BICOLOR MILO (SORGHUM).//P2192
4
F-PLACE1001534//PUTATIVE GENE PROTEIN 54.//0.43:44:40//BACTERIOPHA
GE SP01.//Q48408
F-PLACE1001545//HYPOTHETICAL 7.9 KD PROTEIN IN CELF-KATE INTERGENI
C REGION.//0.99:70:32//ESCHERICHIA COLI.//P37795
F-PLACE1001551//CHLOROPLAST 50S RIBOSOMAL PROTEIN L32.//1.0:66:28/
MARCHANTIA POLYMORPHA (LIVERWORT).//P12196
F-PLACE1001570//SYNAPTONEMAL COMPLEX PROTEIN 1 (SCP-1 PROTEIN).//
0.024:120:27//HOMO SAPIENS (HUMAN).//Q15431
F-PLACE1001602//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.1e-30:90:78//M
US MUSCULUS (MOUSE).//Q60809

【0680】

【表382】

F-PLACE1001603//ACIDIC PROLINE-RICH PROTEIN PRECURSOR (CLONE PRP25) (FRAGMENT).//0.054:77:33//RATTUS NORVEGICUS (RAT).//P10164	E 111.//4.0e-11:174:28//CAENORHABDITIS ELEGANS.//Q09564
F-PLACE1001608	F-PLACE1002090//SIGNAL RECOGNITION PARTICLE 72 KD PROTEIN (SRP72).//2.8e-57:112:99//HOMO SAPIENS (HUMAN).//076094
F-PLACE1001610//PROBABLE E4 PROTEIN.//0.90:58:29//HUMAN PAPILLOMAVIRUS TYPE 28.//P51896	F-PLACE1002115//P8 NTPC-1 PROTEIN (MATURE T-CELL PROLIFERATION-1 TYPE A) (NTPC-1 TYPE A) (P8NTPC1).//1.0:49:30//MUS MUSCULUS (MOUSE).//Q61908
F-PLACE1001611//METALLOTHIONEIN-IG (MT-IG).//0.35:30:40//HOMO SAPIENS (HUMAN).//P13640	F-PLACE1002119//T-LYMPHOCYTE ACTIVATED PROTEIN (CYCLOHEXIMIDE-INDUCED) (CHX1) (IMMEDIATE EARLY RESPONSE 2 PROTEIN).//2.7e-11:118:36//MUS MUSCULUS (MOUSE).//P17950
F-PLACE1001632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.6e-28:144:43//HOMO SAPIENS (HUMAN).//P51523	F-PLACE1002140//HYPOTHETICAL 12.3 KD PROTEIN IN MOBL 3' REGION (ORF 4).//0.0086:39:46//THIOBACILLUS FERROOXIDANS.//P20088
F-PLACE1001634//PHOTOSYSTEM II REACTION CENTRE N PROTEIN.//1.0:36:41//CYANIDIUM CALDARIUM (GALDIERIA SULPHURARIA).//019926	F-PLACE1002150
F-PLACE1001640//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN).//0.24:47:38//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (NDK ISOLATE) (HIV-1).//P18804	F-PLACE1002157//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//2.4e-34:56:82//HOMO SAPIENS (HUMAN).//P39189
F-PLACE1001672//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.0:27:66//HOMO SAPIENS (HUMAN).//P39188	F-PLACE1002163//NEUROTOXIN 1.//1.0:17:52//CENTRUROIDES SCULPTURATUS (BARK SCORPION).//P01492
F-PLACE1001691//HYPOTHETICAL 15.5 KD PROTEIN IN PIK1-POL2 INTERGENIC REGION.//0.40:81:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53842	F-PLACE1002170
F-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//8.3e-41:103:55//RATTUS NORVEGICUS (RAT).//P08635	F-PLACE1002171//TRANSCRIPTION REGULATORY PROTEIN SWI3 (SWI/SNF COMPLEX COMPONENT SWI3) (TRANSCRIPTION FACTOR TFE2).//0.00023:179:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32591
F-PLACE1001705	F-PLACE1002205//HYPOTHETICAL 13.5 KD PROTEIN IN MOBI1-SGA1 INTERGENIC REGION.//0.77:21:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40490
F-PLACE1001716//HYPOTHETICAL 138.5 KD PROTEIN C17H9.01 IN CHROMOSOME 1.//6.1e-07:157:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//013798	F-PLACE1002213//HISTONE H4 (FRAGMENT).//0.62:31:32//BLEPHARISMA JAPONICUM.//P80738
F-PLACE1001720	F-PLACE1002227//HYPOTHETICAL 7.9 KD PROTEIN IN FIXN 5' REGION.//0.41:49:36//RHIZOBIUM LEGUMINOSARUM.//P14310
F-PLACE1001729//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//6.5e-05:196:32//MUS MUSCULUS (MOUSE).//P05143	F-PLACE1002256//CYTOCHROME B (EC 1.10.2.2).//0.61:95:29//CAENORHABDITIS ELEGANS.//P24890
F-PLACE1001739//NEUROFILAMENT TRIPLET N PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//0.00050:213:23//RATTUS NORVEGICUS (RAT).//P12839	F-PLACE1002259//HYPOTHETICAL 9.2 KD PROTEIN IN SPS1-QCR7 INTERGENIC REGION.//0.99:22:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P56508
F-PLACE1001740//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//2.4e-17:90:56//HOMO SAPIENS (HUMAN).//P39188	F-PLACE1002319//HYPOTHETICAL 56.6 KD PROTEIN IN URE2-SSU72 INTERGENIC REGION.//0.91:18:72//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53867
F-PLACE1001745//HYPOTHETICAL PROTEIN KIAA0125.//0.96:38:36//HOMO SAPIENS (HUMAN).//Q14138	F-PLACE1002342//HYPOTHETICAL PROTEIN C16.//1.0:53:32//SWINEPOX VIRUS (STRAIN KASZA) (SPV).//P32219
F-PLACE1001746//CONGLUTIN DELTA-2 SMALL CHAIN.//0.98:23:43//LUPINUS ANGLUSTIFOLIUS (NARROW-LEAVED BLUE LUPINE).//P09930	F-PLACE1002395//CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).//6.4e-05:127:37//PLASMODIUM VIVAX.//P08677
F-PLACE1001748//HYPOTHETICAL 99.0 KD PROTEIN SPBC119.17.//2.9e-28:167:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//042908	F-PLACE1002399
F-PLACE1001756//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//9.2e-43:126:77//HOMO SAPIENS (HUMAN).//P39189	F-PLACE1002433//DYNACTIN, 150 KD ISOFORM (150 KD DYNEIN-ASSOCIATED POLYPEPTIDE) (DP-150) (DAP-150) (P150-GLUED).//0.00094:182:25//RATTUS NORVEGICUS (RAT).//P28023
F-PLACE1001761//50S RIBOSOMAL PROTEIN L35.//0.26:42:38//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//P56057	F-PLACE1002437//ATP-BINDING CASSETTE TRANSPORTER 1.//4.5e-19:62:77//MUS MUSCULUS (MOUSE).//P41233
F-PLACE1001771//TRANSIENT-RECEPTOR-POTENTIAL LIKE PROTEIN.//4.8e-35:223:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48994	F-PLACE1002438//HYPOTHETICAL 141.5 KD ZINC FINGER PROTEIN IN TUB1-CPR3 INTERGENIC REGION.//0.014:63:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04545
F-PLACE1001781//HYPOTHETICAL 71.1 KD PROTEIN IN DSK2-CAT8 INTERGENIC REGION.//9.5e-41:194:46//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q03262	F-PLACE1002450//OOCYTE ZINC FINGER PROTEIN XLCOF6 (FRAGMENT).//3.9e-28:159:38//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18749
F-PLACE1001799	F-PLACE1002465//LARIAT DEBRANCHING ENZYME (EC 3.1.-.-).//0.0014:148:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//013765
F-PLACE1001810	F-PLACE1002474//FIBRILLIN 2 PRECURSOR.//2.1e-24:203:33//MUS MUSCULUS (MOUSE).//Q61555
F-PLACE1001817//SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BET A).//2.8e-40:115:61//NEOCALLIMASTIX FRONTALIS (RUMEN FUNGUS).//P53587	F-PLACE1002477//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!//0.15:65:41//HOMO SAPIENS (HUMAN).//P39193
F-PLACE1001821	F-PLACE1002493//SEMEGELIN II PRECURSOR (SGII).//1.0:72:31//MACACA MULATTA (RHESUS MACAQUE).//Q95196
F-PLACE1001844//IG KAPPA CHAIN V-1 REGION (HAU).//0.59:89:35//HOMO SAPIENS (HUMAN).//P01600	F-PLACE1002499//HYPOTHETICAL 39.3 KD PROTEIN C02B8.6 IN CHROMOSOME X.//2.9e-11:67:35//CAENORHABDITIS ELEGANS.//Q11096
F-PLACE1001845	F-PLACE1002500//COBALT-ZINC-CADMIUM RESISTANCE PROTEIN CZCD (CATION EFFLUX SYSTEM PROTEIN CZCD).//8.4e-11:143:32//ALCALIGENES EUTROPUS.//P13512
F-PLACE1001869//MPA43 PROTEIN.//3.5e-14:153:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53583	F-PLACE1002514//HYPOTHETICAL 8.1 KD PROTEIN IN SPEA-METK INTERGENIC REGION (Q71).//1.0:15:60//ESCHERICHIA COLI.//P46878
F-PLACE1001897//LIGATOXIN A.//1.0:43:27//PHORADENDRON LIGAE (ARGENTINE MISTLETOE).//P01540	F-PLACE1002529
F-PLACE1001912//LONG NEUROTOXIN 2 (TOXIN C).//0.57:44:45//ASTROTIA STOKESI (STOKES'S SEA SNAKE) (DISTERIA STOKESI).//P01381	F-PLACE1002532//HOMEDBOX PROTEIN DLX-5.//1.1e-76:183:81//MUS MUSCULUS (MOUSE).//P70396
F-PLACE1001920//LATE GENES ACTIVATOR (EARLY PROTEIN GP4) (GPF).//0.89:75:29//BACTERIOPHAGE NF.//P09877	F-PLACE1002537//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//2.6e-18:51:86//HOMO SAPIENS (HUMAN).//P39195
F-PLACE1001928	F-PLACE1002571//ACTIN-LIKE PROTEIN I3E.//6.0e-56:140:47//DROSOPHILA MELANOGASTER (FRUIT FLY).//P45890
F-PLACE1001983//IMMEDIATE-EARLY PROTEIN IE180.//0.0049:51:45//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479	F-PLACE1002578
F-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//8.9e-08:125:36//MOXAELLA CATARRHALIS.//Q49091	F-PLACE1002583
F-PLACE1002004	F-PLACE1002591//CORONIN-LIKE PROTEIN P57.//5.5e-26:78:69//BOS TAURUS (BOVINE).//Q92176
F-PLACE1002046//LIGATIN (FRAGMENT).//1.6e-84:191:84//MUS MUSCULUS (MOUSE).//Q61211	F-PLACE1002598
F-PLACE1002052	F-PLACE1002604
F-PLACE1002066	F-PLACE1002625//HYPOTHETICAL 180.2 KD PROTEIN IN FAA4-HOR7 INTERGENIC REGION.//6.4e-08:193:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST)
F-PLACE1002072//AMTER-SPECIFIC PROLINE-RICH PROTEIN APC PRECURSOR.//0.16:77:31//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P40602	
F-PLACE1002073//HYPOTHETICAL 118.2 KD PROTEIN F43C1.1 IN CHROMOSOM	

【0681】

【表383】

ST).//Q04781
 F-PLACE1002655//ADSEVERIN (GELSOLIN-LIKE PROTEIN).//7.1e-100:210:8
 9//MUS MUSCULUS (MOUSE).//Q06004
 F-PLACE1002665//MOBILIZATION PROTEIN MOBS.//0.35:60:30//THIOBACILL
 US FERROXIDANS.//P20086
 F-PLACE1002685//ACTIN BINDING PROTEIN.//0.052:115:29//SACCHAROMYCE
 S EXIGUUS (YEAST).//P38479
 F-PLACE1002714//CIS-GOLGI MATRIX PROTEIN GM130.//1.8e-06:214:30//R
 ATTUS NORVEGICUS (RAT).//Q62839
 F-PLACE1002722//THROMBIN RECEPTOR PRECURSOR.//2.0e-19:134:38//XENO
 PUS LAEVIS (AFRICAN CLAWED FROG).//P47749
 F-PLACE1002768//FOLLICLE STIMULATING HORMONE RECEPTOR PRECURSOR (F
 SH-R) (FOLLITROPIN RECEPTOR) (FRAGMENT).//0.43:40:35//MUS MUSCULUS
 (MOUSE).//P35378
 F-PLACE1002772
 F-PLACE1002775//CENTROMERE/MICROTUBULE BINDING PROTEIN CBF5 (CENTR
 OMERE-BINDING FACTOR 5) (NUCLEOLAR PROTEIN CBF5).//4.8e-07:96:29//
 SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//014007
 F-PLACE1002782//COBALT-ZINC-CADMIUM RESISTANCE PROTEIN CZCD (CATIO
 N EFFLUX SYSTEM PROTEIN CZCD).//1.1e-07:114:35//ALCALIGENES EUTROP
 HUS.//P13512
 F-PLACE1002794//CUTICLE COLLAGEN 12 PRECURSOR.//0.0068:98:39//CAEN
 ORHABDITIS ELEGANS.//P20630
 F-PLACE1002811//CYCLIN-DEPENDENT KINASE 6 INHIBITOR (P18-INK6) (CY
 CLIN-DEPENDENT KINASE 4 INHIBITOR C) (P18-INK4C).//1.1e-09:137:34//
 MUS MUSCULUS (MOUSE).//Q60772
 F-PLACE1002815//C-HORDEIN (CLONE PC HORI-3) (FRAGMENT).//0.46:35:4
 2//HORDEUM VULGARE (BARLEY).//P17991
 F-PLACE1002816//HYPOTHETICAL PROTEIN KIAA0288 (HA6116).//1.0e-86:2
 01:74//HOMO SAPIENS (HUMAN).//P56524
 F-PLACE1002834//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).
 //1.6e-30:54:96//HOMO SAPIENS (HUMAN).//P51522
 F-PLACE1002839//METALLOTHIONEIN-I (MT-I).//1.0:43:37//MUS MUSCULUS
 (MOUSE).//P02802
 F-PLACE1002851//BOHMAN-BIRK TYPE PROTEINASE INHIBITOR (VAI).//0.7
 7:35:37//VICIA ANGLUSTIFOLIA (COMMON VETCH).//P01065
 F-PLACE1002853//HYPOTHETICAL 7.9 KD PROTEIN IN PE 5' REGION (ORF1).
 //1.0:18:55//LYMAETRIA DISPAR MULTICAPSID NUCLEAR POLYHEDROSIS VIR
 US (LONPV).//P36866
 F-PLACE1002881//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.1e-27:9
 1:70//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE1002908//HYPOTHETICAL 33.8 KD PROTEIN R10E11.4 IN CHROMOSOM
 E 111.//2.0e-31:148:46//CAENORHABDITIS ELEGANS.//P34548
 F-PLACE1002941//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.6e-11:
 40:85//HOMO SAPIENS (HUMAN).//P39195
 F-PLACE1002962//ENDOTHELIN-1 PRECURSOR (ET-1) (FRAGMENT).//0.90:3
 8:36//CANIS FAMILIARIS (DOG).//P13206
 F-PLACE1002968//TOXIN IV-5 PRECURSOR (TITYUSTOXIN) (FRAGMENT).//0.
 97:26:38//TITYUS SERRULATUS (BRAZILIAN SCORPION).//P01496
 F-PLACE1002991//PUTATIVE AMIDASE (EC 3.5.1.4).//3.3e-20:120:41//ME
 THANOCCOCCUS JANNASCHII.//Q85860
 F-PLACE1002993//HYPOTHETICAL 17.8 KD PROTEIN IN SMPA-SMPB INTERGEN
 IC REGION (F158).//0.00045:93:23//ESCHERICHIA COLI.//P52121
 F-PLACE1002996//PUTATIVE REGULATORY PROTEIN TSC-22 (TGFB STIMULATE
 D CLONE 22 HOMOLOG).//0.17:91:29//GALLUS GALLUS (CHICKEN).//Q91012
 F-PLACE1003025//SUPPRESSOR PROTEIN SRP40.//0.0079:214:24//SACCHARO
 MYCES CEREVISIAE (BAKER'S YEAST).//P32583
 F-PLACE1003027//HYPOTHETICAL 128.6 KD PROTEIN ZX1098.10 IN CHROMO
 SOME 111.//1.3e-49:167:63//CAENORHABDITIS ELEGANS.//P34609
 F-PLACE1003044//SPORE COAT PROTEIN D.//0.97:24:45//BACILLUS SUBTIL
 IS.//P07791
 F-PLACE1003045
 F-PLACE1003092
 F-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//3.9e-51:188:57//HOMO S
 APIENS (HUMAN).//Q13268
 F-PLACE1003108
 F-PLACE1003136
 F-PLACE1003145//BUTYROPHILIN PRECURSOR (BT).//0.00024:170:24//BOS
 TAURUS (BOVINE).//P18892
 F-PLACE1003153//HUNCHBACK PROTEIN (FRAGMENT).//1.0:32:37//LOCUSTA
 MIGRATORIA (MIGRATORY LOCUST).//Q01777
 F-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.1
 9) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (P442).
 //6.3e-05:54:38//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P42743
 F-PLACE1003176//HYPOTHETICAL 62.3 KD PROTEIN IN PCS60-ABD1 INTERGE
 NIC REGION.//0.24:74:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 //P38319
 F-PLACE1003190//SOF1 PROTEIN.//1.0e-52:158:41//SACCHAROMYCES CEREV
 ISIAE (BAKER'S YEAST).//P33750
 F-PLACE1003200
 F-PLACE1003205//SPERM PROTAMINE P1.//0.074:20:45//CAENOLESTES FULI
 GINOSIUS.//P42131
 F-PLACE1003238//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//0.0
 13:20:55//HOMO SAPIENS (HUMAN).//Q15391
 F-PLACE1003249//HYPOTHETICAL PROTEIN KIAA0125.//0.98:48:37//HOMO S
 APIENS (HUMAN).//Q14138
 F-PLACE1003256//OMEGA-CONOTOXINS GVIA, GVIB AND GVIC PRECURSOR (SH
 AKER PEPTIDE).//0.84:53:30//CONUS GEOGRAPHUS (GEOGRAPHY CONE).//P0
 1522
 F-PLACE1003258//EARLY EMBRYOGENESIS ZYG-11 PROTEIN.//4.1e-18:70:47
 //CAENORHABDITIS ELEGANS.//P21541
 F-PLACE1003296//SPECTRIN BETA CHAIN, ERYTHROCYTE.//0.063:160:24//H
 OMO SAPIENS (HUMAN).//P11277
 F-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).
 //9.4e-69:84:94//HOMO SAPIENS (HUMAN).//P51522
 F-PLACE1003334//NUCLEOBINDIN PRECURSOR (NUCB1) (BONE 63 KD CALCIU
 M-BINDING PROTEIN).//0.029:125:24//RATTUS NORVEGICUS (RAT).//Q6308
 3
 F-PLACE1003342//MALE SPECIFIC SPERM PROTEIN MST84DB.//0.97:44:40//
 DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643
 F-PLACE1003343//GENE 11 PROTEIN.//1.0:37:37//SPIROPLASMA VIRUS SPV
 1-RBA2 B.//P15902
 F-PLACE1003353//SH2/SH3 ADAPTOR CRK (ADAPTER MOLECULE CRK) (CRK2).
 //6.4e-05:69:40//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P87378
 F-PLACE1003361//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.6e-23:
 66:75//HOMO SAPIENS (HUMAN).//P39192
 F-PLACE1003366//SMALL PROLINE-RICH PROTEIN 2-1.//0.62:19:57//HOMO
 SAPIENS (HUMAN).//P35326
 F-PLACE1003369//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//4.3e-0
 6:102:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
 F-PLACE1003373//PROTEIN Q300.//0.042:29:37//MUS MUSCULUS (MOUSE)./
 //Q02722
 F-PLACE1003375//OLFACTORY RECEPTOR 11 (OR11) (FRAGMENT).//0.99:46:3
 4//MUS MUSCULUS (MOUSE).//Q60890
 F-PLACE1003383
 F-PLACE1003394//RAS-RELATED PROTEIN RAB-14.//2.8e-80:166:89//RATTU
 S NORVEGICUS (RAT).//P35287
 F-PLACE1003401
 F-PLACE1003420//PUTATIVE MITOCHONDRIAL CARRIER Y1L006W.//8.1e-17:
 38:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40556
 F-PLACE1003454
 F-PLACE1003478
 F-PLACE1003493//ENDOTHELIAL CELL MULTIMERIN PRECURSOR.//3.4e-11:12
 3:32//HOMO SAPIENS (HUMAN).//Q13201
 F-PLACE1003516//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.0e-32:68
 :76//HOMO SAPIENS (HUMAN).//P08547
 F-PLACE1003519//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//9.2e-17:7
 7:50//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE1003521//HYPOTHETICAL BAMHI-ORF9 PROTEIN.//1.0:38:42//FOWL P
 OX VIRUS (ISOLATE HP-438[MUNICH]).//P14366
 F-PLACE1003528//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.96:
 32:40//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P03931
 F-PLACE1003537//CEF PROTEIN.//0.92:47:29//BACTERIOPHAGE T4.//Q0143
 6
 F-PLACE1003553
 F-PLACE1003566//HYPOTHETICAL BAMHI-ORF9 PROTEIN.//1.0:32:34//FOWL P
 OX VIRUS (ISOLATE HP-438[MUNICH]).//P14366
 F-PLACE1003575
 F-PLACE1003583//PROBABLE E5 PROTEIN.//0.16:64:31//HUMAN PAPILLOMAV
 IRUS TYPE 35.//P27226
 F-PLACE1003584
 F-PLACE1003592//EXCISIONASE.//0.26:19:52//BACTERIOPHAGE PH1-80.//P
 05998
 F-PLACE1003593//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:4
 2:30//OVIS ARIES (SHEEP).//Q078751
 F-PLACE1003596//OLIGOSACCHARYL TRANSFERASE STT3 SUBUNIT HOMOLOG.//
 6.3e-87:238:67//CAENORHABDITIS ELEGANS.//P46975
 F-PLACE1003602//HYPOTHETICAL 11.0 KD PROTEIN IN FAA3-MAS3 INTERGEN
 IC REGION.//8.4e-17:98:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
 T).//P40554
 F-PLACE1003605//HAP5 TRANSCRIPTIONAL ACTIVATOR.//2.0e-09:82:35//SA
 CCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q02516
 F-PLACE1003611//PANCREATIC SECRETORY TRYPSIN INHIBITOR.//0.99:32:4
 3//CANIS FAMILIARIS (DOG).//P04542
 F-PLACE1003618//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.7e-65:22
 9:58//HOMO SAPIENS (HUMAN).//P08547
 F-PLACE1003625//30S RIBOSOMAL PROTEIN S20 (FRAGMENT).//1.0:56:26//
 PROTEUS MIRABILIS.//P42275
 F-PLACE1003638//PROTEIN Q300.//0.079:41:39//MUS MUSCULUS (MOUSE)./
 //Q02722

【0682】

【表384】

F-PLACE1003669//TRICHOHYALIN.//2.9e-07:180:30//OVIS ARIES (SHEEP).
//P22793
F-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA
SPLICING FACTOR SRP75).//3.3e-16:98:40//HOMO SAPIENS (HUMAN).//Q08
170
F-PLACE1003709//HYPOTHETICAL 59.5 KD PROTEIN IN CCT3-CCT8 INTERGEN
IC REGION.//2.8e-07:128:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS
T).//P47074
F-PLACE1003711//ALPHA/BETA-GLIADIN PRECURSOR (PROLAMIN) (CLASS A-1
V).//5.0e-05:88:30//TRITICUM AESTIVUM (WHEAT).//P04724
F-PLACE1003723//TYROSINE-PROTEIN KINASE SRM (EC 2.7.1.112) (PTK70
).//6.0e-06:98:36//MUS MUSCULUS (MOUSE).//Q62270
F-PLACE1003738//DOCTE ZINC FINGER PROTEIN XCOF6 (FRAGMENT).//2.5
e-45:147:46//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P18749
F-PLACE1003760//CYTOCHROME B (EC 1.10.2.2).//0.91:49:34//TRYPANOSO
MA BRUCEI BRUCEI.//P00164
F-PLACE1003762//METALLOTHIONEIN-LIKE PROTEIN TYPE 2.//0.98:28:32//
MALUS DOMESTICA (APPLE) (MALUS SYLVESTRIS).//Q24058
F-PLACE1003768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//8.5e-19:12
3:37//HOMO SAPIENS (HUMAN).//P08547
F-PLACE1003771
F-PLACE1003783//SRY-RELATED PROTEIN ADW2 (FRAGMENT).//1.0:29:37//A
LLIGATOR MISSISSIPPIENSIS (AMERICAN ALLIGATOR).//P40634
F-PLACE1003784//HYPOTHETICAL 98.1 KD PROTEIN IN SP19-CCR2 INTERGE
NIC REGION.//1.2e-13:199:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEA
ST).//P40164
F-PLACE1003795//EC PROTEIN 1/11 (ZINC-METALLOTHIONEIN CLASS 11).//
0.67:53:30//TRITICUM AESTIVUM (WHEAT).//P30569
F-PLACE1003833//METHIONYL-TRNA FORMYLTRANSFERASE (EC 2.1.2.9).//0.
99:158:28//THERMUS AQUATICUS (SUBSP. THERMOPHILUS).//P43523
F-PLACE1003850
F-PLACE1003858//HUNCHBACK PROTEIN (FRAGMENT).//0.37:28:42//LITHOBI
US FORFICATUS.//Q02030
F-PLACE1003864//OUTER MEMBRANE LIPOPROTEIN L0LB PRECURSOR.//0.004
6:116:31//ACTINOBACILLUS ACTINOMYCETEMCOMITANS (HAEMOPHILUS ACTINO
MYCETEMCOMITANS).//Q52727
F-PLACE1003870
F-PLACE1003885//POLY(A) POLYMERASE (EC 2.7.7.19) (PAP) (POLYNUCLEO
TIDE ADENYLYLTRANSFERASE) (FRAGMENT).//1.6e-92:166:75//HOMO SAPIEN
S (HUMAN).//P51003
F-PLACE1003886//IMMEDIATE-EARLY PROTEIN IE180.//0.54:96:34//PSEUDO
RABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675
F-PLACE1003888//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODI
ESTERASE DELTA 1 (EC 3.1.4.11) (PLC-DELTA-1) (PHOSPHOLIPASE C-DELTA
A-1) (PLC-111) (FRAGMENT).//8.8e-54:260:46//BOS TAURUS (BOVINE).//
P10895
F-PLACE1003892//PROBABLE E5 PROTEIN.//1.0:13:61//HUMAN PAPILLOMAVI
RUS TYPE 18.//P06792
F-PLACE1003900//BETA-FRUCTOFURANOSIDASE, SOLUBLE ISOENZYME 1 (EC
3.2.1.26) (SUCROSE-6- PHOSPHATE HYDROLASE) (INVERTASE) (FRAGMENTS
).//0.58:49:36//DAUCUS CAROTA (CARROT).//P80065
F-PLACE1003903//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (C
TP SYNTHETASE).//3.8e-52:92:85//HOMO SAPIENS (HUMAN).//P17812
F-PLACE1003915//PROBABLE ARGINYL-TRNA SYNTHETASE, CYTOPLASMIC (EC
6.1.1.19) (ARGININE--TRNA LIGASE) (ARGRS).//2.6e-26:202:36//SACCH
AROMYCES CEREVISIAE (BAKER'S YEAST).//Q05506
F-PLACE1003923//HISTIDYL-TRNA SYNTHETASE (EC 6.1.1.21) (HISTIDINE
--TRNA LIGASE) (HISRS).//0.94:65:29//STREPTOCOCCUS EQUISIMILIS.//P
30053
F-PLACE1003932//HYPOTHETICAL 17.3 KD PROTEIN IN SEC15-SAP4 INTERGE
NIC REGION.//0.098:79:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST
).//P53074
F-PLACE1003936
F-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT
(AMPK GAMMA-1 CHAIN).//4.7e-68:164:78//RATTUS NORVEGICUS (RAT).//P
80385
F-PLACE1004103//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/1.9e-14:
60:73//HOMO SAPIENS (HUMAN).//P39192
F-PLACE1004104//EXOCYST COMPLEX COMPONENT SECS.//0.020:202:20//SAC
CHAROMYCES CEREVISIAE (BAKER'S YEAST).//P89102
F-PLACE1004114//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/2.1e-15:6
9:60//HOMO SAPIENS (HUMAN).//P39188
F-PLACE1004118//REGULATORY PROTEIN E2.//0.73:58:36//CANINE ORAL PA
PILLOMAVIRUS (COPY).//Q89420
F-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4
(TRANSDUCIN BETA CHAIN 4).//7.7e-62:108:100//MUS MUSCULUS (MOUSE).
//P29387
F-PLACE1004149//PROBABLE NUCLEAR ANTIGEN.//0.0011:73:42//PSEUDORAB
IES VIRUS (STRAIN KAPLAN) (PRV).//P33485
F-PLACE1004155//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//0.0
0061:39:48//OWENIA FUSIFORMIS.//P21260
F-PLACE1004161//PLASMINOGEN-BINDING PROTEIN PAM PRECURSOR (FRAGMEN
T).//0.033:108:27//STREPTOCOCCUS PYOGENES.//P49054
F-PLACE1004183//HYPOTHETICAL 64.3 KD PROTEIN IN CDC12-ERPS INTERGE
NIC REGION.//4.0e-07:146:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEA
ST).//P38817
F-PLACE1004197//BUTYROPHILIN PRECURSOR (BT).//5.9e-11:208:27//MUS
MUSCULUS (MOUSE).//Q62556
F-PLACE1004203//PROTEIN A39.//8.5e-18:139:33//YACCINIA VIRUS (STRA
IN COPENHAGEN).//P21062
F-PLACE1004242//PHOTOSYSTEM II REACTION CENTRE J PROTEIN.//1.0:28:
42//PISUM SATIVUM (GARDEN PEA).//P13555
F-PLACE1004256//MYOSIN HEAVY CHAIN D (MHC D).//0.73:134:25//CAENOR
HABDITIS ELEGANS.//P02567
F-PLACE1004257//HYPOTHETICAL PROTEIN H10490.//0.13:75:29//HAEMOPHI
LUS INFLUENZAE.//P44006
F-PLACE1004258//COLLAGEN ALPHA 2(VI1) CHAIN (ENDOTHELIAL COLLAG
E) (FRAGMENT).//0.027:128:35//HOMO SAPIENS (HUMAN).//P25067
F-PLACE1004270//LARGE TEGUMENT PROTEIN.//1.8e-10:100:44//EPSTEIN-B
ARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03186
F-PLACE1004274//HYPOTHETICAL PROTEIN E-95.//0.44:61:42//HUMAN ADEN
OVIRUS TYPE 2.//P03286
F-PLACE1004277//COLLAGEN ALPHA 1(XI1) CHAIN (FRAGMENTS).//0.0013:5
5:38//BOS TAURUS (BOVINE).//P25508
F-PLACE1004284//T KD PROTEIN (ORF 4).//1.0:63:23//CHRYSANTHEMUM VI
RUS B (CVB).//P37990
F-PLACE1004289//SPERM PROTAMINE P3.//0.00057:22:77//MUS MUSCULUS
(MOUSE).//Q62100
F-PLACE1004302//SERINE/THREONINE PROTEIN KINASE AFSK (EC 2.7.1.-).
//0.0065:148:29//STREPTOMYCES COELICOLOR.//P54741
F-PLACE1004316//AUTOPHAGY PROTEIN APC5.//8.8e-06:117:29//SACCHAROM
YCES CEREVISIAE (BAKER'S YEAST).//Q12380
F-PLACE1004336//COLLAGEN ALPHA 4(IV) CHAIN PRECURSOR.//0.0027:83:3
6//HOMO SAPIENS (HUMAN).//P53420
F-PLACE1004358//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//2.9e-05:2
00:33//CALLUS CALLUS (CHICKEN).//P02457
F-PLACE1004376//AXONEME-ASSOCIATED PROTEIN NST101(2).//2.4e-05:17
9:29//DROSOPHILA HYDEI (FRUIT FLY).//Q08696
F-PLACE1004384//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.6e-28:
46:76//HOMO SAPIENS (HUMAN).//P39194
F-PLACE1004388//HYPOTHETICAL 75.2 KD PROTEIN IN ACS1-GCV3 INTERGEN
IC REGION.//5.7e-34:202:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEA
ST).//P39722
F-PLACE1004405//NEURAMINYLLACTOSE-BINDING HEMAGGLUTININ (N-ACETYL
EURAMINYLLACTOSE- BINDING FIBRILLAR HEMAGGLUTININ RECEPTOR-BINDING
SUBUNIT) (NLBG) (FLAGELLAR SHEATH ADHESIN) (ADHESIN A) (FRAGMENT
).//0.93:74:33//HELICOBACTER ACINONYX.//Q47947
F-PLACE1004425//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.81:70:
42//HOMO SAPIENS (HUMAN).//P39195
F-PLACE1004428//PRISTANDYL-COA OXIDASE (EC 1.3.3.-).//1.9e-31:203:
39//RATTUS NORVEGICUS (RAT).//Q63448
F-PLACE1004437//ISOCITRATE DEHYDROGENASE [NAD]. MITOCHONDRIAL SUBU
NIT BETA PRECURSOR (EC 1.1.1.41) (ISOCITRIC DEHYDROGENASE) (NAD+-S
PECIFIC ICDH) (FRAGMENT).//4.2e-93:140:100//MACACA FASCICULARIS (C
RAB EATING MACAQUE) (CYNOMOLGUS MONKEY).//Q28479
F-PLACE1004451//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00013:4
0:62//HOMO SAPIENS (HUMAN).//P39188
F-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0066:218:23//DROSOPHILA
MELANOGASTER (FRUIT FLY).//P25823
F-PLACE1004467//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/7.8e-10:
33:87//HOMO SAPIENS (HUMAN).//P39193
F-PLACE1004471//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).
//7.0e-56:92:58//HOMO SAPIENS (HUMAN).//P51522
F-PLACE1004473//HYPOTHETICAL 54.3 KD PROTEIN C23D3.03C IN CHROMOSO
ME 1.//0.019:136:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q
09844
F-PLACE1004491//LYSIS PROTEIN.//0.95:53:30//BACTERIOPHAGE FR.//P19
903
F-PLACE1004506//AUTOIMMUNOGENIC CANCER/TESTIS ANTIGEN NY-ESO-1 (LA
GE-1).//0.58:66:34//HOMO SAPIENS (HUMAN).//P78358
F-PLACE1004510//TRANSCRIPTION INITIATION FACTOR TFIID 150 KD SUBUN
IT (TAF11-150) (TAF1150).//3.0e-07:63:46//DROSOPHILA MELANOGASTER
(FRUIT FLY).//Q24325
F-PLACE1004516//HYPOTHETICAL PROTEIN 5' TO ASP-RICH AND HIS-RICH P
ROTEINS (FRAGMENT).//0.95:62:29//PLASMODIUM FALCIPARUM (ISOLATE FC
N17 / SENEGAL).//P14587
F-PLACE1004518//METALLOTHIONEIN 10-III (MT-10-III).//0.91:28:42//M
YTILUS EDULIS (BLUE MUSSEL).//P80248
F-PLACE1004548//DIHYDROPYRIDINE-SENSITIVE L-TYPE, SKELETAL MUSCLE
CALCIUM CHANNEL GAMMA SUBUNIT.//0.94:75:32//ORYCTOLAGUS CUNICULUS

【0683】

【表385】

(RABBIT).//P19518
 F-PLACE1004550//CUTICLE COLLAGEN 2.//0.90:155:31//CAENORHABDITIS ELEGANS.//P17656
 F-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//3.2e-70:121:100//BOS TAURUS (BOVINE).//Q10568
 F-PLACE1004629//PROTEIN OS-9 PRECURSOR.//1.7e-10:132:36//HOMO SAPIENS (HUMAN).//Q13438
 F-PLACE1004645//TRANSCRIPTION INITIATION FACTOR 118 HOMOLOG (TF118).//0.0036:100:30//PYROCOCCUS FURIOSUS.//Q51731
 F-PLACE1004646//PROBABLE UDP-GALACTOPYRANOSE MUTASE (EC 5.4.99.9).//0.91:58:29//KLEBSIELLA PNEUMONIAE.//Q48481
 F-PLACE1004658//GLUTAMATE [NMDA] RECEPTOR SUBUNIT EPSILON 4 PRECURSOR (N-METHYL-D-ASPARTATE RECEPTOR SUBTYPE 2D) (NR2D) (NMDAR2D).//0.031:134:32//MUS MUSCULUS (MOUSE).//Q03391
 F-PLACE1004664//HYPOTHETICAL 180.2 KD PROTEIN IN F4A4-HORT INTERGENIC REGION.//0.025:125:20//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q04781
 F-PLACE1004672//HYPOTHETICAL 36.7 KD PROTEIN C2F7.14C IN CHROMOSOME 1.//7.6e-52:158:56//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09704
 F-PLACE1004674//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//1.4e-88:144:93//MUS MUSCULUS (MOUSE).//P12815
 F-PLACE1004681//CCR4-ASSOCIATED FACTOR 1 (CAF1).//1.0e-34:70:100//MUS MUSCULUS (MOUSE).//Q60809
 F-PLACE1004686//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//3.4e-08:48:62//HOMO SAPIENS (HUMAN).//P39192
 F-PLACE1004691//METALLOTHIONEIN (MT).//0.064:24:45//ARIANTA ARBUSTORUM.//P55946
 F-PLACE1004693
 F-PLACE1004716//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:27:37//PAN PANISCUS (PYGMY CHIMPANZEE) (BONOB0).//Q35587
 F-PLACE1004722//HYPOTHETICAL 61.5 KD PROTEIN IN CLA4-WID1 INTERGENIC REGION.//0.95:53:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48565
 F-PLACE1004736//NEURONAL AXONAL MEMBRANE PROTEIN NAP-22.//0.014:163:30//RATTUS NORVEGICUS (RAT).//Q05175
 F-PLACE1004740//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//1.9e-09:37:70//HOMO SAPIENS (HUMAN).//P39194
 F-PLACE1004743//HYPOTHETICAL 12.6 KD PROTEIN IN ALGR3 3' REGION.//0.99:72:33//PSEUDOMONAS AERUGINOSA.//P21484
 F-PLACE1004751//CMP-N-ACETYLNEURAMINATE-BETA-GALACTOSAMIDE-ALPHA-2,3-SIALYLTRANSFERASE (EC 2.4.99.-) (BETA-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE) (ST3GAL11) (ALPHA 2,3-ST) (GAL-MAC6S) (ST2) (SIA T4-C) (SAT-3) (ST-4).//2.2e-08:90:38//HOMO SAPIENS (HUMAN).//Q11206
 F-PLACE1004773//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN).//3.2e-25:233:32//HOMO SAPIENS (HUMAN).//P16157
 F-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//8.1e-26:210:30//RATTUS NORVEGICUS (RAT).//P30337
 F-PLACE1004793//ENV POLYPROTEIN [CONTAINS: COAT PROTEIN GP52: COAT PROTEIN GP36].//0.0062:106:25//MOUSE MAMMARY TUMOR VIRUS (STRAIN BR6).//P10259
 F-PLACE1004804
 F-PLACE1004813//HYPOTHETICAL PROTEIN UL12.//1.0:22:40//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16777
 F-PLACE1004814//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME 11.//2.8e-06:136:25//CAENORHABDITIS ELEGANS.//Q09217
 F-PLACE1004815
 F-PLACE1004824//HYPOTHETICAL 106.7 KD PROTEIN IN MUP1-SPR3 INTERGENIC REGION.//2.3e-09:70:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53236
 F-PLACE1004827//HYPOTHETICAL 9.4 KD PROTEIN IN FLAL 3' REGION (ORF 3).//0.54:25:56//BACILLUS LICHENIFORMIS.//P22754
 F-PLACE1004836//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.0066:12:66//BOS TAURUS (BOVINE).//P20072
 F-PLACE1004838
 F-PLACE1004840
 F-PLACE1004868//MALE STERILITY PROTEIN 2.//4.0e-16:172:30//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q08891
 F-PLACE1004885
 F-PLACE1004900//MAST CELL DEGRANULATING PEPTIDE PRECURSOR (MCDP) (MCD) (PEPTIDE 401).//1.0:23:47//APIS MELLIFERA (HONEYBEE).//P01499
 F-PLACE1004902//PUTATIVE PRE-mRNA SPLICING FACTOR ATP-DEPENDENT RNASE HELICASE SPAC10F6.02C.//7.3e-15:94:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q42643
 F-PLACE1004913//HYPOTHETICAL 7.2 KD PROTEIN IN BC5A-DEGR INTERGENIC REGION.//1.0:42:33//BACILLUS SUBTILIS.//P54165
 F-PLACE1004918//HYPOTHETICAL 12.4 KD PROTEIN IN RPS218-MRS3 INTERG

ENIC REGION.//0.98:50:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47012
 F-PLACE1004930//HYPOTHETICAL PROTEIN MJ0562.//0.82:44:36//METHANOCOCUS JANNASCHII.//Q57982
 F-PLACE1004934
 F-PLACE1004937//HYPOTHETICAL 67.1 KD TRP-ASP REPEATS CONTAINING PROTEIN C57A10.05C IN CHROMOSOME 1.//9.0e-10:87:33//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P87053
 F-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//4.0e-14:184:25//CAENORHABDITIS ELEGANS.//Q11073
 F-PLACE1004972//BROMELAIN INHIBITOR 2 (BI-11) (BROMELAIN INHIBITOR VI) (BI-VI).//1.0:35:37//ANANAS COMOSUS (PINEAPPLE).//P27478
 F-PLACE1004979//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//5.3e-30:55:72//HOMO SAPIENS (HUMAN).//P39192
 F-PLACE1004982//M PROTEIN, SEROTYPE 12 PRECURSOR (FRAGMENT).//0.0049:124:27//STREPTOCOCCUS PYOGENES.//P19401
 F-PLACE1004985//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:26:34//LUMBRICUS TERRESTRIS (COMMON EARTHWORM).//Q34942
 F-PLACE1005026//TELOMERE-BINDING PROTEIN HOMOLOG.//0.011:179:27//EUPLOTES CRASSUS.//Q06183
 F-PLACE1005027
 F-PLACE1005046//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.082:44:36//BOS TAURUS (BOVINE).//P20072
 F-PLACE1005052//MALE SPECIFIC SPERM PROTEIN MST840D.//0.38:36:44//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01645
 F-PLACE1005055
 F-PLACE1005066//RING CANAL PROTEIN (KELCH PROTEIN).//2.9e-38:194:39//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
 F-PLACE1005077
 F-PLACE1005085//INSECT TOXIN I (BOT ITI).//0.85:36:33//BUTHUS OCCIDENTALIS TUNETANUS (COMMON EUROPEAN SCORPION).//P55902
 F-PLACE1005086//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//8.5e-38:93:76//HOMO SAPIENS (HUMAN).//P39194
 F-PLACE1005101//HYPOTHETICAL PROTEIN ZAP128 (FRAGMENT).//1.6e-11:35:100//HOMO SAPIENS (HUMAN).//P49753
 F-PLACE1005102//ZINC FINGER PROTEIN 151 (POLYOMAVIRUS LATE INITIATOR PROMOTER BINDING PROTEIN) (LP-1) (ZINC FINGER PROTEIN 213).//3.0e-14:110:38//MUS MUSCULUS (MOUSE).//Q60821
 F-PLACE1005108//METALLOTHIONEIN-III (MT-III) (GROWTH INHIBITORY FACTOR) (GIF).//0.41:35:34//BOS TAURUS (BOVINE).//P37359
 F-PLACE1005111//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L) (CHARGE RIM 11).//1.0:29:41//RATTUS NORVEGICUS (RAT).//P11608
 F-PLACE1005128//RABPHILIN-3A (FRAGMENT).//5.9e-05:95:36//MUS MUSCULUS (MOUSE).//P47708
 F-PLACE1005146//FIBROBLAST GROWTH FACTOR INDUCIBLE PROTEIN 15 (FIN 15).//0.17:48:35//MUS MUSCULUS (MOUSE).//Q61075
 F-PLACE1005162//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//1.0e-31:60:76//HOMO SAPIENS (HUMAN).//P39189
 F-PLACE1005176
 F-PLACE1005181//HYPOTHETICAL 7 KD PROTEIN.//1.0:31:45//MEASLES VIRUS (STRAIN HALLE) (SUBACUTE SCLEROSING PANENCEPHALITIS VIRUS).//P06831
 F-PLACE1005187//GLUCAN SYNTHASE-1 (EC 2.4.1.34) (1,3-BETA-GLUCAN SYNTHASE) (UDP-GLUCOSE-1,3-BETA-D-GLUCAN GLUCOSYLTRANSFERASE).//0.025:58:34//NEUROSPORA CRASSA.//P36678
 F-PLACE1005206//HYPOTHETICAL 10.7 KD PROTEIN.//0.34:57:42//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20511
 F-PLACE1005232//AMELOGENIN, Y ISOFORM PRECURSOR.//0.70:60:35//HOMO SAPIENS (HUMAN).//Q99218
 F-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//0.0017:114:27//PHYCOMYCES BLAKESLEENUS.//Q01577
 F-PLACE1005261//HYPOTHETICAL 90.8 KD PROTEIN TOSH10.7 IN CHROMOSOME 11.//1.2e-38:206:41//CAENORHABDITIS ELEGANS.//Q10003
 F-PLACE1005266
 F-PLACE1005277//PROTEIN GURKEN PRECURSOR.//0.58:95:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//P42287
 F-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.0e-12:211:29//GALLUS GALLUS (CHICKEN).//P53352
 F-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//1.8e-78:205:78//BOS TAURUS (BOVINE).//P08760
 F-PLACE1005308//WOUND-INDUCED BASIC PROTEIN.//0.99:40:40//PHASEOLUS VULGARIS (KIDNEY BEAN) (FRENCH BEAN).//Q09020
 F-PLACE1005313//HYPOTHETICAL 8.7 KD PROTEIN IN LEUX-FECE INTERGENIC REGION (O67).//0.15:38:41//ESCHERICHIA COLI.//P39355
 F-PLACE1005327//DNA-BINDING PS2/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//1.0:19:52//HOMO SAPIENS (HUMAN).//P30808
 F-PLACE1005331//BREAKPOINT CLUSTER REGION PROTEIN.//0.00021:98:35//HOMO SAPIENS (HUMAN).//P11274
 F-PLACE1005335//IROQUOIS-CLASS HOMEODOMAIN PROTEIN IRX-3.//0.37:98:33//MUS MUSCULUS (MOUSE).//P81067

【0684】

【表386】

F-PLACE1005373//PSEUDOURIDYLATE SYNTHASE 4 (EC 4.2.1.70) (PSEUDOURIDINE SYNTHASE 4) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PS155 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYTASE) //0.010:96:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P48567

F-PLACE1005374

F-PLACE1005409

F-PLACE1005453//LICHENASE PRECURSOR (EC 3.2.1.73) (ENDO-BETA-1,3-1,4 GLUCANASE) //1.0:50:32//NICOTIANA PLUMBAGINIFOLIA (LEADWORT-LEAVED TOBACCO) //P07979

F-PLACE1005467//KERATIN, FEATHER (F-KER) //0.0095:42:35//LARUS NOVAE-HOLLANDIAE (SILVER GULL) //P02451

F-PLACE1005471//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3) //0.23:49:32//PHYTOPHTHORA INFESTANS (POTATO LATE BLIGHT FUNGUS) //Q37598

F-PLACE1005477//HYPOTHETICAL PROTEIN ORF-1137 //9.6e-13:115:38//MUS MUSCULUS (MOUSE) //P11260

F-PLACE1005480//C-HORDEIN (CLONE PC MORI-3) (FRAGMENT) //0.97:33:30//HORDEUM VULGARE (BARLEY) //P17991

F-PLACE1005481//HUNCHBACK PROTEIN (FRAGMENT) //0.30:52:38//APIS MELIFERA (HONEYBEE) //P31504

F-PLACE1005494//TRANSIENT-RECEPTOR-POTENTIAL PROTEIN //3.9e-05:87:33//DROSOPHILA MELANOGASTER (FRUIT FLY) //P19334

F-PLACE1005502

F-PLACE1005526//IMMEDIATE-EARLY PROTEIN IE180 //4.6e-05:132:32//PSUDORABIES VIRUS (STRAIN KAPLAN) (PRV) //P33479

F-PLACE1005528//!!!! ALU SUBFAMILY SX WARNING ENTRY !!! //3.4e-09:31:74//HOMO SAPIENS (HUMAN) //P39195

F-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME E111 //9.7e-50:148:58//CAENORHABDITIS ELEGANS //Q09251

F-PLACE1005550//HYPOTHETICAL 40.2 KD PROTEIN K12H4.3 IN CHROMOSOME 111 //3.0e-21:127:37//CAENORHABDITIS ELEGANS //P34524

F-PLACE1005554//CYTOCHROME B (EC 1.10.2.2) (FRAGMENT) //0.84:38:31//DIPODOMYS CALIFORNICUS (KANGAROO RAT) //P16359

F-PLACE1005557//60S RIBOSOMAL PROTEIN L27 //4.8e-09:60:48//CRYPTOCOCUS NEOFORMANS (FILOBASIDIELLA NEOFORMANS) //P46288

F-PLACE1005574//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L) //0.89:44:29//BOS TAURUS (BOVINE) //P03929

F-PLACE1005584//MALE SPECIFIC SPERM PROTEIN MST87F //0.00030:33:48//DROSOPHILA MELANOGASTER (FRUIT FLY) //P08175

F-PLACE1005595//IMMEDIATE-EARLY PROTEIN IE180 //0.00048:162:30//PSUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV) //P11675

F-PLACE1005603//HIGH-MOBILITY-GROUP PROTEIN (NONHISTONE CHROMOSOMAL PROTEIN) //0.00034:83:30//TETRAHYMENA PYRIFORMIS //P40625

F-PLACE1005611//DNAJ PROTEIN //8.6e-20:108:48//CLOSTRIDIUM ACETOBI TYLICUM //P30725

F-PLACE1005623//EXTRACELLULAR SIGNAL-REGULATED KINASE 5 (EC 2.7.1.1) (ERK5) (ERK4) (BIRK1 KINASE) //0.80:116:31//HOMO SAPIENS (HUMAN) //Q13164

F-PLACE1005630//INTERLEUKIN-14 PRECURSOR (IL-14) (HIGH MOLECULAR WEIGHT B-CELL GROWTH FACTOR) (HBM-BCGF) //0.0024:74:39//HOMO SAPIENS (HUMAN) //P40222

F-PLACE1005639//EXTRACELLULAR MATRIX PROTEIN 1 (SECRETORY COMPONENT T85) (FRAGMENT) //0.72:18:61//RATTUS NORVEGICUS (RAT) //Q62894

F-PLACE1005646//RNA HELICASE-LIKE PROTEIN DB10 //4.8e-29:172:45//NICOTIANA SYLVESTRIS (WOOD TOBACCO) //P46942

F-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE) //3.7e-64:133:75//MESOCRITETUS AURATUS (GOLDEN HAMSTER) //Q60561

F-PLACE1005666//CHLOROPLAST 50S RIBOSOMAL PROTEIN L28 //0.57:36:41//PORPHYRA PURPUREA //P51224

F-PLACE1005698//HYPOTHETICAL PROTEIN IN SIGD 3' REGION (ORFC) (FRAGMENT) //0.50:61:29//BACILLUS SUBTILIS //P40405

F-PLACE1005727//ANTER-SPECIFIC PROLINE-RICH PROTEIN APC (PROTEIN C EX) (FRAGMENT) //0.46:27:51//BRASSICA NAPUS (RAPE) //P40603

F-PLACE1005730//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT) //0.95:21:52//ORYZOLAGUS CUNICULUS (RABBIT) //P02456

F-PLACE1005739//INTERFERON-GAMMA INDUCIBLE PROTEIN MG11 //3.4e-46:111:53//MUS MUSCULUS (MOUSE) //Q60710

F-PLACE1005755//HYPOTHETICAL 70.2 KD PROTEIN IN GSH1-CHS6 INTERGENIC REGION //2.6e-12:66:51//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P42951

F-PLACE1005763//3-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II) //1.5e-26:69:57//RATTUS NORVEGICUS (RAT) //P08635

F-PLACE1005799//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN) //0.028:96:32//HOMO SAPIENS (HUMAN) //P26371

F-PLACE1005802//PROTEIN PROSPERO //0.86:64:42//DROSOPHILA MELANOGASTER (FRUIT FLY) //P29617

F-PLACE1005803//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN M

YD116 //1.0:95:25//MUS MUSCULUS (MOUSE) //P17564

F-PLACE1005804//PROCESSING ALPHA-1,2-MANNOSIDASE (EC 3.2.1.-) (ALPHA-1,2-MANNOSIDASE 1B) //2.8e-73:198:73//MUS MUSCULUS (MOUSE) //P39098

F-PLACE1005813//HYPOTHETICAL 49.0 KD PROTEIN IN NSPI-KAR2 INTERGENIC REGION //0.022:78:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P47057

F-PLACE1005828//!!!! ALU SUBFAMILY SX WARNING ENTRY !!! //1.8e-23:56:76//HOMO SAPIENS (HUMAN) //P39195

F-PLACE1005834//LATE CONTROL GENE B PROTEIN (CPB) //0.97:33:39//BACTERIOPHAGE 186 //P08711

F-PLACE1005845

F-PLACE1005850//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!! //5.5e-28:96:73//HOMO SAPIENS (HUMAN) //P39194

F-PLACE1005851

F-PLACE1005876//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSP 100 KD SUBUNIT) //2.2e-99:155:95//BOS TAURUS (BOVINE) //Q10568

F-PLACE1005884

F-PLACE1005890//BEM46 PROTEIN (FRAGMENT) //1.8e-33:137:49//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //P54069

F-PLACE1005898//NADH-UBIQUINONE OXIDOREDUCTASE MLRQ SUBUNIT (EC 1.6.5.3) (EC 1.6.9.3) (COMPLEX I-MLRQ) (CI-MLRQ) //0.77:58:34//HOMO SAPIENS (HUMAN) //Q00483

F-PLACE1005921//AIG1 PROTEIN //1.4e-23:165:38//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS) //P54120

F-PLACE1005923//HYPOTHETICAL 22.4 KD PROTEIN (ORF16) //0.90:118:28//PARAMECIUM TETRAURELIA //P15617

F-PLACE1005925//HYPOTHETICAL GENE 30 PROTEIN //0.94:57:29//HERPESVIRUS SAIMIRI (STRAIN 11) //Q01010

F-PLACE1005932//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) //0.42:128:32//NICOTIANA TABACUM (COMMON TOBACCO) //P13983

F-PLACE1005934//DNA-DIRECTED RNA POLYMERASE II LARGEST SUBUNIT (EC 2.7.7.6) (RPB1) (FRAGMENT) //0.40:76:35//CRICETULUS GRISEUS (CHINESE HAMSTER) //P11414

F-PLACE1005936//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) //0.50:15:66//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (CLONE 12) (HIV-1) //P04326

F-PLACE1005951//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) //0.0025:135:32//NICOTIANA TABACUM (COMMON TOBACCO) //P13983

F-PLACE1005953//HIGH POTENTIAL IRON-SULFUR PROTEIN (HIP1P) //0.64:57:33//RHODOSPIRILLUM RUBRUM //P08882

F-PLACE1005955//HYPOTHETICAL 54.2 KD PROTEIN IN ERPS-ORC6 INTERGENIC REGION //1.0e-32:110:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P38821

F-PLACE1005966//TACHYPLESLIN II PRECURSOR //0.97:31:35//TACHYPLEUS TENDENTATUS (JAPANESE HORSESHOE CRAB) //P14214

F-PLACE1005968//GATA FACTOR SREP //0.17:52:40//PENICILLIUM CHRYSOGENUM //Q92259

F-PLACE1005990//CELL PATTERN FORMATION-ASSOCIATED PROTEIN //0.36:5:36//EMERICELLA NIDULANS (ASPERGILLUS NIDULANS) //P36011

F-PLACE1006002//!!!! ALU SUBFAMILY SC WARNING ENTRY !!! //1.5e-36:102:75//HOMO SAPIENS (HUMAN) //P39192

F-PLACE1006003//HYPOTHETICAL 6.8 KD PROTEIN IN COX3-NAD1 INTERGENIC REGION (ORF 61) //1.0:22:40//MARCHANTIA POLYMORPHA (LIVERWORT) //P38473

F-PLACE1006011//POLY [ADP-RIBOSE] POLYMERASE (EC 2.4.2.30) (PARP) (ADPRT) (NAD+) ADP-RIBOSYLTRANSFERASE (POLY[ADP-RIBOSE] SYNTHETASE) //2.8e-21:163:36//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS) //Q11207

F-PLACE1006017//!!!! ALU SUBFAMILY SC WARNING ENTRY !!! //1.1e-10:43:67//HOMO SAPIENS (HUMAN) //P39192

F-PLACE1006037//VITELLOGENIN I PRECURSOR (VTG I) [CONTAINS: LIPOVITELLIN 1 (LV1), PHOSVITIN (PV), LIPOVITELLIN 2 (LV2)] //0.00019:12:3:37//FUNDULUS HETEROCLOTUS (KILLIFISH) (MUMMICHOG) //Q90508

F-PLACE1006040//CAMP-REGULATED PHOSPHOPROTEIN 19 (ARPP-19) //3.2e-40:110:76//HOMO SAPIENS (HUMAN) //P56211

F-PLACE1006076//BOWMAN-BIRK TYPE PROTEINASE INHIBITOR A-II //0.99:30:40//ARACHIS HYPOGAEA (PEANUT) //P01066

F-PLACE1006119//IMPORTIN BETA-3 SUBUNIT (KARYOPHERIN BETA-3 SUBUNIT) (RAN-BINDING PROTEIN 5) //8.8e-94:218:76//HOMO SAPIENS (HUMAN) //Q00410

F-PLACE1006129//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR //0.0009:2:228:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P32323

F-PLACE1006139//HYPOTHETICAL 52.9 KD PROTEIN IN SAPI55-YMR31 INTERGENIC REGION //5.9e-55:128:50//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P43616

F-PLACE1006143//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!! //1.4e-25:

【0685】

【表387】

107:63//HOMO SAPIENS (HUMAN).//P39194
 F-PLACE1006157//E-SELECTIN PRECURSOR (ENDOTHELIAL LEUKOCYTE ADHESION MOLECULE 1) (ELAM-1) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION MOLECULE 2) (LECAM2) (CD62E).//1.3e-21:168:32//SUS SCROFA (PIG).//P98110
 F-PLACE1006159//COLD SHOCK INDUCED PROTEIN TIRI PRECURSOR (SERINE-RICH PROTEIN 1).//0.46:98:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P10863
 F-PLACE1006164//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.3).//0.70:28:42//ARTEMIA SALINA (BRINE SHRIMP).//P19049
 F-PLACE1006167//GLUCOAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//8.9e-05:167:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640
 F-PLACE1006170//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HAZ/AP2 ADAPTIN ALPHA C SUBUNIT).//1.1e-67:157:88//MUS MUSCULUS (MOUSE).//P17427
 F-PLACE1006187//G1/S-SPECIFIC CYCLIN E.//5.6e-75:224:62//HOMO SAPIENS (HUMAN).//P24864
 F-PLACE1006195//T-RELATED PROTEIN (TRP) (BRACHYENTERON PROTEIN).//0.99:177:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//P55965
 F-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//2.0e-33:183:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09747
 F-PLACE1006205
 F-PLACE1006223//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.00015:22:50//MUS MUSCULUS (MOUSE).//P15265
 F-PLACE1006225//VIRION INFECTIVITY FACTOR (SOR PROTEIN).//1.0:63:34//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (MDK ISOLATE) (HIV-1).//P18805
 F-PLACE1006236
 F-PLACE1006239//60S ACIDIC RIBOSOMAL PROTEIN P2 (FRAGMENT).//0.48:23:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P51407
 F-PLACE1006246//CMP-SIALIC ACID TRANSPORTER (CMP-SIA-TR).//0.012:84:30//MUS MUSCULUS (MOUSE).//Q61420
 F-PLACE1006248//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140).//0.017:203:22//RATTUS NORVEGICUS (RAT).//P41777
 F-PLACE1006267//L-FRUCTULOSE PHOSPHATE ALDOLASE (EC 4.1.2.17).//0.84:25:52//HAEMOPHILUS INFLUENZAE.//P44777
 F-PLACE1006288
 F-PLACE1006318//CYSTEINE-RICH ANTIFUNGAL PROTEIN 1 (AFP1) (M1).//1.0:29:48//SINAPIS ALBA (WHITE MUSTARD) (BRASSICA HIRTA).//P30231
 F-PLACE1006325//CYCLIN-DEPENDENT KINASE INHIBITOR 1C (CYCLIN-DEPENDENT KINASE INHIBITOR P57) (P57KIP2).//0.99:97:32//HOMO SAPIENS (HUMAN).//P49918
 F-PLACE1006335//PROLINE-RICH PEPTIDE P-8.//0.56:19:52//HOMO SAPIENS (HUMAN).//P02814
 F-PLACE1006357
 F-PLACE1006360
 F-PLACE1006368//RUF1 PROTEIN (SPINDLE POLY BODY SPACER PROTEIN SPC110).//0.0057:122:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32380
 F-PLACE1006371//ARS BINDING PROTEIN 1.//0.00030:142:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P49777
 F-PLACE1006387//NEUROTOXIN V.//0.85:28:39//ANDROCTONUS MAURETANICUS MAURETANICUS (SCORPION).//P01482
 F-PLACE1006385//HYPOTHETICAL 45.1 KD PROTEIN IN RP55-ZMS1 INTERGENIC REGION.//3.1e-35:165:47//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P47160
 F-PLACE1006412//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//4.3e-08:40:47//HOMO SAPIENS (HUMAN).//P08547
 F-PLACE1006414//FORKHEAD-RELATED TRANSCRIPTION FACTOR 4 (FREAC-4).//3.8e-05:123:39//HOMO SAPIENS (HUMAN).//Q16676
 F-PLACE1006438//ZINC FINGER PROTEIN 165.//2.8e-21:76:64//HOMO SAPIENS (HUMAN).//P49910
 F-PLACE1006445//SUPPRESSOR OF HAIRY WING PROTEIN.//0.058:99:29//DROSOPHILA VIRILIS (FRUIT FLY).//Q08876
 F-PLACE1006469//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACYL- ACTIVATING ENZYME).//1.8e-64:177:50//ESCHERICHIA COLI.//P27550
 F-PLACE1006470
 F-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//2.0e-47:120:85//GALLUS GALLUS (CHICKEN).//Q90595
 F-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.8e-85:173:95//CANIS FAMILIARIS (DOG).//Q00004
 F-PLACE1006492//VERY HYPOTHETICAL 11.2 KD PROTEIN CS6F8.13 IN CHROMOSOME 1.//0.75:32:56//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10261
 F-PLACE1006506
 F-PLACE1006521
 F-PLACE1006531//HYPOTHETICAL 115.4 KD PROTEIN ZX757.3 IN CHROMOSOME 111.//1.3e-53:167:61//CAENORHABDITIS ELEGANS.//P34681
 F-PLACE1006534
 F-PLACE1006540
 F-PLACE1006552//MYOSIN HEAVY CHAIN, CLONE 203 (FRAGMENT).//1.3e-07:242:23//HYDRA ATTENUATA (HYDRA) (HYDRA VULGARIS).//P39922
 F-PLACE1006598//!!!! ALU SUBFAMILY S81 WARNING ENTRY !!!!!//0.17:43:51//HOMO SAPIENS (HUMAN).//P39190
 F-PLACE1006615//ACROSIN PRECURSOR (EC 3.4.21.10).//3.6e-05:66:43//ORYZOLAGUS CUNICULUS (RABBIT).//P48038
 F-PLACE1006617//HYPOTHETICAL 14.6 KD PROTEIN (READING FRAME C) (REPLICATION).//1.0:74:29//STAPHYLOCOCCUS AUREUS.//P03861
 F-PLACE1006626//HYPOTHETICAL HELICASE K12H4.8 IN CHROMOSOME 111.//2.9e-10:73:46//CAENORHABDITIS ELEGANS.//P34529
 F-PLACE1006629//HYPOTHETICAL PROTEIN B80410.//1.0:23:43//BORRELIA BURGDORFERI (LYME DISEASE SPIROCHETE).//Q51371
 F-PLACE1006640
 F-PLACE1006673
 F-PLACE1006678//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENT).//1.0:36:41//ORYZOLAGUS CUNICULUS (RABBIT).//P02456
 F-PLACE1006704//BROAD-COMPLEX CORE-TNT1-Q1-Z1 PROTEIN (BRCORE-TNT1-Q1-Z1) (CONTAINS: BROAD-COMPLEX CORE-Q1-Z1 PROTEIN).//0.00062:157:26//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01295
 F-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//1.3e-07:127:36//CORYNEBACTERIUM AMMONIAGENES (BREVIBACTERIUM AMMONIAGENES).//Q59263
 F-PLACE1006754//CARCINOEMBRYONIC ANTIGEN CCM1 PRECURSOR (CD66D ANTIGEN).//1.9e-19:78:53//HOMO SAPIENS (HUMAN).//P40198
 F-PLACE1006760//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//0.21:107:30//RATTUS NORVEGICUS (RAT).//P13941
 F-PLACE1006779//CYTOTOXIN 5 (CTX V).//1.0:20:30//NAJIA MOSSAMBICA (MOZAMBIQUE COBRA).//P25517
 F-PLACE1006782//ZINC FINGER PROTEIN 1.//0.00052:178:28//CANDIDA ALBICANS (YEAST).//P28875
 F-PLACE1006792
 F-PLACE1006795//VOLTAGE-GATED POTASSIUM CHANNEL PROTEIN SHAW (SHAW2).//1.0:80:30//DROSOPHILA MELANOGASTER (FRUIT FLY).//P17972
 F-PLACE1006800//HYPOTHETICAL 9.4 KD PROTEIN.//0.99:62:33//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20569
 F-PLACE1006805
 F-PLACE1006815//HYPOTHETICAL PROTEIN UL61.//0.038:146:32//HUMAN CYTOMEGALOVIRUS (STRAIN AD169).//P16818
 F-PLACE1006819//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//7.3e-98:239:76//HOMO SAPIENS (HUMAN).//P08547
 F-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8).//0.061:34:58//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P50102
 F-PLACE1006860
 F-PLACE1006867
 F-PLACE1006878//HYPOTHETICAL 8.2 KD PROTEIN IN MOBL 3'REGION (ORF3).//0.85:27:37//THIOBACILLUS FERROOXIDANS.//P20087
 F-PLACE1006883//VITAMIN D3 RECEPTOR (VDR) (1,25-DIHYDROXYVITAMIN D3 RECEPTOR).//0.78:51:37//MUS MUSCULUS (MOUSE).//P48281
 F-PLACE1006901//HYPOTHETICAL 8.1 KD PROTEIN.//0.99:55:23//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20567
 F-PLACE1006904//MATING-TYPE LOCUS ALLELE B1 PROTEIN.//0.95:86:26//USTILAGO MAYDIS (SMUT FUNGUS).//P22015
 F-PLACE1006917//HYPOTHETICAL 40.9 KD PROTEIN C08B11.5 IN CHROMOSOME 11.//6.9e-15:101:45//CAENORHABDITIS ELEGANS.//Q09442
 F-PLACE1006932//HISTIDINE-RICH, METAL BINDING POLYPEPTIDE.//0.089:28:39//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//Q48251
 F-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME 111.//0.93:35:48//CAENORHABDITIS ELEGANS.//Q10000
 F-PLACE1006956//TRANSCRIPTION INITIATION FACTOR TF110 135 KD SUBUNIT (TAF11-135) (TAF11135) (TAF11-130) (TAF11130).//0.00079:122:36//HOMO SAPIENS (HUMAN).//Q00268
 F-PLACE1006958//OSMOTIC STRESS PROTEIN 94 (HEAT SHOCK 70-RELATED PROTEIN APG-1).//8.8e-70:140:98//MUS MUSCULUS (MOUSE).//P48722
 F-PLACE1006961
 F-PLACE1006962//APOLIPOPROTEIN C-I PRECURSOR (APO-C1).//1.0:25:40//PAPIO HAMADRYAS (HAMADRYAS BABOON).//P34929
 F-PLACE1006966//HYPOTHETICAL 49.1 KD PROTEIN IN SSB2-SPX18 INTERGENIC REGION.//1.6e-47:221:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40160
 F-PLACE1006989//HYPOTHETICAL 13.1 KD HIT-LIKE PROTEIN IN P37 5'REGION.//0.15:46:32//MYCOPLASMA HYORHINIS.//P32083
 F-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PROTEIN 12) (DER12).//3.4e-09:120:29//HOMO SAPIENS (HUMAN).//Q14542

【0686】

【表388】

F-PLACE1007021/!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//0.00046:42:59//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE1007045//HYPOTHETICAL PROTEIN ORF-1137.//8.1e-14:115:35//MUS MUSCULUS (MOUSE).//P11260
 F-PLACE1007053//SMALL PROLINE RICH PROTEIN 11 (SPR-11) (CLONE 930).//0.038:48:39//HOMO SAPIENS (HUMAN).//P22531
 F-PLACE1007068//PROTEIN-LYSINE 6-OXIDASE PRECURSOR (EC 1.4.3.13) (LYSYL OXIDASE).//0.0040:113:39//GALLUS GALLUS (CHICKEN).//Q05063
 F-PLACE1007097//HYPOTHETICAL 6.8 KD PROTEIN IN HE65-PK2 INTERGENIC REGION.//0.97:47:29//AUTOGRAPH A CALIFORNICA NUCLEAR POLYTHEODROSIS VIRUS (ACMPV).//P41663
 F-PLACE1007105//HYPOTHETICAL 83.6 KD PROTEIN C15A10.10 IN CHROMOSOME 1.//2.9e-33:219:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//013730
 F-PLACE1007111
 F-PLACE1007112//HYPOTHETICAL 9.2 KD PROTEIN.//0.47:75:28//ESCHERICHIA COLI.//P03853
 F-PLACE1007132/!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//1.8e-11:56:57//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE1007140//CAR2 PROTEIN.//0.72:185:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891
 F-PLACE1007178//HYPOTHETICAL 8.5 KD PROTEIN CY274.40C.//0.97:79:30//MYCOBACTERIUM TUBERCULOSIS.//Q10826
 F-PLACE1007226//HYPOTHETICAL 42.6 KD PROTEIN IN CSHB-AN5B INTERGENIC REGION (Q378).//1.9e-15:123:32//ESCHERICHIA COLI.//P52062
 F-PLACE1007238//MYOSIN HEAVY CHAIN 1B (MYOSIN HEAVY CHAIN 1L).//5.5e-10:98:44//ACANTHAMOEBA CASTELLANI (AMOEBA).//P19706
 F-PLACE1007239//TRANSCRIPTION ELONGATION FACTOR S-11 (TRANSCRIPTION ELONGATION FACTOR A).//3.9e-19:96:57//HOMO SAPIENS (HUMAN).//P23193
 F-PLACE1007242//GUANINE NUCLEOTIDE DISSOCIATION STIMULATOR RALGDS FORM B (RALGEF).//1.0:132:30//RATTUS NORVEGICUS (RAT).//Q03386
 F-PLACE1007243//HYPOTHETICAL 53.3 KD PROTEIN IN HXB-CAN1 INTERGENIC REGION.//0.041:114:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39981
 F-PLACE1007257//DIAPHANOUS PROTEIN.//1.3e-42:205:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//P48608
 F-PLACE1007274//CADMIUM-METALLOTHIONEIN (CD-MT).//0.054:60:30//HELIX POMATIA (ROMAN SNAIL) (EDIBLE SNAIL).//P33187
 F-PLACE1007276//BETA-DEFENSIN 1 PRECURSOR (RHBD-1) (DEFENSIN, BETA 1).//1.0:42:28//SUS SCROFA (PIG).//Q62697
 F-PLACE1007282//OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4) [CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8].//0.070:126:27//HUMAN ROTAVIRUS (SEROTYPE 4 / STRAIN ST. THOMAS 3).//P11200
 F-PLACE1007286
 F-PLACE1007301//HYPOTHETICAL PROTEIN KIAA0168.//0.042:61:39//HOMO SAPIENS (HUMAN).//P50749
 F-PLACE1007317
 F-PLACE1007342//PROTEIN GRAINY-HEAD (DNA-BINDING PROTEIN ELF-1) (ELEMENT 1-BINDING ACTIVITY) (TRANSCRIPTION FACTOR NTF-1).//1.7e-06:77:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//P13002
 F-PLACE1007346//TRANSCRIPTION INTERMEDIARY FACTOR 1-BETA (KRAB-A 1 INTERACTING PROTEIN) (KRIP-1).//0.0026:147:27//MUS MUSCULUS (MOUSE).//Q62318
 F-PLACE1007367/!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//1.3e-37:110:76//HOMO SAPIENS (HUMAN).//P39189
 F-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13.//4.7e-07:71:39//CAENORHABDITIS ELEGANS.//P27715
 F-PLACE1007386//HYPOTHETICAL 7.6 KD PROTEIN IN FLO1-PHO11 INTERGENIC REGION.//0.74:48:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P39561
 F-PLACE1007402//TRANSCRIPTIONAL REGULATORY PROTEIN ENTR (ENTERICIDIN R).//0.99:63:36//CITROBACTER FREUNDII.//Q69280
 F-PLACE1007409//WHITE PROTEIN.//7.9e-38:179:41//DROSOPHILA MELANOGASTER (FRUIT FLY).//P10090
 F-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADAP).//0.031:159:23//HOMO SAPIENS (HUMAN).//P27487
 F-PLACE1007450//ZINC FINGER PROTEIN 39 (ZINC FINGER PROTEIN KOX27) (FRAGMENT).//0.023:36:50//HOMO SAPIENS (HUMAN).//P17038
 F-PLACE1007452//HYPOTHETICAL 22.1 KD PROTEIN IN CCP1-NET1 INTERGENIC REGION.//2.2e-18:85:54//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36149
 F-PLACE1007454//PHOTOSYSTEM II REACTION CENTRE N PROTEIN.//0.66:13:53//CHLAMYDOMONAS REINHARDTII.//Q06480
 F-PLACE1007460//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.93:45:33//SUS SCROFA (PIG).//Q35914
 F-PLACE1007478//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//5.3e-08:50:56//MUS MUSCULUS (MOUSE).//P11369
 F-PLACE1007484//HYPOTHETICAL 6.8 KD PROTEIN IN REPLICATION ORIGIN REGION.//0.87:43:37//ESCHERICHIA COLI.//P03849
 F-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN).//1.2e-25:202:37//HOMO SAPIENS (HUMAN).//P98174
 F-PLACE1007507//HYPOTHETICAL 16.0 KD PROTEIN IN TAF60-GAP1 INTERGENIC REGION.//0.12:128:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53139
 F-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19).//2.1e-45:209:48//BOS TAURUS (BOVINE).//P08728
 F-PLACE1007524//HYPOTHETICAL 9.2 KD PROTEIN.//0.74:80:30//VACCINIA VIRUS (STRAIN COPENHAGEN).//P20550
 F-PLACE1007525
 F-PLACE1007537//MYOTROPHIN (V-1 PROTEIN) (GRANULE CELL DIFFERENTIATION PROTEIN).//0.045:92:30//MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT).//P80144
 F-PLACE1007544//IMMEDIATE-EARLY PROTEIN IE180.//1.5e-07:59:50//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479
 F-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R0SD3.4 IN CHROMOSOME 111.//2.5e-16:188:34//CAENORHABDITIS ELEGANS.//P34537
 F-PLACE1007557
 F-PLACE1007583//PROLINE RICH 33 KD EXTENSIN-RELATED PROTEIN PRECURSOR (FRAGMENT).//0.98:72:33//DAUCUS CAROTA (CARROT).//P06600
 F-PLACE1007598//ZINC FINGER PROTEIN 92 (ZINC FINGER PROTEIN HTF12) (FRAGMENT).//1.7e-11:88:43//HOMO SAPIENS (HUMAN).//Q03936
 F-PLACE1007618//ANION EXCHANGE PROTEIN 2 (NON-ERYTHROID BAND 3-LIKE PROTEIN) (B3RP).//0.19:109:27//MUS MUSCULUS (MOUSE).//P13808
 F-PLACE1007621//PHOSPHATE REGULATOR SENSOR PROTEIN PHOR (EC 2.7.3.-) (FRAGMENT).//0.98:34:41//PSEUDOMONAS AERUGINOSA.//P23621
 F-PLACE1007632//COLLAGEN ALPHA 2(I) CHAIN (FRAGMENT).//0.70:110:34//BOS TAURUS (BOVINE).//P02465
 F-PLACE1007645//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.99:20:45//STRUTHIO CAMELUS (OSTRICH).//Q21401
 F-PLACE1007649//GLUCANAMYLASE S1/S2 PRECURSOR (EC 3.2.1.3) (GLUCAN 1,4-ALPHA-GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE).//8.1e-06:197:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P08640
 F-PLACE1007677/!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!//1.0:47:46//HOMO SAPIENS (HUMAN).//P39192
 F-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG).//2.7e-06:116:28//AEDES ALBOPICTUS (FOREST DAY MOSQUITO).//Q26457
 F-PLACE1007690//SPERM PROTAMINE P1.//0.12:26:50//TACHYGLOSSUS ACULEATUS ACULEATUS (AUSTRALIAN ECHIDNA).//P35311
 F-PLACE1007697//SPERM PROTAMINE P1.//0.19:34:52//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM), AND MONODELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM).//P35305
 F-PLACE1007705//BIOM PROTEIN.//0.015:97:29//ESCHERICHIA COLI.//P13001
 F-PLACE1007706//HYPOTHETICAL 112.2 KD PROTEIN IN TIF35-NPL3 INTERGENIC REGION (ORF1).//5.3e-55:190:56//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32898
 F-PLACE1007725
 F-PLACE1007729//PROTEASE (EC 3.4.23.-).//1.8e-21:136:42//MOUSE MAMMARY TUMOR VIRUS (STRAIN BR6).//P10271
 F-PLACE1007730//SALIVARY PROLINE-RICH PROTEIN 11-1 (FRAGMENT).//0.0031:77:40//HOMO SAPIENS (HUMAN).//P81489
 F-PLACE1007737/!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!//8.78:39:56//HOMO SAPIENS (HUMAN).//P39195
 F-PLACE1007743
 F-PLACE1007746//RRP5 PROTEIN HOMOLOG (KIAA0185) (FRAGMENT).//0.0066:168:25//HOMO SAPIENS (HUMAN).//Q14690
 F-PLACE1007791//KRUEPPEL PROTEIN (FRAGMENT).//0.62:17:41//LITHOBIOUS FORFICATUS.//Q01872
 F-PLACE1007807//HYPOTHETICAL 6.4 KD PROTEIN IN BLTR-SPO11IC INTERGENIC REGION.//1.0:40:30//BACILLUS SUBTILIS.//P54446
 F-PLACE1007810//ANTHOPEURIN A (TOXIN AP-A).//0.79:28:46//ANTHOPELURA XANTHOGRAMMICA (GIANT GREEN SEA ANEMONE).//Q15669
 F-PLACE1007829//SPORE COAT PROTEIN G.//1.0:65:38//BACILLUS SUBTILIS.//P39801
 F-PLACE1007843
 F-PLACE1007846//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-32:37:94//HOMO SAPIENS (HUMAN).//P08547
 F-PLACE1007852//RHO-RELATED GTP-BINDING PROTEIN RHOD (GTP-BINDING PROTEIN TTF).//8.7e-05:138:30//HOMO SAPIENS (HUMAN).//Q15669
 F-PLACE1007858//ANAPHASE SPINDLE ELONGATION PROTEIN.//0.0039:127:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P50275
 F-PLACE1007866
 F-PLACE1007877

【0687】

【表389】

F-PLACE1007897//CD44 ANTIGEN PRECURSOR (PHAGOCYTTIC GLYCOPROTEIN 1) (PGP-1) (HJTC-1) (EXTRACELLULAR MATRIX RECEPTOR-111) (ECMR-111) (GPI LYMPHOCYTE HOMING/ADHESION RECEPTOR) (HERMES ANTIGEN) (HYALURONATE RECEPTOR) (HEPARAN SULFATE PROTEOGLYCAN) (HAM1 ANTIGEN) //0.44:128:28//MESOCRICETUS AURATUS (GOLDEN HAMSTER) //Q06022
F-PLACE1007908//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/5.5e-28:61:65//HOMO SAPIENS (HUMAN) //P39192
F-PLACE1007946//HYPOTHETICAL MERCURIC RESISTANCE PROTEIN MERC. //0.84:48:37//PSEUDOMONAS AERUGINOSA. //P04139
F-PLACE1007954//HYPOTHETICAL 45.5 KD PROTEIN IN FIG1-GPI1 INTERGENIC REGION. //0.00070:96:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P38226
F-PLACE1007955//HYPOTHETICAL 84.3 KD PROTEIN ZK945.10 IN CHROMOSOME 11. //0.00027:255:23//CAENORHABDITIS ELEGANS. //Q09625
F-PLACE1007958//HIGH-AFFINITY CAMP-SPECIFIC 3',5'-CYCLIC PHOSPHODIESTERASE (EC 3.1.4.17) //1.7e-09:127:30//MUS MUSCULUS (MOUSE) //P70453
F-PLACE1007969//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION. //2.4e-05:104:37//AUTOPHAGAL CALIFORNICA NUCLEAR POLYHEDRIN VIRUS (ACMPV) //P41479
F-PLACE1007990//SPERM PROTEIN P1. //0.78:35:47//ORNITHORHYNCHUS NATIVUS (DUCKBILL PLATYPUS) //P35307
F-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSIN-110) (SYNAPTIC DENSITY PROTEIN PSD-93) //1.2e-16:128:39//RATTUS NORVEGICUS (RAT) //Q63622
F-PLACE1008002
F-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN N UP107) (107 KD NUCLEOPORIN) (P105) //3.9e-106:208:93//RATTUS NORVEGICUS (RAT) //P52590
F-PLACE1008045//COLLAGEN ALPHA 1(XII) CHAIN (FRAGMENTS) //3.9e-09:49:53//BOS TAURUS (BOVINE) //P25508
F-PLACE1008080//RNA REPLICASE POLYPROTEIN (EC 2.7.7.48) //0.00025:100:27//EGGPLANT MOSAIC VIRUS. //P20126
F-PLACE1008095//PROTOPORPHYRINOGEN OXIDASE (EC 1.3.3.4) (PPO) //0.90:74:25//MYCOBACTERIUM TUBERCULOSIS. //O53230
F-PLACE1008111//HYPOTHETICAL PROTEIN MJCS12. //0.30:38:42//METHANOCOCCUS JANNASCHII. //Q60311
F-PLACE1008122//PEA2 PROTEIN (PPF2 PROTEIN) //0.0085:117:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P40091
F-PLACE1008129//PROCOLLAGEN ALPHA 2(I) CHAIN PRECURSOR (FRAGMENTS) //1.8e-06:154:36//GALLUS GALLUS (CHICKEN) //P02467
F-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME 111. //1.4e-13:227:36//CAENORHABDITIS ELEGANS. //Q09531
F-PLACE1008177//TRICHOHYALIN. //2.7e-10:230:26//OVIS ARIES (SHEEP) //P22793
F-PLACE1008181
F-PLACE1008198//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN) //0.00044:121:34//XENOPUS LAEVIS (AFRICAN CLAWED FROG) //P17437
F-PLACE1008201//ZINC FINGER PROTEIN ZFMSA12A. //3.0e-05:82:37//MICROPTERUS SALMOIDES (LARGEMOUTH BASS) //P38621
F-PLACE1008209//METALLOTHIONEIN-1 (MT-1) //0.95:39:35//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET) //P02797
F-PLACE1008231//PROCYCLIC FORM SPECIFIC POLYPEPTIDE B1-ALPHA PRECURSOR (PROCYCLIN) (PARP) //0.028:23:52//TRYPANOSOMA BRUCEI BRUCEI //P08469
F-PLACE1008244//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1. //2.2e-23:148:38//PODOSPORA ANSERINA. //Q08008
F-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA-A-COP) //1.1e-97:222:81//BOS TAURUS (BOVINE) //P53620
F-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-) //5.8e-20:161:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P12689
F-PLACE1008280//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. //6.1e-23:124:42//HOMO SAPIENS (HUMAN) //P08547
F-PLACE1008309//HYPOTHETICAL 98.3 KD PROTEIN C9G1.05C IN CHROMOSOME 1. //0.47:99:37//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //O14302
F-PLACE1008329//PUTATIVE Z PROTEIN. //0.73:52:28//OVIS ARIES (SHEEP) //P08105
F-PLACE1008330//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.0e-37:75:81//HOMO SAPIENS (HUMAN) //P39194
F-PLACE1008331//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.1e-08:70:50//HOMO SAPIENS (HUMAN) //P39188
F-PLACE1008356//FRUIT PROTEIN PKIWI501. //0.0037:148:29//ACTINIDIA CHINENSIS (KIWI) (YANGTAO) //P43393
F-PLACE1008368//RING CANAL PROTEIN (KELCH PROTEIN) //3.5e-18:205:30//DROSOPHILA MELANOGASTER (FRUIT FLY) //Q04652
F-PLACE1008369
F-PLACE1008392
F-PLACE1008398//GENE 33 POLYPEPTIDE. //1.5e-102:225:84//RATTUS NORVEGICUS (RAT) //P05432
F-PLACE1008401//PROLINE-RICH PROTEIN MP-3 (FRAGMENT) //2.9e-08:186:34//MUS MUSCULUS (MOUSE) //P05143
F-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS ASSOCIATED PROTEIN) (TAP) //9.4e-105:207:98//BOS TAURUS (BOVINE) //P41541
F-PLACE1008405
F-PLACE1008424//PROTEIN UL56. //1.0:65:33//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN HFEM) //P36297
F-PLACE1008426//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN I) //4.4e-05:185:28//DROSOPHILA MELANOGASTER (FRUIT FLY) //Q99323
F-PLACE1008429//NEURONAL AXONAL MEMBRANE PROTEIN NAP-22. //0.00054:172:25//RATTUS NORVEGICUS (RAT) //Q05175
F-PLACE1008437//HYPOTHETICAL 115.4 KD PROTEIN ZK757.3 IN CHROMOSOME 111. //1.9e-23:226:34//CAENORHABDITIS ELEGANS. //P34681
F-PLACE1008455//DNA-BINDING PROTEIN (AGNOPROTEIN) //0.97:23:52//BURGERICAR FLEDGLING DISEASE VIRUS (BFDV) //P13893
F-PLACE1008457//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/2.1e-12:89:47//HOMO SAPIENS (HUMAN) //P39188
F-PLACE1008465//ZINC FINGER PROTEIN 31 (ZINC FINGER PROTEIN K0X29) (FRAGMENT) //0.00017:23:43//HOMO SAPIENS (HUMAN) //P17040
F-PLACE1008488//HYPOTHETICAL PROTEIN UL61. //9.1e-05:204:30//HUMAN CYTOMEGALOVIRUS (STRAIN AD169) //P16818
F-PLACE1008524//HOMEBOX PROTEIN HLX1 (HOMEBOX PROTEIN HB24) //0.95:74:36//HOMO SAPIENS (HUMAN) //Q14774
F-PLACE1008531//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.1e-05:86:45//HOMO SAPIENS (HUMAN) //P39192
F-PLACE1008532//HYPOTHETICAL 36.4 KD PROTEIN IN SMP1-NBA1 INTERGENIC REGION. //3.9e-21:62:45//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P38298
F-PLACE1008533//HYPOTHETICAL 86.2 KD PROTEIN C4G8.04 IN CHROMOSOME 1. //3.5e-06:118:29//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST) //Q09830
F-PLACE1008568//NEUROMATIN. //0.046:34:52//HOMO SAPIENS (HUMAN) //Q16517
F-PLACE1008584//HUNCHBACK PROTEIN (FRAGMENT) //0.94:30:43//LITHOBIUS FORFICATUS. //Q02030
F-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN N UP155) (155 KD NUCLEOPORIN) (P140) //3.9e-123:224:96//RATTUS NORVEGICUS (RAT) //P37199
F-PLACE1008621//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD) //5.0e-05:31:67//HOMO SAPIENS (HUMAN) //P20931
F-PLACE1008625//DISAGREGIN (PLATELET AGGREGATION ACTIVATION INHIBITOR) //0.87:17:52//ORNITHODOROS MOUBATA (SOFT TICK) //P36235
F-PLACE1008626//METALLOTHIONEIN-1 (MT-1) //0.77:33:36//SCYLLA SERRATA (MUD CRAB) //P02805
F-PLACE1008627//METALLOTHIONEIN-111 (MT-111) (GROWTH INHIBITORY FACTOR) (GIF) (GIFB) //0.14:44:31//HOMO SAPIENS (HUMAN) //P25713
F-PLACE1008629
F-PLACE1008630//PROTAMINE 23 (SCYLLIORHININE 23) //0.78:33:36//SCYLLIORHINUS CANICULA (SPOTTED DOGFISH) (SPOTTED CATSHARK) //P30258
F-PLACE1008643//INTER-ALPHA-TRYPSIN INHIBITOR HEAVY CHAIN H4 PRECURSOR (ITI HEAVY CHAIN H4) (INTER-ALPHA-TRYPSIN INHIBITOR FAMILY HEAVY CHAIN-RELATED PROTEIN) (PLASMA KALLIKREIN SENSITIVE GLYCOPROTEIN 120) (PK-120) //1.7e-30:220:41//HOMO SAPIENS (HUMAN) //Q14624
F-PLACE1008650//PPI/PP2A PHOSPHATASES PLEIOTROPIC REGULATOR PRL1. //2.5e-10:106:31//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS) //Q42384
F-PLACE1008693//BOHRMAN-BIRK TYPE PROTEINASE INHIBITOR (MST1) //1.0:36:38//MEDICAGO SCUTELLATA (SNAIL MEDIC) //P80321
F-PLACE1008696//NADH-UBIQUINONE OXIDOREDUCTASE 23 KD SUBUNIT PRECURSOR (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-23KD) (C1-23KD) (TYK3 SUBUNIT) //4.8e-14:47:80//HOMO SAPIENS (HUMAN) //O00217
F-PLACE1008715//HYPOTHETICAL 13.4 KD PROTEIN IN ACT5-YCK1 INTERGENIC REGION. //0.66:105:24//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P38834
F-PLACE1008748//HYPOTHETICAL 57.5 KD PROTEIN IN VMA7-RPS25A INTERGENIC REGION. //0.10:178:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST) //P53214
F-PLACE1008757//HYPOTHETICAL 10.1 KD PROTEIN IN RHSD-GCL INTERGENIC REGION (ORFD3) //0.60:44:34//ESCHERICHIA COLI. //P33669
F-PLACE1008790//IMPORTIN ALPHA-6 SUBUNIT (KARYOPHERIN ALPHA-6 SUBUNIT) (IMPORTIN ALPHA S2) //3.0e-69:191:80//MUS MUSCULUS (MOUSE) //O35345
F-PLACE1008798//BACTERIOCIN LACTOBIN A. //1.0:34:41//LACTOBACILLUS AMYLVOORUS. //P06096
F-PLACE1008807//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. //0.91:77:36//HOMO SAPIENS (HUMAN) //P08547
F-PLACE1008808//REC1 PROTEIN. //0.45:39:30//USTILAGO MAYDIS (SMUT FUNGUS) //P14746
F-PLACE1008813

【0688】

【表390】

F-PLACE1008851//VERY HYPOTHETICAL 11.8 KD PROTEIN IN KTR3-DURI.2 I
NTERGENIC REGION.//1.0:62:30//SACCHAROMYCES CEREVISIAE (BAKER'S YE
AST).//P38309
F-PLACE1008854//HYPOTHETICAL 182.0 KD PROTEIN IN NMDS-HOMS INTERGE
NIC REGION.//1.0:82:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//
/P47170
F-PLACE1008867//PATATIN T5 PRECURSOR (POTATO TUBER PROTEIN).//0.6
5:61:36//SOLANUM TUBEROSUM (POTATO).//P15478
F-PLACE1008887//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.5e-56:18
0:54//NYCTICEBUS COUCANG (SLOW LORIS).//P08548
F-PLACE1008902
F-PLACE1008920
F-PLACE1008925//HYPOTHETICAL 41.2 KD PROTEIN IN GAPA-RND INTERGENI
C REGION.//0.90:77:33//ESCHERICHIA COLI.//P76242
F-PLACE1008934//HYPOTHETICAL PROTEIN IN ADHS 5' REGION (ORF3) (FRAG
MENT).//0.14:77:45//GLUCONOBACTER SUBOXYDANS.//005543
F-PLACE1008941//ZINC FINGER PROTEIN 141.//1.1e-17:45:95//HOMO SAPI
ENS (HUMAN).//Q15928
F-PLACE1008947//MAJOR CENTROMERE AUTOANTIGEN B (CENTROMERE PROTEIN
B) (CENP-B).//4.1e-14:136:39//MUS MUSCULUS (MOUSE).//P27790
F-PLACE1009020//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.74:37:48//BOS
TAURUS (BOVINE).//P20072
F-PLACE1009027//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4L (EC 1.6.5.
3).//0.39:57:36//BALAENOPTERA MUSCULUS (BLUE WHALE).//P41301
F-PLACE1009039
F-PLACE1009045//HYPOTHETICAL 9.5 KD PROTEIN IN SPEA-METX INTERGENI
C REGION (F83).//0.48:32:43//ESCHERICHIA COLI.//P46879
F-PLACE1009048
F-PLACE1009050
F-PLACE1009060//HYPOTHETICAL 98.3 KD PROTEIN R10E12.1 IN CHROMOSOM
E 111.//4.9e-23:244:31//CAENORHABDITIS ELEGANS.//P34552
F-PLACE1009090//50S RIBOSOMAL PROTEIN L35.//1.0:27:51//MYCOPLASMA
GENITALIUM.//P47439
F-PLACE1009091
F-PLACE1009094//HEL-LIKE PROTEIN (FRAGMENT).//3.6e-15:180:30//HOMO
SAPIENS (HUMAN).//Q92832
F-PLACE1009099//ZINC FINGER PROTEIN 27 (ZFP-27) (MKR4 PROTEIN) (FR
AGMENT).//1.4e-94:228:71//MUS MUSCULUS (MOUSE).//P10077
F-PLACE1009110//HIRUDIN HVI (BUFRUDIN).//1.0:49:34//HIRUDINARIA MA
NILLENSIS (BUFFALO LEECH).//P81492
F-PLACE1009111//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.4e-05:
30:83//HOMO SAPIENS (HUMAN).//P39195
F-PLACE1009113//ANNEXIN VII (SYNEXIN) (FRAGMENT).//0.032:40:52//BO
S TAURUS (BOVINE).//P20072
F-PLACE1009130//HYPOTHETICAL PROTEIN KIAA0032.//3.3e-37:214:38//HO
MO SAPIENS (HUMAN).//Q15034
F-PLACE1009150//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/1.6e-32:
56:76//HOMO SAPIENS (HUMAN).//P39195
F-PLACE1009155//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.2e-17:
101:57//HOMO SAPIENS (HUMAN).//P39194
F-PLACE1009158//HYPOTHETICAL PROTEIN HKRFJ (J11).//0.0058:73:42//H
UMAN CYTOMEGALOVIRUS (STRAIN AD169).//P09711
F-PLACE1009166//CYTOSOLIC PURINE 5'-NUCLEOTIDASE (EC 3.1.3.5).//0.
0086:96:30//HOMO SAPIENS (HUMAN).//P49902
F-PLACE1009172//HYPOTHETICAL 8.7 KD PROTEIN IN GAPA-RND INTERGENIC
REGION.//1.0:19:52//ESCHERICHIA COLI.//P76246
F-PLACE1009174//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.1e-17:
47:82//HOMO SAPIENS (HUMAN).//P39194
F-PLACE1009183
F-PLACE1009186//HYPOTHETICAL 11.4 KD PROTEIN C13G6.04 IN CHROMOSOM
E 1.//0.019:62:24//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09
783
F-PLACE1009190//PALMITOYL-COA HYDROLASE (EC 3.1.2.2) (LONG-CHAIN F
ATTY-ACYL-COA HYDROLASE) (FRAGMENT).//0.027:53:28//RATTUS NORVEGIC
US (RAT).//P80250
F-PLACE1009200//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/5.4e-28:
84:71//HOMO SAPIENS (HUMAN).//P39194
F-PLACE1009230//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.8e-12:
50:74//HOMO SAPIENS (HUMAN).//P39189
F-PLACE1009246//UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 7.8 KD PR
OTEIN (EC 1.10.2.2) (MITOCHONDRIAL HINGE PROTEIN) (CR7).//1.0:17:5
2//SOLANUM TUBEROSUM (POTATO).//P48504
F-PLACE1009298//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.
//6.6e-41:177:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P3411
0
F-PLACE1009308//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (HNS KER
ATIN).//0.0034:108:33//HOMO SAPIENS (HUMAN).//P26371
F-PLACE1009319//PRESYNAPTIC DENSITY PROTEIN 95 (PSD-95).//5.3e-16:
84:50//HOMO SAPIENS (HUMAN).//P78352
F-PLACE1009328//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//6.9e-82:26
3:67//HOMO SAPIENS (HUMAN).//P08547
F-PLACE1009335//60S RIBOSOMAL PROTEIN L32.//0.95:71:36//HOMO SAPI
ENS (HUMAN), MUS MUSCULUS (MOUSE), AND RATTUS NORVEGICUS (RAT).//P0
2433
F-PLACE1009338//TRANSCRIPTION FACTOR HES-5 (HAIRY AND ENHANCER OF
SPLIT 5).//0.90:42:40//MUS MUSCULUS (MOUSE).//P70120
F-PLACE1009368//BASIC PROLINE-RICH PEPTIDE 1B-1.//0.013:33:48//HOM
O SAPIENS (HUMAN).//P04281
F-PLACE1009375//HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOM
E 111.//0.0022:135:21//CAENORHABDITIS ELEGANS.//P34492
F-PLACE1009388//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/4.8e-22:
73:65//HOMO SAPIENS (HUMAN).//P39195
F-PLACE1009398//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).
//8.1e-83:223:65//HOMO SAPIENS (HUMAN).//P51523
F-PLACE1009404//GLUTENIN, HIGH MOLECULAR WEIGHT SUBUNIT PW212 PREC
URSOR.//0.047:145:29//TRITICUM AESTIVUM (WHEAT).//P08489
F-PLACE1009410//TOXIN C13S1C1 PRECURSOR.//0.22:21:47//DENDROASPIS
ANGUSTICEPS (EASTERN GREEN MAMBA).//P18329
F-PLACE1009434//NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT K (EC 1.6.
5.3) (FRAGMENT).//0.81:61:29//ANTHOCEROS FORMOSAE.//Q31791
F-PLACE1009443//SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A6
6).//9.1e-05:93:32//MUS MUSCULUS (MOUSE).//Q62203
F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67)
(PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//6.4e-15:41:97//HOMO
SAPIENS (HUMAN).//P42356
F-PLACE1009459//HYPOTHETICAL 42.3 KD PROTEIN C12G12.11C IN CHROMOS
OME 1.//0.0011:119:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//
/Q09874
F-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//4.2
e-34:101:75//RATTUS NORVEGICUS (RAT).//P54319
F-PLACE1009476//DNA-BINDING PS2/P100 COMPLEX, 100 KD SUBUNIT (FRAG
MENTS).//0.086:21:52//HOMO SAPIENS (HUMAN).//P30808
F-PLACE1009477
F-PLACE1009493//HYPOTHETICAL 127.3 KD PROTEIN B0416.1 IN CHROMOSOM
E X.//1.4e-18:138:39//CAENORHABDITIS ELEGANS.//Q11069
F-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN)
(ARF EXCHANGE FACTOR).//9.4e-80:155:85//HOMO SAPIENS (HUMAN).//Q99
418
F-PLACE1009539//GTP-BINDING NUCLEAR PROTEIN RAM/TC4.//1.0:76:26//G
IARDIA LAMBLIA (GIARDIA INTESTINALIS).//P38543
F-PLACE1009542//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.00016:3
1:77//HOMO SAPIENS (HUMAN).//P39188
F-PLACE1009571//ATP SYNTHASE B CHAIN (EC 3.6.1.34) (SUBUNIT 1).//
0.88:116:29//STREPTOCOCCUS PNEUMONIAE.//Q59952
F-PLACE1009581//50S RIBOSOMAL PROTEIN L32.//0.0023:37:51//RHODOBA
CTER CAPSULATUS (RHODOSPIRILLUM RUBRUM).//P30788
F-PLACE1009595
F-PLACE1009596//HYPOTHETICAL 40.4 KD TRP-ASP REPEATS CONTAINING PR
OTEIN C14B1.4 IN CHROMOSOME 111.//2.1e-36:116:49//CAENORHABDITIS E
LEGANS.//Q17963
F-PLACE1009607//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.8e-43:7
3:69//HOMO SAPIENS (HUMAN).//P39188
F-PLACE1009613
F-PLACE1009621//TRANSCRIPTION FACTOR BTF3 HOMOLOG 2.//0.91:29:44//
HOMO SAPIENS (HUMAN).//Q13891
F-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN.//1.3e-22:132:47//
DROSOPHILA MELANOGASTER (FRUIT FLY).//P25159
F-PLACE1009637//HYPOTHETICAL 18.1 KD PROTEIN IN CFXA 3' REGION.//0.
30:28:57//BACTEROIDES VULGATUS.//P30905
F-PLACE1009639//LIPASE MODULATOR PRECURSOR (LIPASE HELPER PROTEIN
) .//0.23:79:31//PSEUDOMONAS AERUGINOSA.//Q04591
F-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (BRAIN PROTEIN H
19) (HM19) (FRAGMENT).//3.9e-126:227:96//MUS MUSCULUS (MOUSE).//P2
8660
F-PLACE1009665//IG KAPPA CHAIN V-1 REGION (HAU).//0.52:89:35//HOMO
SAPIENS (HUMAN).//P01600
F-PLACE1009670//CYCLOMALTODEXTRIN GLUCANOTRANSFERASE PRECURSOR (EC
2.4.1.19) (CYCLODEXTRIN-GLYCOSYLTRANSFERASE) (CGTASE).//0.16:114:
29//PAENIBACILLUS MACERANS (BACILLUS MACERANS).//P31835
F-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING P
ROTEIN C12G12.13C IN CHROMOSOME 1.//9.6e-19:156:36//SCHIZOSACCHARO
MYCES POMBE (FISSION YEAST).//Q09876
F-PLACE1009721//MSF1 PROTEIN.//7.7e-23:176:33//SACCHAROMYCES CEREV
ISIAE (BAKER'S YEAST).//P35200
F-PLACE1009731//AIG1 PROTEIN.//1.1e-09:91:43//ARABIDOPSIS THALIANA
(MOUSE-EAR CRESS).//P54120
F-PLACE1009763//HYPOTHETICAL 48.9 KD PROTEIN C24H6.12C IN CHROMOSO
ME 1.//8.3e-42:171:51//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//
/Q09765
F-PLACE1009794//C-HORDEIN (CLONE PC HOR1-3) (FRAGMENT).//0.99:36:3

【0689】

【表391】

3//HORDIUM VULGARE (BARLEY).//P17991
 F-PLACE1009798//HYPOTHETICAL PROTEIN C2F3.14C IN CHROMOSOME 1 (FRAGMENT).//2.6e-34:191:38//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09779
 F-PLACE1009845//WEB1 PROTEIN (PROTEIN TRANSPORT PROTEIN SEC31).//2.2e-19:190:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38968
 F-PLACE1009861//CATHEPSIN B PRECURSOR (EC 3.4.22.1).//4.4e-20:171:33//BOS TAURUS (BOVINE).//P07688
 F-PLACE1009879//HYPOTHETICAL 8.7 KD PROTEIN IN RPL22-RPL23 INTERGENIC REGION (ORF70).//0.99:30:33//ASTASIA LONGA (EUGLENOPHYCEAN ALGAE).//P34779
 F-PLACE1009886
 F-PLACE1009888//NONSTRUCTURAL POLYPROTEIN [CONTAINS: NONSTRUCTURAL PROTEIN NSP4] (FRAGMENT).//1.0:33:42//WESTERN EQUINE ENCEPHALITIS VIRUS.//P13896
 F-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN C3F10.16C IN CHROMOSOME 1.//3.1e-42:205:46//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10190
 F-PLACE1009921
 F-PLACE1009924//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.70:128:29//TRYPANOSOMA BRUCEI BRUCEI.//P24499
 F-PLACE1009925//ATP SYNTHASE D CHAIN, MITOCHONDRIAL (EC 3.6.1.34).//0.99:111:21//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P30902
 F-PLACE1009935//HYPOTHETICAL PROTEIN MJ0258.//0.063:75:32//METHANOCOCCUS JANNASCHII.//Q57706
 F-PLACE1009947//NEUROGRANIN (NG) (P17) (8-50 IMMUNOREACTIVE C-KINASE SUBSTRATE) (BICKS) (FRAGMENT).//0.33:51:45//BOS TAURUS (BOVINE).//P35722
 F-PLACE1009971//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//0.022:84:27//MUS MUSCULUS (MOUSE).//P28575
 F-PLACE1009992//BONE MORPHOGENETIC PROTEIN 1 PRECURSOR (EC 3.4.24.-) (BMP-1).//0.00011:35:51//HOMO SAPIENS (HUMAN).//P13497
 F-PLACE1009995//TROPOMYOSIN, SMOOTH MUSCLE/FIBROBLAST CTN1.//0.052:185:22//CICOMA INTESTINALIS.//Q07068
 F-PLACE1009997//TRANSCRIPTION ELONGATION FACTOR S-11 (RNA POLYMERASE II ELONGATION FACTOR DNS-11) (TF11S).//0.68:98:28//DROSOPHILA MELANOGASTER (FRUIT FLY).//P20232
 F-PLACE1010023//HYPOTHETICAL 83.8 KD PROTEIN C2F2.7 IN CHROMOSOME 111.//6.6e-06:111:32//CAENORHABDITIS ELEGANS.//Q18262
 F-PLACE1010031//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//0.0024:72:33//AUTOTRAPHIA CALIFORNICA NUCLEAR POLYTHEDROSIS VIRUS (ACNPV).//P41479
 F-PLACE1010053//HYPOTHETICAL PROTEIN H10593.//0.83:24:45//HAEMOPHILUS INFLUENZAE.//P44022
 F-PLACE1010069
 F-PLACE1010074//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VP55.//0.0027:192:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q92331
 F-PLACE1010076//HUNCHBACK PROTEIN (FRAGMENT).//0.80:39:30//SCIARA COPROPHILA (FUNGUS GNAT).//Q01790
 F-PLACE1010083//RHO-GAP HEMATOPOIETIC PROTEIN C1 (P115) (K1AA0131).//2.7e-48:177:46//HOMO SAPIENS (HUMAN).//P98171
 F-PLACE1010089//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 11 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 11) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 13) (DEUBIQUITINATING ENZYME 11) (K1AA0055).//7.9e-07:55:43//HOMO SAPIENS (HUMAN).//P40818
 F-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-).//1.0e-107:232:90//RATTUS NORVEGICUS (RAT).//Q62671
 F-PLACE1010102//DNA-DIRECTED RNA POLYMERASE SUBUNIT N (EC 2.7.7.6).//1.0:33:45//METHANOCOCCUS JANNASCHII.//Q57649
 F-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-47:200:46//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
 F-PLACE1010106//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE TRANSCRIPTASE (EC 2.7.7.49); ENDONUCLEASE].//1.2e-14:94:41//MUS MUSCULUS (MOUSE).//P11369
 F-PLACE1010134//HYPOTHETICAL 171.5 KD HELICASE IN MUT1-AR02 INTERGENIC REGION.//4.0e-28:78:76//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53115
 F-PLACE1010148//GAR2 PROTEIN.//2.6e-05:180:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P41891
 F-PLACE1010152//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E).//2.1e-59:227:54//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q24574
 F-PLACE1010181//MALE SPECIFIC SPERM PROTEIN MST87F.//0.39:12:58//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175
 F-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//1.4e-07:95:43//GALLUS GALLUS (CHICKEN).//P30352
 F-PLACE1010202//TRISTETRAPROLINE (TTP) (T1S11A) (T1S11) (ZFP-36).//0.094:109:29//RATTUS NORVEGICUS (RAT).//P47973

F-PLACE1010231//LANTIBIOTIC NISIN A PRECURSOR.//0.99:42:35//LACTOCOCCUS LACTIS (SUBSP. LACTIS) (STREPTOCOCCUS LACTIS).//P13068
 F-PLACE1010261//SEGREGATION DISTORTER PROTEIN.//6.0e-71:201:62//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25722
 F-PLACE1010270
 F-PLACE1010274//HYPOTHETICAL 16.2 KD PROTEIN CAF8.01 IN CHROMOSOME 1.//4.4e-08:100:26//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q14177
 F-PLACE1010293//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!//3.9e-26:94:64//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE1010310//SYNAPSINS 1A AND 1B.//5.7e-09:89:37//RATTUS NORVEGICUS (RAT).//P09951
 F-PLACE1010321//IMMEDIATE-EARLY PROTEIN IE180.//0.033:145:31//PSEUDORABIES VIRUS (STRAIN KAPLAN) (PRV).//P33479
 F-PLACE1010324//MAST CELL DEGRANULATING PEPTIDE (MCDP) (MCD).//0.60:25:48//MEGABOMBUS PENNSYLVANICUS (AMERICAN COMMON BUMBLEBEE).//P04567
 F-PLACE1010329//TOXIN SSC10.//1.0:39:33//DENDROASPIS JAMESONI KAIMOSA (EASTERN JAMESON'S MAMBA).//P01419
 F-PLACE1010341//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!//0.0049:49:55//HOMO SAPIENS (HUMAN).//P39189
 F-PLACE1010362//VARIANT-SURFACE-GLYCOPROTEIN PHOSPHOLIPASE C (EC 3.1.4.47) (VSG LIPASE) (GLYCOSYLPHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (GPI-PLC).//0.0034:89:30//TRYPANOSOMA CRUZI.//Q15886
 F-PLACE1010364//NADH-UBIQUINONE OXIDOREDUCTASE B17 SUBUNIT (EC 1.6.5.3) (EC 1.6.99.3) (COMPLEX I-B17) (CI-B17).//1.0:40:35//SUS SCROFA (PIG).//Q29259
 F-PLACE1010383
 F-PLACE1010401//140 KD NUCLEOLAR PHOSPHOPROTEIN (NOPP140).//0.10:174:22//RATTUS NORVEGICUS (RAT).//P41777
 F-PLACE1010481//HYPOTHETICAL 71.9 KD PROTEIN B0285.5 IN CHROMOSOME 111.//1.5e-21:170:35//CAENORHABDITIS ELEGANS.//P46555
 F-PLACE1010491//HYPOTHETICAL 13.5 KD PROTEIN IN MOBI-SGA1 INTERGENIC REGION.//1.0:31:41//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P40490
 F-PLACE1010492//HYPOTHETICAL 42.3 KD PROTEIN C12G12.11C IN CHROMOSOME 1.//0.77:97:30//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09874
 F-PLACE1010522//SMALL PROLINE RICH PROTEIN 11 (SPR-11) (CLONE 930).//0.74:45:37//HOMO SAPIENS (HUMAN).//P22531
 F-PLACE1010529//DELTA 1-PYRROLINE-5-CARBOXYLATE SYNTHETASE (PSCS) [CONTAINS: GLUTAMATE 5-KINASE (EC 2.7.2.11) (GAMMA-GLUTAMYL KINASE) (CK); GAMMA-GLUTAMYL PHOSPHATE REDUCTASE (GPR) (EC 1.2.1.41) (GLUTAMATE-5-SEMIALDEHYDE DEHYDROGENASE) (GLUTAMYL-GAMMA-SEMIALDEHYDE DEHYDROGENASE)].//0.70:58:39//VIGNA ACONITIFOLIA (MOTHBEAN).//P32296
 F-PLACE1010547//HYPOTHETICAL 31.0 KD PROTEIN IN BUD9-RME1 INTERGENIC REGION.//0.17:68:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53227
 F-PLACE1010562//CHLOROPLAST 50S RIBOSOMAL PROTEIN L33.//0.50:48:29//PORPHYRA PURPUREA.//P51255
 F-PLACE1010579//HYPOTHETICAL PROTEIN H11571.//0.29:37:43//HAEMOPHILUS INFLUENZAE.//P44260
 F-PLACE1010580//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//3.3e-38:178:48//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09747
 F-PLACE1010599//PEROXISOMAL MEMBRANE PROTEIN PERO (PEROXIN-14).//4.6e-17:192:31//PICHIA ANGUSTA (YEAST) (HANSENULA POLYMORPHA).//P78723
 F-PLACE1010616//HYPOTHETICAL 9.2 KD PROTEIN IN RNPA 3' REGION.//0.44:32:37//PSEUDOMONAS PUTIDA.//P25753
 F-PLACE1010622//A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.//5.0e-06:102:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32323
 F-PLACE1010624//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.00036:134:32//HOMO SAPIENS (HUMAN).//P10162
 F-PLACE1010628
 F-PLACE1010629//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!//2.7e-12:37:81//HOMO SAPIENS (HUMAN).//P39194
 F-PLACE1010630
 F-PLACE1010631//WNT-5B PROTEIN (FRAGMENT).//0.49:62:30//EUMECES SKILTONIANUS (WESTERN SKINK).//P28118
 F-PLACE1010661//MATERNAL EXUPERANTIA 2 PROTEIN.//1.0:95:30//DROSOPHILA PSEUDOBURSICA (FRUIT FLY).//Q24617
 F-PLACE1010662//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (EC 2.4.1.-) (DUGT).//3.2e-05:117:24//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q09332
 F-PLACE1010702//ZINC FINGER PROTEIN 195.//1.4e-62:117:62//HOMO SAPIENS (HUMAN).//Q14628
 F-PLACE1010714
 F-PLACE1010720//CHROMOSOME ASSEMBLY PROTEIN XCAP-C.//1.1e-64:176:7

【0690】

【表392】

6//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P50532
 F-PLACE1010739//TAT PROTEIN (TRANSACTIVATING REGULATORY PROTEIN) (FRAGMENT).//0.97:31:41//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 (BHS ISOLATE) (HIV-1).//P04512
 F-PLACE1010743//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//3.8e-05:25:3:30//MUS MUSCULUS (MOUSE).//P05143
 F-PLACE1010761//HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME 11.//1.5e-14:175:25//CAENORHABDITIS ELEGANS.//Q09217
 F-PLACE1010771//TRANSCRIPTIONAL REGULATOR PROTEIN HONGP.//1.3e-12:0:216:89//MUS MUSCULUS (MOUSE).//Q02614
 F-PLACE1010786//CENTROSOMIN (ARROW PROTEIN).//0.97:133:24//DROSOPHILA MELANOGASTER (FRUIT FLY).//P54623
 F-PLACE1010800//HYPOTHETICAL 31.7 KD PROTEIN IN TRAX-FINO INTERGENIC REGION (ORFC).//0.0060:111:31//ESCHERICHIA COLI.//Q99390
 F-PLACE1010802//UREASE ACCESSORY PROTEIN UREI.//0.82:44:29//BACILLUS SP. (STRAIN TB-90).//Q07415
 F-PLACE1010811//CYTOCHROME C-551 (C551).//0.99:42:38//ECTOTHORHODOSPIRA HALOCHLORIS.//P38587
 F-PLACE1010833//CALTRACTIN, ISOFORM 1 (CENTRIN).//2.8e-09:90:34//HOMO SAPIENS (HUMAN).//P41208
 F-PLACE1010856//MOLT-INHIBITING HORMONE (MIH).//1.0:32:37//PROCAMBARUS CLARKII (RED SWAMP CRAYFISH).//P55848
 F-PLACE1010857//IG ALPHA-1 CHAIN C REGION.//0.49:73:34//GORILLA GORILLA GORILLA (LOWLAND GORILLA).//P20758
 F-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.2e-56:173:58//HOMO SAPIENS (HUMAN).//Q05481
 F-PLACE1010877//HEAT SHOCK PROTEIN 82.//0.13:130:25//ZEA MAYS (MAIZE).//Q08277
 F-PLACE1010891//HYPOTHETICAL 8.2 KD PROTEIN-IN BLTR-SPOIIC INTERGENIC REGION.//0.95:51:27//BACILLUS SUBTILIS.//P54436
 F-PLACE1010896//SERINE/THREONINE-PROTEIN KINASE PTK1/STK1 (EC 2.7.1.-).//0.98:71:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36002
 F-PLACE1010900//HYPOTHETICAL PROTEIN H10840.//1.0:42:30//HAEMOPHILUS INFLUENZAE.//P44897
 F-PLACE1010916//KERATIN, HIGH-SULFUR MATRIX PROTEIN, 11B3.//0.06:0:59:35//OVIS ARIES (SHEEP).//P02444
 F-PLACE1010917//E2 GLYCOPROTEIN PRECURSOR (SPIKE GLYCOPROTEIN) (PE PLONER PROTEIN).//0.71:141:24//BOVINE CORONAVIRUS (STRAIN L9).//P25191
 F-PLACE1010925//HYPOTHETICAL 8.1 KD PROTEIN.//1.0:17:58//THERMOPROTEUS TENAX VIRUS 1 (STRAIN KRA1) (TTV1).//P19285
 F-PLACE1010926//HYPOTHETICAL PROLINE-RICH PROTEIN KIAA0269.//0.01:1:51:45//HOMO SAPIENS (HUMAN).//Q92558
 F-PLACE1010942//EPIDERMAL GROWTH FACTOR RECEPTOR SUBSTRATE SUBSTRATE 15 (PROTEIN EPS15).//3.1e-09:64:37//MUS MUSCULUS (MOUSE).//P42567
 F-PLACE1010944//GAP JUNCTION ALPHA-3 PROTEIN (CONNEXIN 44) (CX44).//0.17:71:38//BOS TAURUS (BOVINE).//P41987
 F-PLACE1010947
 F-PLACE1010954//TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE.//0.011:44:26//HOMO SAPIENS (HUMAN).//P09493
 F-PLACE1010960//ACTIN-LIKE PROTEIN 13E.//1.1e-60:136:52//DROSOPHILA MELANOGASTER (FRUIT FLY).//P45890
 F-PLACE1010965
 F-PLACE1011026//PERIOD CLOCK PROTEIN (FRAGMENT).//1.0:64:31//DROSOPHILA ANANASSAE (FRUIT FLY).//Q03293
 F-PLACE1011032//RIBONUCLEASE HI (EC 3.1.26.4) (RNASE HI) (RIBONUCLEASE H) (RNASE H).//1.0:32:37//SALMONELLA TYPHIMURIUM.//P23329
 F-PLACE1011041//HOMEBOX PROTEIN VAB-7.//0.36:65:30//CAENORHABDITIS ELEGANS.//Q93899
 F-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 1 (EC 3.1.4.11) (PLC-BETA-1) (PHOSPHOLIPASE C-BETA-1) (PLC-1) (PLC-154).//1.3e-22:58:93//RATTUS NORVEGICUS (RAT).//P10687
 F-PLACE1011054//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//1.6e-07:38:73//HOMO SAPIENS (HUMAN).//P39195
 F-PLACE1011056//HISTONE H1.//2.2e-10:109:41//PISUM SATIVUM (GARDEN PEA).//P08283
 F-PLACE1011057
 F-PLACE1011090//HYPOTHETICAL 33.8 KD PROTEIN IN TWT1-FLOS INTERGENIC REGION.//1.8e-07:133:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38892
 F-PLACE1011109//ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEFG).//5.4e-25:63:88//RATTUS NORVEGICUS (RAT).//Q07803
 F-PLACE1011114//PUTATIVE ATP-DEPENDENT RNA HELICASE C1F7.02C.//8.4e-31:157:45//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q09916
 F-PLACE1011133//SERUM AMYLOID P-COMPONENT PRECURSOR (SAP) (9.55 ALPHA-1-GLYCOPROTEIN).//0.92:58:31//HOMO SAPIENS (HUMAN).//P02743
 F-PLACE1011143//PROBABLE E5 PROTEIN.//0.24:42:35//HUMAN PAPILLOMAVIRUS TYPE 31.//P17385
 F-PLACE1011160//EARLY NODULIN 55-2 PRECURSOR (N-55-2) (NODULIN-315).//0.88:98:27//GLYCINE MAX (SOYBEAN).//Q02917
 F-PLACE1011165//HISTIDINE-RICH PROTEIN.//0.013:13:76//PLASMODIUM FALCIPARUM (ISOLATE FCM17 / SENEGAL).//P14586
 F-PLACE1011185//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.4e-13:9:8:50//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE1011203
 F-PLACE1011214//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:4:8:27//EQUUS ASINUS (DONKEY).//P92479
 F-PLACE1011219//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).//1.9e-15:16:2:31//STREPTOMYCES ANTIBIOTICUS.//Q03326
 F-PLACE1011221//ANTITHROMBIN-III HOMOLOG.//0.84:74:33//FOWLPOX VIRUS (ISOLATE HP-438[MUNICH]).//P14369
 F-PLACE1011229//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN HOMOLOG).//3.5e-86:218:68//HOMO SAPIENS (HUMAN).//Q13107
 F-PLACE1011263//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NON ERYTHROID) (FRAGMENT).//3.0e-07:99:36//HOMO SAPIENS (HUMAN).//Q01485
 F-PLACE1011273
 F-PLACE1011291//PROTEIN KINASE C SUBSTRATE 80 KD PROTEIN (FRAGMENT S).//0.011:36:50//RATTUS NORVEGICUS (RAT).//P20468
 F-PLACE1011296//HOMEBOX PROTEIN DLX-6.//0.76:55:32//BRACHYDANIO ERIO (ZEBRAFISH) (ZEBRA DANIO).//Q98877
 F-PLACE1011310//ATP SYNTHASE PROTEIN 9, MITOCHONDRIAL (EC 3.6.1.3:4) (LIPID-BINDING PROTEIN).//0.46:43:44//PETUNIA SP. (PETUNIA).//Q07060
 F-PLACE1011325//HYPOTHETICAL 222.8 KD PROTEIN CIF3.06C IN CHROMOSOME 1.//0.00021:171:27//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10411
 F-PLACE1011332//DNA-DAMAGE-REPAIR/TOLERATION PROTEIN DRT101 PRECURSOR.//7.3e-27:113:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q05211
 F-PLACE1011340//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.6e-07:4:0:62//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE1011371//INTER-ALPHA-TRYPsin INHIBITOR HEAVY CHAIN H2 PRECURSOR (I1 HEAVY CHAIN H2).//2.2e-54:227:44//MUS MUSCULUS (MOUSE).//Q61703
 F-PLACE1011375//PROBABLE E5 PROTEIN.//0.93:28:57//HUMAN PAPILLOMAVIRUS TYPE 51.//P26553
 F-PLACE1011399//HISTONE H2B-IV.//0.19:129:27//VOLVOX CARTERI.//P16868
 F-PLACE1011419
 F-PLACE1011433//ZINC FINGER PROTEIN GLI3 (FRAGMENT).//3.4e-05:133:24//GALLUS GALLUS (CHICKEN).//P55879
 F-PLACE1011452//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//3.9e-25:76:63//HOMO SAPIENS (HUMAN).//P08547
 F-PLACE1011465//ECTODERMAL DYSPLASIA PROTEIN (EDA PROTEIN).//0.97:36:41//HOMO SAPIENS (HUMAN).//Q92838
 F-PLACE1011472//METALLOTHIONEIN-1 (CUNT-1).//0.084:55:30//HOMARUS AMERICANUS (AMERICAN LOBSTER).//P29499
 F-PLACE1011477//CELL SURFACE GLYCOPROTEIN 1 PRECURSOR (OUTER LAYER PROTEIN B) (S-LAYER PROTEIN 1).//0.028:129:34//CLOSTRIDIUM THERMOCELLUM.//Q06852
 F-PLACE1011492//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PRECURSOR (CTPT).//2.9e-13:147:31//BRASSICA OLERACEA (CAULIFLOWER).//P52178
 F-PLACE1011503//PUTATIVE FERREDOXIN-LIKE PROTEIN IN PURL-DPJ INTERGENIC REGION (086).//0.66:32:40//ESCHERICHIA COLI.//P52102
 F-PLACE1011520
 F-PLACE1011563//LORICRIN.//0.00023:112:39//HOMO SAPIENS (HUMAN).//P23490
 F-PLACE1011567//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//9.2e-31:78:76//HOMO SAPIENS (HUMAN).//P39195
 F-PLACE1011576//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.5e-32:45:86//HOMO SAPIENS (HUMAN).//Q05481
 F-PLACE1011586//N-TYPE CALCIUM CHANNEL ALPHA-1B SUBUNIT (OMEGA-CONOTOXIN-SENSITIVE N-TYPE, BRAIN CALCIUM CHANNEL ALPHA-1 SUBUNIT).//0.26:81:37//HOMO SAPIENS (HUMAN).//Q00975
 F-PLACE1011635//IMMEDIATE-EARLY PROTEIN IE18D.//0.00045:170:30//PSUDORABIES VIRUS (STRAIN INDIANA-FUNKHAUSER / BECKER) (PRV).//P11675
 F-PLACE1011641
 F-PLACE1011643//CUTICLE COLLAGEN 40.//1.0:128:32//CAENORHABDITIS ELEGANS.//P34804
 F-PLACE1011646//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-15:4:4:63//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE1011649//HYPOTHETICAL PROTEIN F-215.//0.48:106:34//HUMAN AD

【0691】

【表393】

ENOVIRUS TYPE 2.//P03291
 F-PLACE1011650
 F-PLACE1011664//CROOKED NECK PROTEIN.//1.2e-79:201:68//DROSOPHILA MELANOCASTER (FRUIT FLY).//P17886
 F-PLACE1011675//FERREDOXIN.//1.0:44:29//METHANOCOCCUS THERMOLITHOTROPHICUS.//P21305
 F-PLACE1011682//HYPOTHETICAL 7.0 KD PROTEIN IN RPS26A-COX4 INTERGENIC REGION.//1.0:40:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53098
 F-PLACE1011719//NEUROTOXIN TX2-6.//0.90:31:35//PHONEUTRIA NIGRIVENTER (BRAZILIAN ARMED SPIDER).//P29425
 F-PLACE1011725//NUCLEOBINDIN PRECURSOR (NUCB1) (BONE 63 KD CALCIUM-BINDING PROTEIN).//0.0065:125:25//RATTUS NORVEGICUS (RAT).//Q63083
 F-PLACE1011729//SRY-RELATED PROTEIN LG27 (FRAGMENT).//0.97:48:39//EUBLEPHARIS MACULARIUS.//P40654
 F-PLACE1011749
 F-PLACE1011762//D-BINDING PROTEIN (DBP) (ALBUMIN D BOX-BINDING PROTEIN).//0.028:91:39//MUS MUSCULUS (MOUSE).//Q60925
 F-PLACE1011778
 F-PLACE1011783//EMBRYONIC GROWTH/DIFFERENTIATION FACTOR 1 PRECURSOR (GDF-1).//0.97:48:43//MUS MUSCULUS (MOUSE).//P20863
 F-PLACE1011858//COLLAGEN 1(X) CHAIN PRECURSOR.//0.0027:154:33//BOSTAURUS (BOVINE).//P23206
 F-PLACE1011874//BACTERIOCHLOROPHYLL A PROTEIN (BCHL A PROTEIN) (BCP).//1.0:60:26//PROTHECOCHLORIS AESTUARII.//P11741
 F-PLACE1011875//HYPOTHETICAL 6.6 KD PROTEIN IN GP54-ALT INTERGENIC REGION.//0.99:34:35//BACTERIOPHAGE T4.//P39495
 F-PLACE1011891//SMOOTH ELIN.//0.018:122:31//HOMO SAPIENS (HUMAN).//P53814
 F-PLACE1011896//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//6.3e-09:203:35//XENOPUS LAEVIS (AFRICAN CLAWED FROG).//P17437
 F-PLACE1011922//CRYPTIDIN-RELATED PROTEIN 4C-2 PRECURSOR (CR54C).//0.067:37:48//MUS MUSCULUS (MOUSE).//P50715
 F-PLACE1011923//SERINE/THREONINE-PROTEIN KINASE SNK (EC 2.7.1.-) (SERUM INDUCIBLE KINASE).//1.5e-83:175:89//MUS MUSCULUS (MOUSE).//P53351
 F-PLACE1011962//MATING-TYPE PHEROMONE BAP1(2) PRECURSOR.//0.50:46:41//SCHIZOPHYLLUM COMMUNE (BRACKET FUNGUS).//Q02593
 F-PLACE1011964//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//1.6e-05:47:51//MYCTICEBUS COUCANG (SLOW LORIS).//P08548
 F-PLACE1011982//APICAL MEMBRANE ANTIGEN 1 PRECURSOR (MEZOZOITE SURFACE ANTIGEN).//0.98:83:31//PLASMODIUM FRAGILE.//P22622
 F-PLACE1011995
 F-PLACE1012031//HYPOTHETICAL PROTEIN KIAA0254.//0.032:62:33//HOMO SAPIENS (HUMAN).//Q92543
 F-PLACE2000003//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//5.4e-18:63:73//HOMO SAPIENS (HUMAN).//P39193
 F-PLACE2000006//ANHEXIN VII (SYNEXIN) (FRAGMENT).//0.14:20:50//BOSTAURUS (BOVINE).//P20072
 F-PLACE2000007//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.0045:176:30//MUS MUSCULUS (MOUSE).//P05143
 F-PLACE2000011//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.6e-25:57:78//HOMO SAPIENS (HUMAN).//P39194
 F-PLACE2000014//HYPOTHETICAL HELICASE C28H8.3 IN CHROMOSOME III.//0.00013:237:27//CAENORHABDITIS ELEGANS.//Q09475
 F-PLACE2000015//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.4e-33:60:80//HOMO SAPIENS (HUMAN).//P39193
 F-PLACE2000017//FOLATE RECEPTOR BETA PRECURSOR (FR-BETA) (FOLATE RECEPTOR 2) (FOLATE RECEPTOR, FETAL/PLACENTAL) (PLACENTAL FOLATE-BINDING PROTEIN) (FBP).//1.0:83:31//HOMO SAPIENS (HUMAN).//P14207
 F-PLACE2000021//EPHRAIN TYPE-A RECEPTOR 4 PRECURSOR (EC 2.7.1.112) (TYROSINE-PROTEIN KINASE RECEPTOR CEK8).//0.99:103:26//GALLUS GALLUS (CHICKEN).//Q07496
 F-PLACE2000030//MALE SPECIFIC SPERM PROTEIN MST84DA.//0.69:29:44//DROSOPHILA MELANOCASTER (FRUIT FLY).//Q01642
 F-PLACE2000033//PROBABLE OXIDOREDUCTASE (EC 1.-.-.-).//1.1e-05:74:41//STREPTOMYCES ANTIBIOTICUS.//Q03326
 F-PLACE2000034//AXONIN-1 PRECURSOR (AXONAL GLYCOPROTEIN TAG-1) (TRANSIENT AXONAL GLYCOPROTEIN 1).//6.7e-18:191:35//HOMO SAPIENS (HUMAN).//Q02246
 F-PLACE2000039//DYNEIN HEAVY CHAIN, CYTOSOLIC (DYHC) (MAP 1C).//4.7e-80:163:96//RATTUS NORVEGICUS (RAT).//P38650
 F-PLACE2000047//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//6.4e-06:63:49//HOMO SAPIENS (HUMAN).//P39191
 F-PLACE2000050//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//3.2e-22:74:64//HOMO SAPIENS (HUMAN).//P39192
 F-PLACE2000061
 F-PLACE2000062//GLUCOSE STARVATION-INDUCIBLE PROTEIN B (GENERAL STRESS PROTEIN B).//1.9e-06:108:37//BACILLUS SUBTILIS.//P26907
 F-PLACE2000072//ZINC FINGER PROTEIN 165.//3.5e-34:175:49//HOMO SAPIENS (HUMAN).//P49910
 F-PLACE2000097//RIBONUCLEASE PANCREATIC (EC 3.1.27.5) (RNASE 1) (RNASE A).//0.36:39:38//ONDATRA ZIBETHICUS (MUSKRAT).//P00681
 F-PLACE2000100
 F-PLACE2000103//TUBULIN ALPHA-4 CHAIN (FRAGMENTS).//0.18:32:37//ZEAMAYS (MAIZE).//P33626
 F-PLACE2000111//CNR35 ANTIGEN PRECURSOR.//0.056:107:27//HOMO SAPIENS (HUMAN).//Q08708
 F-PLACE2000115//DIAMINOPIMELATE EPIMERASE (EC 5.1.1.7) (DAP EPIMERASE) (FRAGMENT).//1.0:21:52//CLOSTRIDIUM PERFRINGENS.//Q46185
 F-PLACE2000124//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.4e-37:108:68//HOMO SAPIENS (HUMAN).//P39194
 F-PLACE2000132//PROBABLE MEMBRANE ANTIGEN GP85.//0.99:133:29//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03224
 F-PLACE2000136//VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 2 PRECURSOR (VIP-R-2) (PITUITARY ADENYLATE CYCLASE ACTIVATING POLYPEPTIDE TYPE III RECEPTOR) (PACAP TYPE III RECEPTOR) (PACAP-R-3).//0.83:65:32//MUS MUSCULUS (MOUSE).//P41588
 F-PLACE2000140
 F-PLACE2000164//TIPD PROTEIN.//5.7e-12:190:28//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//Q15736
 F-PLACE2000170//BACTERIOCIN CARNOBACTERIOCIN BMI PRECURSOR (CARNOBACTERIOCIN BI).//1.0:30:26//CARNOBACTERIUM PISCICOLA.//P38579
 F-PLACE2000172
 F-PLACE2000176//HYPOTHETICAL PROTEIN AF0526.//0.76:44:43//ARCHAEOGLOBUS FULGIDUS.//Q02974
 F-PLACE2000187//EEN-LIKE PROTEIN GE46.//0.84:42:35//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//Q02973
 F-PLACE2000216
 F-PLACE2000223//NEUROTOXIN III (LQX III).//0.99:38:34//LEIURUS QUINQUESTRIATUS QUINQUESTRIATUS (EGYPTIAN SCORPION).//P01487
 F-PLACE2000235
 F-PLACE2000246//RING CANAL PROTEIN (KELCH PROTEIN).//5.1e-37:121:42//DROSOPHILA MELANOCASTER (FRUIT FLY).//Q04652
 F-PLACE2000264//!!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!!!//2.4e-05:77:42//HOMO SAPIENS (HUMAN).//P39191
 F-PLACE2000274//DYNEIN BETA CHAIN, CILIARY.//5.3e-46:232:45//TRIPN EUSTES GRATILLA (HAWAIIAN SEA URCHIN).//P23098
 F-PLACE2000302//TRICHOHYALIN.//1.5e-06:215:29//ORYCTOLAGUS CUNICULUS (RABBIT).//P37709
 F-PLACE2000305//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//5.3e-06:33:66//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE2000317//TOXIN C13S1C1 PRECURSOR.//0.44:45:33//DENDROASPIS ANGSTICEPS (EASTERN GREEN MAMBA).//P18329
 F-PLACE2000335//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//7.9e-08:35:71//HOMO SAPIENS (HUMAN).//P39195
 F-PLACE2000341//SODIUM/GLUCOSE COTRANSORTER 1 (NA(+)/GLUCOSE COTRANSORTER 1) (HIGH AFFINITY SODIUM-GLUCOSE COTRANSORTER).//0.014:141:24//ORYCTOLAGUS CUNICULUS (RABBIT).//P11170
 F-PLACE2000342//HYPOTHETICAL 24.1 KD PROTEIN IN LEF4-P33 INTERGENIC REGION.//5.7e-09:96:38//AUTOGRAPH A CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACNPV).//P41479
 F-PLACE2000347//ZINC FINGER PROTEIN 177.//5.9e-05:49:53//HOMO SAPIENS (HUMAN).//Q13360
 F-PLACE2000359//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.5e-10:69:52//HOMO SAPIENS (HUMAN).//P39194
 F-PLACE2000366
 F-PLACE2000371//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUSIAN ATROPHY PROTEIN).//1.5e-05:216:29//HOMO SAPIENS (HUMAN).//P54259
 F-PLACE2000373//MAX BINDING PROTEIN MMT (ROX PROTEIN) (MYC ANTAGONIST MMT).//0.27:63:33//HOMO SAPIENS (HUMAN).//Q99583
 F-PLACE2000379//HYPOTHETICAL GENE 1 PROTEIN.//0.72:120:31//EQUINE HERPESVIRUS TYPE 1 (STRAIN AB4P) (EHV-1).//P28978
 F-PLACE2000394//BASIC PROLINE-RICH PEPTIDE P-E (18-9).//0.95:40:42//HOMO SAPIENS (HUMAN).//P02811
 F-PLACE2000398//RIBONUCLEASE PRECURSOR (EC 3.1.27.-).//0.88:88:31//AEROMONAS HYDROPHILA.//Q07465
 F-PLACE2000399//T-CELL SURFACE GLYCOPROTEIN E2 PRECURSOR (E2 ANTIGEN) (CD99) (MIC2 PROTEIN) (I2E7).//7.6e-16:180:39//HOMO SAPIENS (HUMAN).//P14209
 F-PLACE2000404//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE-TRNA LIGASE) (LEURS).//1.7e-94:243:64//CAENORHABDITIS ELEGANS.//Q09996
 F-PLACE2000411//SERINE/THREONINE PROTEIN PHOSPHATASE 5 (EC 3.1.3.16) (PP5) (PROTEIN PHOSPHATASE T) (PPT) (FRAGMENT).//1.2e-09:78:39//MUS MUSCULUS (MOUSE).//Q60676
 F-PLACE2000419//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.6e-20:61:62//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE2000425//HYPOTHETICAL 11.9 KD PROTEIN IN MSB2-UGA1 INTERGEN

【0692】

【表394】

IC REGION.//0.98:75:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53211
 F-PLACE2000427//INSULIN PRECURSOR.//0.98:55:34//CERCOPITHECUS AETHIOPS (GREEN MONKEY) (GRIVET).//P30407
 F-PLACE2000433//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//7.5e-07:65:50//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE2000435
 F-PLACE2000438//HYPOTHETICAL 67.9 KD PROTEIN ZK688.8 IN CHROMOSOME 111.//4.7e-66:178:47//CAENORHABDITIS ELEGANS.//P34678
 F-PLACE2000450//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//2.1e-23:88:62//HOMO SAPIENS (HUMAN).//P39195
 F-PLACE2000455//TOXIN II (TOXIN II.10.9.2) (FRAGMENT).//0.093:18:44//CENTRURIOIDES LIMPIDUS LIMPIDUS (MEXICAN SCORPION).//P45630
 F-PLACE2000458//ADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT P ROTEIN).//3.1e-23:165:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P33450
 F-PLACE2000465//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.6e-23:73:63//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE2000477//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.4e-37:90:78//HOMO SAPIENS (HUMAN).//P39194
 F-PLACE2000004//EYES ABSENT HOMOLOG 3.//1.1e-09:27:100//MUS MUSCULUS (MOUSE).//P97480
 F-PLACE2000009//PUTATIVE CUTICLE COLLAGEN C9G5.6.//0.0061:148:34//CAENORHABDITIS ELEGANS.//Q09457
 F-PLACE2000020//ADENYLATE CYCLASE, OLFACTORY TYPE (EC 4.6.1.1) (TYPE III) (ATP PYROPHOSPHATE-LYASE) (ADENYLATE CYCLASE).//8.8e-93:193:92//RATTUS NORVEGICUS (RAT).//P21932
 F-PLACE2000029//50S RIBOSOMAL PROTEIN L31E.//0.15:50:38//METHANOCOCCUS JANNASCHII.//P54009
 F-PLACE2000059//TCP1-CHAPERONIN COFACTOR A.//0.96:50:34//BOS TAURUS (BOVINE).//P48427
 F-PLACE2000070//HYPOTHETICAL 17.1 KD PROTEIN IN PURS 3' REGION.//0.29:22:59//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38898
 F-PLACE2000103//LYSIS PROTEIN (E PROTEIN) (GPE).//0.99:53:32//BACTERIOPHAGE ALPHA-3.//P31280
 F-PLACE2000119//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//5.4e-41:87:78//HOMO SAPIENS (HUMAN).//P39189
 F-PLACE2000121//VESICULAR TRAFFIC CONTROL PROTEIN SEC15.//1.0e-07:269:22//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P22224
 F-PLACE2000124//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.2e-29:97:73//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE2000136//PARS INTERCEREBRALIS MAJOR PEPTIDE D1 (PMP-D1).//0.77:26:42//LOCUSTA MIGRATORIA (MIGRATORY LOCUST).//P80059
 F-PLACE2000142//HYPOTHETICAL 7.1 KD PROTEIN IN MAD2 3' REGION (ORF 63).//0.82:34:41//MARCHANTIA POLYMORPHA (LIVERWORT).//P38468
 F-PLACE2000145//TENSIN.//3.5e-91:238:74//GALLUS GALLUS (CHICKEN).//Q04205
 F-PLACE2000147//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.4e-30:61:65//HOMO SAPIENS (HUMAN).//P39194
 F-PLACE2000148//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-). REVERSE TRANSCRIPTASE (EC 2.7.7.49): ENDONUCLEASE].//1.4e-18:226:34//GIBBON APE LEUKEMIA VIRUS.//P21414
 F-PLACE2000155//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//0.00014:107:33//ZEA MAYS (MAIZE).//P14918
 F-PLACE2000156//POL POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-). REVERSE TRANSCRIPTASE (EC 2.7.7.49): ENDONUCLEASE].//2.7e-19:169:30//BABOON ENDOGENOUS VIRUS (STRAIN W7).//P10272
 F-PLACE2000157//PROBABLE SERINE/THREONINE-PROTEIN KINASE CY50.16 (EC 2.7.1.-).//0.0061:92:30//MYCOBACTERIUM TUBERCULOSIS.//Q11053
 F-PLACE2000158//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!//5.7e-49:56:80//HOMO SAPIENS (HUMAN).//P39189
 F-PLACE2000160//DNA TRANSFORMATION PROTEIN TFOX (COMPETENCE ACTIVATOR) (PROTEIN SX).//0.39:94:34//HAEMOPHILUS INFLUENZAE.//P43779
 F-PLACE2000169//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//5.6e-28:99:59//HOMO SAPIENS (HUMAN).//P39193
 F-PLACE2000194//PROLINE-RICH PROTEIN LAS17.//0.91:80:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q12446
 F-PLACE2000197//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//0.24:119:32//GALLUS GALLUS (CHICKEN).//P16053
 F-PLACE2000199//EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN).//0.76:87:37//NICOTIANA TABACUM (COMMON TOBACCO).//P13983
 F-PLACE2000207//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//4.5e-09:32:78//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE2000208
 F-PLACE2000218//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.2e-34:96:70//HOMO SAPIENS (HUMAN).//P39194
 F-PLACE2000220//OSTEOCALCIN (GAMMA-CARBOXYGLUTAMIC ACID-CONTAINING PROTEIN) (BONE GLA- PROTEIN) (BGP).//0.46:13:53//CANIS FAMILIARIS

(DOG).//P81455

F-PLACE2000221//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.8e-24:178:45//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE2000226//30S RIBOSOMAL PROTEIN S18.//0.98:38:34//WEISSERIA GONORRHOEA.//Q07815
 F-PLACE2000230//METALLOTHIONEIN (MT).//0.97:25:48//OREOCHROMIS MOS SAMBICUS (MOZAMBIQUE TILAPIA) (TILAPIA MOSSAMBICA).//P52726
 F-PLACE2000242//MELANOMA-ASSOCIATED ANTIGEN 8 (MAGE-8 ANTIGEN).//8.0e-21:121:39//HOMO SAPIENS (HUMAN).//P43361
 F-PLACE2000244//PROTEIN TSC24 (MEIOTIC CHECK POINT REGULATOR).//2.3e-125:264:87//MUS MUSCULUS (MOUSE).//P53995
 F-PLACE2000254//RTOA PROTEIN (RAT10-A).//0.99:142:23//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P54681
 F-PLACE2000271//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.2e-12:63:53//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE2000276//COLLAGEN ALPHA 1(VIII) CHAIN PRECURSOR (ENDOTHELIAL COLLAGEN).//1.0:55:38//HOMO SAPIENS (HUMAN).//P27658
 F-PLACE2000304//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.0028:31:54//HOMO SAPIENS (HUMAN).//P30808
 F-PLACE2000310//ATROPHIN-1 (DENTATORUBRAL-PALLIDOLUTSIAN ATROPHY PROTEIN).//0.98:82:34//RATTUS NORVEGICUS (RAT).//P54258
 F-PLACE2000320
 F-PLACE2000322//GLYCINE-RICH CELL WALL STRUCTURAL PROTEIN 1 PRECURSOR.//2.2e-22:61:52//ORYZA SATIVA (RICE).//P25074
 F-PLACE2000331//SMALL PROLINE-RICH PROTEIN II (SPR-II) (CLONE 174 N).//0.32:15:53//HOMO SAPIENS (HUMAN).//P22532
 F-PLACE2000339//CHORION PROTEIN S19.//0.34:89:37//DROSOPHILA VIRILIS (FRUIT FLY).//P24516
 F-PLACE2000341//NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 (EC 1.6.5.3) (FRAGMENT).//1.0:47:38//COTURNIX COTURNIX JAPONICA (JAPANESE QUAIL).//P24968
 F-PLACE2000350//SERINE/THREONINE-PROTEIN KINASE SULKU (EC 2.7.1.-).//3.9e-50:168:60//CAENORHABDITIS ELEGANS.//P46549
 F-PLACE2000352//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.8e-29:76:71//HOMO SAPIENS (HUMAN).//P39194
 F-PLACE2000353//POLYPEPTIDE N-ACETYL GALACTOSAMINYLTRANSFERASE (EC 2.4.1.41) (PROTEIN- UOP ACETYL GALACTOSAMINYLTRANSFERASE) (UOP-GALNAC-POLYPEPTIDE, N- ACETYL GALACTOSAMINYLTRANSFERASE) (GALNAC-TI).//3.0e-09:102:41//HOMO SAPIENS (HUMAN).//Q10472
 F-PLACE2000362//HYPOTHETICAL PROTEIN TP0064.//1.0:75:26//TREPONEMA PALLIDUM.//Q03103
 F-PLACE2000363//METALLOTHIONEIN (MT).//0.067:42:33//ASTACUS FLUVIA TILIS (BROAD-FINGERED CRAYFISH) (ASTACUS ASTACUS).//P55951
 F-PLACE2000365//LYSIS PROTEIN (E PROTEIN) (GPE).//1.0:65:27//BACTERIOPHAGE PHI-K.//Q38040
 F-PLACE2000373//RETROVIRUS-RELATED ENV POLYPROTEIN.//1.5e-18:90:47//HOMO SAPIENS (HUMAN).//P10267
 F-PLACE2000388
 F-PLACE2000399//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//6.3e-45:60:75//HOMO SAPIENS (HUMAN).//P39193
 F-PLACE2000400
 F-PLACE2000401//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//3.6e-09:46:73//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE2000402//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//0.036:43:44//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE2000405//POSTERIOR PITUITARY PEPTIDE.//0.70:25:40//BOS TAURUS (BOVINE).//P01154
 F-PLACE2000406//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//4.3e-09:49:67//HOMO SAPIENS (HUMAN).//P39195
 F-PLACE2000413//MALE SPECIFIC SPERM PROTEIN MST87F.//0.12:42:40//DROSOPHILA MELANOGASTER (FRUIT FLY).//P08175
 F-PLACE2000416//CYCLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//0.67:23:6:21//BOS TAURUS (BOVINE).//P35662
 F-PLACE2000425//PROLINE-RICH PEPTIDE P-8.//0.45:19:42//HOMO SAPIENS (HUMAN).//P02814
 F-PLACE2000455//AMELOCENIN, CLASS I PRECURSOR.//0.0073:81:43//BOS TAURUS (BOVINE).//P02817
 F-PLACE2000475//8.6 KD TRANSGLUTAMINASE SUBSTRATE.//1.0:53:32//TACHYLEUS TRIDENTATUS (JAPANESE HORSESHOE CRAB).//P01281
 F-PLACE2000477//MUSCARINIC TOXIN 7 (MT-7).//0.13:55:32//DENDROASPIS ANGSTICEPS (EASTERN GREEN MAMBA).//P09070
 F-PLACE2000009//MYOSIN HEAVY CHAIN, SMOOTH MUSCLE ISOFORM (SMHC) (FRAGMENT).//7.0e-19:180:27//HOMO SAPIENS (HUMAN).//P35749
 F-PLACE2000014//X-LINKED HELICASE II (X-LINKED NUCLEAR PROTEIN) (XNP).//3.2e-15:193:30//HOMO SAPIENS (HUMAN).//P46100
 F-PLACE2000034//BRIDE OF SEVENLESS PROTEIN PRECURSOR.//0.0024:97:29//DROSOPHILA MELANOGASTER (FRUIT FLY).//P22815
 F-PLACE2000049//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.0e-32:79:75//HOMO SAPIENS (HUMAN).//P39194
 F-PLACE2000052//ATP-BINDING CASSETTE TRANSPORTER 1.//2.2e-99:178:9

【0693】

【表395】

7//MUS MUSCULUS (MOUSE).//P41233
 F-PLACE4000063//IMMEDIATE-EARLY PROTEIN.//0.0017:159:25//HERPESVIRUS SAIMIRI (STRAIN 11).//Q01042
 F-PLACE4000089
 F-PLACE4000093
 F-PLACE4000100//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-14:6
 8:60//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE4000106//1A PROTEIN [CONTAINS: HELICASE: METHYLTRANSFERASE
].//1.0:45:41//BROAD BEAN WATTLE VIRUS.//Q00020
 F-PLACE4000128//HYPOTHETICAL PROTEIN E-115.//0.00020:101:30//HUMAN
 ADENOVIRUS TYPE 2.//P03290
 F-PLACE4000129//CORNIFIN B (SMALL PROLINE-RICH PROTEIN 1B) (SPR-1
 B) (14.9 KD PANCORNULIN).//0.15:57:31//HOMO SAPIENS (HUMAN).//P225
 28
 F-PLACE4000131
 F-PLACE4000147//COMPETENCE PHEROMONE PRECURSOR.//1.0:45:24//BACILLUS
 SUBTILIS.//P45453
 F-PLACE4000156//ZINC FINGER PROTEIN 136.//2.1e-88:194:59//HOMO SAPIENS
 (HUMAN).//P52737
 F-PLACE4000192//ZINC FINGER PROTEIN 142 (K1AA0236) (HA4654).//0.08
 3:148:26//HOMO SAPIENS (HUMAN).//P52746
 F-PLACE4000211//CALPHOTIN.//0.20:43:39//DROSOPHILA MELANOGASTER (FRUIT
 FLY).//Q02910
 F-PLACE4000222//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.1e-05:2
 0:85//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE4000230//DIHYDROFOLATE REDUCTASE (EC 1.5.1.3) / THYMIDYLATE
 SYNTHASE (EC 2.1.1.45) (DHFR-TS).//1.0:96:28//TRYPANOSOMA BRUCEI
 BRUCEI.//Q27783
 F-PLACE4000233
 F-PLACE4000247//METALLOTHIONEIN (MT).//1.0e-05:34:41//PLEUROMECTES
 PLATESSA (PLAICE).//P07216
 F-PLACE4000250//VPU PROTEIN (ORF-X PROTEIN) (UPX PROTEIN).//0.99:3
 3:42//CAPRINE ARTHRITIS ENCEPHALITIS VIRUS (CAEV).//P31834
 F-PLACE4000252//MALE SPECIFIC SPERM PROTEIN MST840B.//0.42:24:45//
 DROSOPHILA MELANOGASTER (FRUIT FLY).//Q01643
 F-PLACE4000259//PRE-MRNA SPLICING HELICASE BRR2 (EC 3.6.1.-).//3.5
 e-09:189:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32639
 F-PLACE4000261//PEREGRIN (BR140 PROTEIN).//5.0e-11:103:37//HOMO SAPIENS
 (HUMAN).//P55201
 F-PLACE4000269//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.0
 37:181:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25386
 F-PLACE4000270//COAGULATION FACTOR VII PRECURSOR (EC 3.4.21.21).//
 1.0:46:39//MUS MUSCULUS (MOUSE).//P70375
 F-PLACE4000300//50S RIBOSOMAL PROTEIN L32.//0.81:28:46//THERMUS AQUATICUS
 (SUBSP. THERMOPHILUS).//P80339
 F-PLACE4000320//PKBP-RAPAMYCIN ASSOCIATED PROTEIN (FRAP) (RAPAMYCIN
 TARGET PROTEIN).//1.6e-29:44:93//HOMO SAPIENS (HUMAN).//P42345
 F-PLACE4000323
 F-PLACE4000326//PARATHYROSIN.//0.0018:54:48//HOMO SAPIENS (HUMAN).
 //P20962
 F-PLACE4000344//EPIDERMAL GROWTH FACTOR (EGF) (FRAGMENT).//0.97:2
 8:42//SUS SCROFA (PIC).//Q00968
 F-PLACE4000367//NEUROTOXIN 1 (TOXIN SHP-1) (SHNA) (NEUROTOXIN SHI
).//1.0:33:36//STOICHAETIS HELIANTHUS (CARRIBEAN SEA ANEMONE) (STI
 CHODACTYLA HELIANTHUS).//P19651
 F-PLACE4000369//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN).//
 0.071:42:42//SORGHUM VULGARE (SORGHUM).//P24152
 F-PLACE4000379//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//1.4e-16:
 54:77//HOMO SAPIENS (HUMAN).//P39193
 F-PLACE4000387//PHOTOSYSTEM II 4 KD REACTION CENTRE PROTEIN PRECURSOR.
 //0.25:21:52//HORDEUM VULGARE (BARLEY). AND SECALE CEREALE (RYE).
 //P25877
 F-PLACE4000392//FERROCHELATASE (EC 4.99.1.1) (PROTOHEME FERRO-LYASE)
 (HEME SYNTHETASE) (FRAGMENT).//0.91:36:50//YERSINIA PSEUDOTUBERCULOSIS.
 //Q05338
 F-PLACE4000401//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//4.4e-29:
 96:67//HOMO SAPIENS (HUMAN).//P39194
 F-PLACE4000411//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.3e-18:4
 1:73//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE4000431//PRE-MRNA SPLICING HELICASE BRR2 (EC 3.6.1.-).//5.4
 e-21:237:33//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32639
 F-PLACE4000445//HYPOTHETICAL 99.7 KD PROTEIN IN SOL1 5' REGION PRECURSOR.
 //0.00081:210:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//
 P40442
 F-PLACE4000450//TRANSCRIPTION FACTOR HBP-1A (HISTONE-SPECIFIC TRANSCRIPTION
 FACTOR HBP1).//0.020:87:33//TRITICUM AESTIVUM (WHEAT).//
 P23922
 F-PLACE4000465//METALLOTHIONEIN-IL (MT-IL) (MT1X).//0.20:18:38//HOMO
 SAPIENS (HUMAN).//P80297
 F-PLACE4000487//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//1.5e-19:7
 3:52//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE4000489
 F-PLACE4000494//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//0.1
 7:130:30//MUS MUSCULUS (MOUSE).//Q03173
 F-PLACE4000521//RETROVIRUS-RELATED POLYPROTEIN [CONTAINS: REVERSE
 TRANSCRIPTASE (EC 2.7.7.49): ENDONUCLEASE] (FRAGMENT).//3.0e-0
 5:50:36//MUS MUSCULUS (MOUSE).//P10400
 F-PLACE4000522//NEUROGENIC LOCUS NOTCH HOMOLOG PROTEIN 1 PRECURSOR
 R.//1.8e-45:231:47//RATTUS NORVEGICUS (RAT).//Q07008
 F-PLACE4000548//CYTOCHROME C-551 (C551).//0.96:50:34//ECTOTHORHOD
 OSPIRA HALOPHILA.//P00122
 F-PLACE4000558//PROBABLE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE FAF
 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE FAF) (UBIQUITIN-SPECIFIC
 PROCESSING PROTEASE FAF) (DEUBIQUITINATING ENZYME FAF) (FAT FACETS
 PROTEIN).//1.6e-28:223:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//P
 55824
 F-PLACE4000581//P-SELECTIN PRECURSOR (GRANULE MEMBRANE PROTEIN 14
 0) (GMP-140) (PADGEM) (CD62P) (LEUKOCYTE-ENDOTHELIAL CELL ADHESION
 MOLECULE 3) (LECAM3).//9.7e-11:166:28//HOMO SAPIENS (HUMAN).//P16
 109
 F-PLACE4000590//POLYPROTEIN [CONTAINS: PROTEASE (EC 3.4.23.-):
 REVERSE TRANSCRIPTASE (EC 2.7.7.49): ENDONUCLEASE].//1.6e-17:134:
 35//GIBBON APE LEUKEMIA VIRUS.//P21414
 F-PLACE4000593//GONADOTROPIN-RELEASING HORMONE RECEPTOR (GNRH-R).//
 1.0:54:29//RATTUS NORVEGICUS (RAT).//P30969
 F-PLACE4000612//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15: INNER
 COAT PROTEIN P12: CORE SHELL PROTEIN P30].//2.6e-14:221:32//MOLOMYRIS
 SARCOMA VIRUS (STRAIN TS110).//P32594
 F-PLACE4000638//HYPOTHETICAL 9.3 KD PROTEIN IN NR0B-INAA INTERGENIC
 REGION.//0.65:37:40//ESCHERICHIA COLI.//P37910
 F-PLACE4000650//ZINC FINGER PROTEIN 16 (ZINC FINGER PROTEIN K0X9)
 (FRAGMENT).//1.0:33:33//HOMO SAPIENS (HUMAN).//P17020
 F-PLACE4000654
 F-PLACE4000670//HYPOTHETICAL 44.1 KD PROTEIN IN RPBS-CDC28 INTERGENIC
 REGION.//1.6e-07:161:25//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).
 //P33313
 F-PLACE4000681//PUTATIVE IMPORTIN BETA-4 SUBUNIT (KARYOPHERIN BETA-4
 SUBUNIT).//7.4e-15:223:31//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).
 //P06100
 F-PLACE4000683//TRANSCRIPTION FACTOR BF-2 (BRAIN FACTOR 2) (BF2)
 (CBF-2) (T-14-6).//0.0013:128:35//GALLUS GALLUS (CHICKEN).//Q98937
 F-PLACE4000684//CUTICLE COLLAGEN 1.//0.0010:154:33//CAENORHABDITIS
 ELEGANS.//P08124
 F-PLACE4000685//CALPAIN 2. LARGE [CATALYTIC] SUBUNIT (EC 3.4.22.17)
 (CALCIUM-ACTIVATED NEUTRAL PROTEINASE) (CAMP) (M-TYPE).//3.2e-4
 1:87:98//HOMO SAPIENS (HUMAN).//P17655
 F-PLACE4000691//NTAK PROTEIN (NEURAL AND THYMUS-DERIVED ACTIVATOR
 FOR ERBB KINASES).//0.0032:154:35//HOMO SAPIENS (HUMAN).//Q14511
 F-PLACE4000692//PUTATIVE PYRIDOXALINE 5'-PHOSPHATE OXIDASE (EC 1.
 4.3.5) (PMP/PMP OXIDASE).//1.6e-23:124:37//CAENORHABDITIS ELEGANS.
 //Q20939
 F-PLACE4000693//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//3.0e-13:
 54:66//HOMO SAPIENS (HUMAN).//P39192
 F-PLACE4000694//HYPOTHETICAL 10.4 KD PROTEIN.//0.16:44:34//HEPATITIS
 B VIRUS (SUBTYPE AYV).//P03163
 F-PLACE4000695//CAMPATH-1 ANTIGEN PRECURSOR (CD52 ANTIGEN) (CD52)
 (CAMBRIDGE PATHOLOGY 1 ANTIGEN).//0.83:59:37//MACACA FASCICULARIS
 (CRAB EATING MACAQUE) (CYNOMOLGUS MONKEY).//P32763
 F-PLACE4000696//60S RIBOSOMAL PROTEIN L37 (FRAGMENT).//0.25:23:39//
 BOS TAURUS (BOVINE).//P79244
 F-PLACE4000697//HYPOTHETICAL 29.3 KD PROTEIN (ORF92).//2.3e-11:13
 3:36//ORGYIA PSEUDOTSUGATA MULTICAPSID POLYHEDROSIS VIRUS (OPMV)
).//Q10341
 F-PLACE4000698//C-PROTEIN. SKELETAL MUSCLE SLOW-ISOFORM.//1.5e-14:
 205:29//HOMO SAPIENS (HUMAN).//Q00872
 F-PLACE4000699
 F-PLACE4000700//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//
 0.063:59:33//HOMO SAPIENS (HUMAN).//P49901
 F-PLACE4000701
 F-PLACE4000702//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.0e-58:11
 0:67//NYCTICEBUS COUCANG (SLOW LORIS).//P08548
 F-PLACE4000703//SPLICEDSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A6)
 6).//2.6e-06:134:35//MUS MUSCULUS (MOUSE).//Q62203
 F-PLACE4000704//TENECIN 3 PRECURSOR.//0.047:76:35//TENEbrio MOLTIO
 R (YELLOW MEALWORM).//Q27270
 F-PLACE4000705//FIBROSIN (FRAGMENT).//0.35:43:34//MUS MUSCULUS (MOUSE).
 //Q60791
 F-PLACE4000706//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//8.7e-14:1
 04:42//HOMO SAPIENS (HUMAN).//P39188
 F-PLACE4000707

【0694】

【表396】

F-THYR01000163//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/3.7e-20: 71:71//HOMO SAPIENS (HUMAN).//P39189
 F-THYR01000173//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//6.7e-88:216:76//MUS MUSCULUS (MOUSE).//P35585
 F-THYR01000186//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/2.9e-24: 72:77//HOMO SAPIENS (HUMAN).//P39192
 F-THYR01000187
 F-THYR01000190//PROTEIN TRANSPORT PROTEIN SEC61 BETA 2 SUBUNIT.//0.060:50:42//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P52871
 F-THYR01000197
 F-THYR01000199//HYPOTHETICAL 49.8 KD PROTEIN D2007.5 IN CHROMOSOME 111.//2.0e-06:88:35//CAENORHABDITIS ELEGANS.//P34379
 F-THYR01000206
 F-THYR01000221
 F-THYR01000241//HYPOTHETICAL 11.8 KD PROTEIN IN H655-PK2 INTERGENIC REGION.//1.0:51:35//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACNPV).//P41661
 F-THYR01000242//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//7.4e-37:137:36//HOMO SAPIENS (HUMAN).//P51523
 F-THYR01000253//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.11:21:52//HOMO SAPIENS (HUMAN).//P30808
 F-THYR01000270//WDM1 PROTEIN PRECURSOR.//0.40:52:32//MUS MUSCULUS (MOUSE).//Q62477
 F-THYR01000279//BETA CRYSTALLIN A4.//0.97:64:26//BOS TAURUS (BOVIN E).//P11842
 F-THYR01000288//POTENTIAL CAAX PRENYL PROTEASE 1 (EC 3.4.24.-) (PRENYL PROTEIN-SPECIFIC ENDOPEPTASE 1) (PPSEP 1).//3.4e-48:142:42//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10071
 F-THYR01000320//ZINC FINGER PROTEIN 14 (ZFP-14) (KROX-9 PROTEIN) (FRAGMENT).//0.87:35:45//MUS MUSCULUS (MOUSE).//P10755
 F-THYR01000327//HYPOTHETICAL 64.7 KD PROTEIN F26E4.11 IN CHROMOSOME 1.//0.00010:75:26//CAENORHABDITIS ELEGANS.//P90859
 F-THYR01000343//CHROMOGRAIN A PRECURSOR (CGA) [CONTAINS: PANCREAS TATIN; BETA-CRANIN; WE-14].//0.88:107:26//MUS MUSCULUS (MOUSE).//P26339
 F-THYR01000358//SELENIUM-BINDING LIVER PROTEIN.//4.6e-25:49:81//MUS MUSCULUS (MOUSE).//P17563
 F-THYR01000368//LOCOMOTION-RELATED PROTEIN MIKARU GENKI PRECURSOR.//1.0:136:26//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q09101
 F-THYR01000381//GAG POLYPROTEIN [CONTAINS: CORE PROTEIN P15; INNER COAT PROTEIN P12; CORE SHELL PROTEIN P30; NUCLEOPROTEIN P10].//0.032:99:35//SIMIAN SARCOMA VIRUS.//P03330
 F-THYR01000387//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//0.90: 46:30//HALICHERUS GRYPUS (GRAY SEAL).//P38592
 F-THYR01000394//SMALL PROLINE RICH PROTEIN 11 (SPR-11) (CLONE 930).//0.00019:48:37//HOMO SAPIENS (HUMAN).//P22531
 F-THYR01000395//RING CANAL PROTEIN (KELCH PROTEIN).//1.2e-33:186:3 8//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
 F-THYR01000401//50S RIBOSOMAL PROTEIN L7/L12 (FRAGMENT).//0.57:67: 31//STAPHYLOCOCCUS AUREUS.//P48860
 F-THYR01000438//ATP SYNTHASE PROTEIN 8 (EC 3.6.1.34) (A6L).//1.0:4 2:38//STRONGYLOCENTROTUS PURPURATUS (PURPLE SEA URCHIN).//P15997
 F-THYR01000452//BACTERIOCIN CARNOBACTERIOCIN A PRECURSOR (PISCICOL IN 61).//0.31:34:44//CARNOBACTERIUM PISCICOLA.//P38578
 F-THYR01000471//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.1e-31: 94:72//HOMO SAPIENS (HUMAN).//P39194
 F-THYR01000484//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/5.9e-08: 30:86//HOMO SAPIENS (HUMAN).//P39195
 F-THYR01000488//EARLY NODULIN 55-2 PRECURSOR (N-55-2) (NODULIN-31 5).//0.93:98:27//GLYCINE MAX (SOYBEAN).//Q02917
 F-THYR01000501//DOWN REGULATORY PROTEIN OF INTERLEUKIN 2 RECEPTOR.//2.4e-51:198:50//MUS MUSCULUS (MOUSE).//P15533
 F-THYR01000502//HUNCHBACK PROTEIN (FRAGMENT).//0.84:41:43//APIS ME LLIFERA (HONEYBEE).//P31504
 F-THYR01000505//HYPOTHETICAL BHLF1 PROTEIN.//0.99:231:33//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
 F-THYR01000558//ANTITHROMBIN-III PRECURSOR (ATIII) (FRAGMENT).//0. 47:58:37//GALLUS GALLUS (CHICKEN).//Q03352
 F-THYR01000569//COLLAGEN ALPHA 1(I) CHAIN (FRAGMENTS).//0.00048:6 4:42//RATTUS NORVEGICUS (RAT).//P02454
 F-THYR01000570//HYPOTHETICAL 11.6 KD PROTEIN IN ACS1-GCV3 INTERGEN IC REGION.//0.94:61:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).// P39725
 F-THYR01000585//SPLICING FACTOR, ARGININE/SERINE-RICH 6 (PRE-MRNA SPLICING FACTOR SRP55).//0.050:104:36//HOMO SAPIENS (HUMAN).//Q132 47
 F-THYR01000596//INFECTED CELL PROTEIN ICP34.5 (NEUROVIRULENCE FACT OR ICP34.5).//0.99:37:40//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN MG H-10).//P37319
 F-THYR01000602//EAMZP30-47 PROTEIN (FRAGMENT).//0.88:61:34//EIMERI A ACERVULINA.//P21959
 F-THYR01000605//SUPPRESSOR PROTEIN SRP40.//0.0016:116:26//SACCHAR OMYES CEREVISIAE (BAKER'S YEAST).//P32583
 F-THYR01000625//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.4e-33: 88:78//HOMO SAPIENS (HUMAN).//P39194
 F-THYR01000637//METALLOTHIONEIN A (MT A).//1.0:23:43//SPARUS AURAT A (GILTHEAD SEA BREAM).//P52727
 F-THYR01000641//PHOTOSYSTEM 11 10 KD PHOSPHOPROTEIN.//0.99:26:46// CYANIDIUM CALDARIUM (GALDIERIA SULPHURARIA).//019925
 F-THYR01000658//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.5e-49: 116:69//HOMO SAPIENS (HUMAN).//P39189
 F-THYR01000662//DNA-DAMAGE-INDUCIBLE PROTEIN P.//3.7e-15:119:43//E SCHERICHIA COLI.//Q47155
 F-THYR01000666//KINESIN-LIKE PROTEIN KLP1.//1.0e-44:232:41//CHLAMY DOMONAS REINHARDTII.//P46870
 F-THYR01000676//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/2.1e-15: 144:39//HOMO SAPIENS (HUMAN).//P39193
 F-THYR01000684//HYPOTHETICAL 73.5 KD PROTEIN IN SCS3-RPS2 INTERGEN IC REGION.//0.00033:84:30//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS T).//P53129
 F-THYR01000699//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/0.97:20: 85//HOMO SAPIENS (HUMAN).//P39192
 F-THYR01000712//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/4.2e-10:6 9:59//HOMO SAPIENS (HUMAN).//P39188
 F-THYR01000715//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP 3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE 18-6; PEPTIDE P-H].//4.6 e-10:204:32//HOMO SAPIENS (HUMAN).//P04280
 F-THYR01000734
 F-THYR01000748//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.8e-4 6:130:70//HOMO SAPIENS (HUMAN).//043295
 F-THYR01000756//ALPHA-N-ACETYLGLACTOSAMINIDE ALPHA-2,6-SIALYLTRAN SFERASE (EC 2.4.99.-) (ST6GALNAC11) (STY).//1.1e-06:95:31//RATTUS NORVEGICUS (RAT).//Q64686
 F-THYR01000777//CUTICLE COLLAGEN 2C (FRAGMENT).//0.0031:119:34//NA EMONCHUS CONTORTUS.//P16252
 F-THYR01000783//MYOSIN IC HEAVY CHAIN.//0.0014:121:37//ACANTHAMOEBA CASTELLANII (AMOEBA).//P10569
 F-THYR01000787//HUNCHBACK PROTEIN (FRAGMENT).//0.54:25:52//PHOLCUS PHALANGIODES.//Q02031
 F-THYR01000793//PRE-MRNA SPLICING FACTOR PRP9.//0.91:30:36//SACCHA ROMYCES CEREVISIAE (BAKER'S YEAST).//P19736
 F-THYR01000796
 F-THYR01000805//HYPOTHETICAL 7.3 KD PROTEIN IN 100 KD PROTEIN REGI ON.//0.081:31:38//HUMAN ADENOVIRUS TYPE 41.//P23691
 F-THYR01000815//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/6.0e-30: 81:70//HOMO SAPIENS (HUMAN).//P39195
 F-THYR01000829//NEUROTOXIN III (BOM III).//0.022:32:34//BUTHUS OCC ITANUS MARDOCHEI (MOROCCAN SCORPION).//P13488
 F-THYR01000843//HYPOTHETICAL 7.7 KD PROTEIN IN GENES 5-4 INTERGEN IC REGION (ORF 109).//0.98:25:44//BACTERIOPHAGE P22.//P26750
 F-THYR01000852//SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185).//7.3 e-09:83:42//VOLVOX CARTERI.//P21997
 F-THYR01000855//ANTIFREEZE PEPTIDE 4 PRECURSOR.//1.0:54:35//PSEUDO PLEURONECTA AMERICANUS (WINTER FLOUNDER).//P02734
 F-THYR01000865//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.2e-17:6 6:57//HOMO SAPIENS (HUMAN).//P39188
 F-THYR01000895//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/1.0e-12: 58:62//HOMO SAPIENS (HUMAN).//P39189
 F-THYR01000916//!!!! ALU SUBFAMILY SB WARNING ENTRY !!!!!/2.0e-32: 101:69//HOMO SAPIENS (HUMAN).//P39189
 F-THYR01000926//NITROGEN FIXATION REGULATORY PROTEIN.//5.5e-05:10 8:27//KLEBSIELLA OXYTOCA.//P56267
 F-THYR01000934//PYRROLINE-5-CARBOXYLATE REDUCTASE (EC 1.5.1.2) (P5 CR) (P5C REDUCTASE).//3.9e-50:147:40//HOMO SAPIENS (HUMAN).//P3232 2
 F-THYR01000951//DIHYDROXYACETONE KINASE (EC 2.7.1.29) (GLYCERONE K INASE).//1.8e-31:136:56//CITROBACTER FREUNDII.//P45510
 F-THYR01000952//HYPOTHETICAL 182.0 KD PROTEIN IN NM05-HOM6 INTERGE NIC REGION.//2.4e-05:91:34//SACCHAROMYCES CEREVISIAE (BAKER'S YEAS T).//P47170
 F-THYR01000974//MITOCHONDRIAL ATP-DEPENDENT RNA HELICASE SUV3 PREC URSOR.//1.0:35:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P125 80
 F-THYR01000975
 F-THYR01000983//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//1.3e-20:96:51//CAENORHABDITIS ELEGANS.//Q11076
 F-THYR01000984//GTP-BINDING ADP-RIBOSYLATION FACTOR HOMOLOG 1 PROT EIN.//0.011:76:34//DROSOPHILA MELANOGASTER (FRUIT FLY).//P25160

【0695】

【表397】

F-THYR01000988
F-THYR01001003//HYPOTHETICAL 8.1 KD PROTEIN IN MSCL-RPLQ INTERGENE C REGION.//0.97:60:31//ESCHERICHIA COLI.//P36675
F-THYR01001031//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/9.5e-18:56:66//HOMO SAPIENS (HUMAN).//P39195
F-THYR01001033//TRANSFORMATION-SENSITIVE PROTEIN IEF SSP 3521.//5.0e-13:126:35//HOMO SAPIENS (HUMAN).//P31948
F-THYR01001062//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.1e-35:97:79//HOMO SAPIENS (HUMAN).//P39194
F-THYR01001093//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/6.4e-13:70:57//HOMO SAPIENS (HUMAN).//P39194
F-THYR01001100//ZINC FINGER X-LINKED PROTEIN ZXDA (FRAGMENT).//4.2e-63:219:63//HOMO SAPIENS (HUMAN).//P98168
F-THYR01001120//SPLICEOSOME ASSOCIATED PROTEIN 49 (SAP 49) (SF3B5 3).//0.00068:160:31//HOMO SAPIENS (HUMAN).//Q15427
F-THYR01001121//VERY HYPOTHETICAL 20.6 KD PROTEIN C56F8.15 IN CHROMOSOME 1.//0.37:158:28//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10263
F-THYR01001133//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/7.3e-15:59:66//HOMO SAPIENS (HUMAN).//P39188
F-THYR01001134//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.00088:159:29//HOMO SAPIENS (HUMAN).//P10161
F-THYR01001142//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.0e-29:81:71//HOMO SAPIENS (HUMAN).//P39194
F-THYR01001173//CYTOCHROME C OXIDASE POLYPEPTIDE VIIIS (EC 1.9.3.1).//0.88:51:35//DICTYOSTELIUM DISCOIDEUM (SLIME MOLD).//P20610
F-THYR01001177//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/3.0e-24:91:68//HOMO SAPIENS (HUMAN).//P39192
F-THYR01001189//MKR2 PROTEIN (ZINC FINGER PROTEIN 2).//7.3e-27:16:53//MUS MUSCULUS (MOUSE).//P08043
F-THYR01001204//BASIC PROLINE-RICH PEPTIDE P-E (18-9).//0.67:42:42//HOMO SAPIENS (HUMAN).//P02811
F-THYR01001213//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/2.9e-16:61:68//HOMO SAPIENS (HUMAN).//P39194
F-THYR01001262//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.4e-36:50:84//HOMO SAPIENS (HUMAN).//P39193
F-THYR01001271//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.62:126:30//STREPTOMYCES FRADIAE.//P20186
F-THYR01001287//HYPOTHETICAL 91.2 KD PROTEIN IN RPS4B-SCH9 INTERGENE REGION.//1.9e-26:208:37//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38888
F-THYR01001290//GIANT HEMOGLOBIN A1V CHAIN (FRAGMENT).//1.0:31:38//LAMELLIBRACHIA SP. (DEEP-SEA GIANT TUBE WORM).//P20413
F-THYR01001313//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VP55.//0.00042:105:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q92331
F-THYR01001320//COLLAGEN ALPHA 1(III) CHAIN.//0.27:57:38//BOS TAURUS (BOVINE).//P04258
F-THYR01001321//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/5.5e-20:74:64//HOMO SAPIENS (HUMAN).//P39188
F-THYR01001322//HYPOTHETICAL 7.2 KD PROTEIN.//0.66:49:30//VACCINIA VIRUS (STRAIN COPENHAGEN).//P21123
F-THYR01001347//TOXIN F-VIII PRECURSOR (TOXIN TAZ) (TOXIN DAF8).//0.94:61:36//DENDROASPIS ANGIUSTICEPS (EASTERN GREEN MANGA).//P01404
F-THYR01001363//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/0.0025:23:73//HOMO SAPIENS (HUMAN).//P39188
F-THYR01001365//MERCADIDIN PRECURSOR.//0.35:38:42//BACILLUS SP. (STRAIN HIL-Y85/54728).//P43683
F-THYR01001374//PROTEIN VOLD.//1.6e-13:140:31//HELICOBACTER PYLORI (CAMPYLOBACTER PYLORI).//005729
F-THYR01001401//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!/0.047:43:48//HOMO SAPIENS (HUMAN).//P39192
F-THYR01001403
F-THYR01001405//SMALL PROLINE RICH PROTEIN II (SPR-II) (CLONE 930).//0.0068:26:42//HOMO SAPIENS (HUMAN).//P22531
F-THYR01001406//PUTATIVE STEROID DEHYDROGENASE KIX-1 (EC 1.1.1.-).//3.1e-81:97:83//MUS MUSCULUS (MOUSE).//070503
F-THYR01001411//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.9e-26:89:74//HOMO SAPIENS (HUMAN).//P39193
F-THYR01001426//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!/1.4e-09:55:61//HOMO SAPIENS (HUMAN).//P39193
F-THYR01001434//BETA-DEFENSIN 4 PRECURSOR (BNDB-4).//0.68:44:34//BOS TAURUS (BOVINE).//P46162
F-THYR01001458//MYOSIN HEAVY CHAIN, NONMUSCLE TYPE B (CELLULAR MYOSIN HEAVY CHAIN, TYPE B) (NMHC-B).//3.8e-64:216:62//HOMO SAPIENS (HUMAN).//P35580
F-THYR01001480//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/9.3e-29:88:75//HOMO SAPIENS (HUMAN).//P39194
F-THYR01001487//HOMEOBOX PROTEIN HOX-B4 (HOX-2.6).//0.99:59:37//MUS MUSCULUS (MOUSE).//P10284
F-THYR01001534//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/1.4e-14:40:82//HOMO SAPIENS (HUMAN).//P39194
F-THYR01001537//HYPOTHETICAL 33.8 KD PROTEIN IN TWI1-FLOS INTERGENE C REGION.//2.4e-07:142:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38892
F-THYR01001541//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.98:26:61//HOMO SAPIENS (HUMAN).//P39195
F-THYR01001559//PROTEIN Q300.//2.6e-05:20:75//MUS MUSCULUS (MOUSE).//Q02722
F-THYR01001570
F-THYR01001573//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS).//0.033:71:36//MUS MUSCULUS (MOUSE).//P15265
F-THYR01001584//SUPPRESSOR PROTEIN SRP40.//2.1e-05:188:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P32583
F-THYR01001595//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//6.1e-21:35:91//HOMO SAPIENS (HUMAN).//Q15404
F-THYR01001602//TRK SYSTEM POTASSIUM UPTAKE PROTEIN TRKH.//1.0:57:42//HAEMOPHILUS INFLUENZAE.//P44843
F-THYR01001605//VENOM BASIC PROTEASE INHIBITORS IX AND VIIIB.//1.0:34:38//BUNGARUS FASCIATUS (BANDER KRAIT).//P25660
F-THYR01001617//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/7.0e-18:55:81//HOMO SAPIENS (HUMAN).//P39194
F-THYR01001637//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!/0.00020:25:80//HOMO SAPIENS (HUMAN).//P39195
F-THYR01001656//PROLINE-RICH PROTEIN NP-2 PRECURSOR.//0.0091:54:42//MUS MUSCULUS (MOUSE).//P05142
F-THYR01001661//HYPOTHETICAL 21.1 KD PROTEIN IN SSR-SERA INTERGENE C REGION (O182).//0.033:77:35//ESCHERICHIA COLI.//P09160
F-THYR01001671//((2'-5') OLIGOADENYLATE SYNTHETASE 1 (EC 2.7.7.-) ((2'-5') OLIGO(A) SYNTHETASE 1) (2-SA SYNTHETASE 1) (P46/P41) (E18/E16).//4.3e-34:207:34//HOMO SAPIENS (HUMAN).//P00973
F-THYR01001673//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!/3.9e-08:49:65//HOMO SAPIENS (HUMAN).//P39194
F-THYR01001703//HYPOTHETICAL 69.8 KD PROTEIN IN BDF1-SFP1 INTERGENE C REGION.//6.4e-16:134:35//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//Q06053
F-THYR01001706
F-THYR01001721//RING CANAL PROTEIN (KELCH PROTEIN).//2.7e-27:191:36//DROSOPHILA MELANOGASTER (FRUIT FLY).//Q04652
F-THYR01001738//MATING PROCESS PROTEIN MID2 (SERINE-RICH PROTEIN S M2) (PROTEIN KINASE A INTERFERENCE PROTEIN).//0.0032:105:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P36027
F-THYR01001745
F-THYR01001746//GENE 10 PROTEIN.//1.0:55:30//SPIROPLASMA VIRUS SPV 1-RBA2 8.//P15901
F-THYR01001772//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/1.2e-05:41:63//HOMO SAPIENS (HUMAN).//P39188
F-THYR01001793//HYPOTHETICAL 21.6 KD PROTEIN F37A4.2 IN CHROMOSOME III.//1.5e-26:161:42//CAENORHABDITIS ELEGANS.//P41880
F-THYR01001809//LATENCY-RELATED PROTEIN 2.//0.49:74:27//HERPES SIMPLEX VIRUS (TYPE 1 / STRAIN F).//P17589
F-THYR01001828//PROTEINASE INHIBITOR.//0.11:34:50//SOLANUM MELONGENA (EGGPLANT) (AUBERGINE).//P01078
F-THYR01001854//ACYL-COA-BINDING PROTEIN HOMOLOG (ACBP) (DIAZEPAM BINDING INHIBITOR HOMOLOG) (DBI).//0.63:50:38//RAMA RIDIBUNDA (LAUGHING FROG) (MARSH FROG).//P45883
F-THYR01001895//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!/6.1e-09:72:47//HOMO SAPIENS (HUMAN).//P39188
F-THYR01001907//TRYPMASITICOTIDE DECAY-ACCELERATING FACTOR (T-DAF) (FRAGMENT).//0.79:36:44//TRYPMASITICOTIDE CRUZ1.//Q26327
F-VESEN1000122//HOMEOBOX PROTEIN HB9.//0.57:64:32//HOMO SAPIENS (HUMAN).//P50219
F-Y79AA1000013//METALLOTHIONEIN B (MT-B).//0.034:35:48//SALMO SALAR (ATLANTIC SALMON).//P52720
F-Y79AA1000033//CHOLECYSTOKININ.//0.97:49:30//PSEUDOMYXUS SCRIPPA (SLIDER TURTLE).//P80345
F-Y79AA1000037//DNA-BINDING PROTEIN BMI-1.//1.4e-23:80:60//HOMO SAPIENS (HUMAN).//P35226
F-Y79AA1000059//HYPOTHETICAL 35.5 KD PROTEIN IN TRANSPOSON TN4556.//0.0075:127:36//STREPTOMYCES FRADIAE.//P20186
F-Y79AA1000065//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT).//0.022:135:29//HOMO SAPIENS (HUMAN).//P10162
F-Y79AA1000131//REGULATORY PROTEIN E2.//1.1e-05:175:26//HUMAN PAPILLOMAVIRUS TYPE 24.//P50770
F-Y79AA1000181//PROLINE-RICH PROTEIN NP-3 (FRAGMENT).//1.4e-06:18:7:29//MUS MUSCULUS (MOUSE).//P05143
F-Y79AA1000202//HYPOTHETICAL PROLINE-RICH PROTEIN (FRAGMENT).//6.2e-05:47:53//OWENIA FUSIFORMIS.//P21260
F-Y79AA1000214//HISTONE H2A VARIANT.//1.7e-50:107:100//GALLUS GALLUS

【0696】

【表398】

US (CHICKEN).//P02272
 F-Y79AA1000230//GONADOLIBERIN 1 PRECURSOR (LHRH 1) (LUTEINIZING HORMONE RELEASING HORMONE 1) (GONADOTROPIN RELEASING HORMONE 1) (GNRH 1) (LULIBERIN 1).//0.27:64:34//HOMO SAPIENS (HUMAN).//P01148
 F-Y79AA1000231//HYPOTHETICAL 47.9 KD PROTEIN MD21804.12.//2.5e-72:277:53//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//004658
 F-Y79AA1000258//PROLINE-RICH PROTEIN MP-2 PRECURSOR.//2.8e-08:174:35//MUS MUSCULUS (MOUSE).//P05142
 F-Y79AA1000268//COLLAGEN ALPHA 1(III) CHAIN (FRAGMENT).//0.00020:176:33//RATTUS NORVEGICUS (RAT).//P13941
 F-Y79AA1000313//HYPOTHETICAL 54.0 KD PROTEIN C32A.1 IN CHROMOSOME 111.//0.092:127:21//CAENORHABDITIS ELEGANS.//Q09260
 F-Y79AA1000328//SEL-10 PROTEIN.//5.3e-05:129:28//CAENORHABDITIS ELEGANS.//Q03794
 F-Y79AA1000342//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//1.0:73:30//OVIS ARIES (SHEEP).//P26372
 F-Y79AA1000346//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA A-COP).//1.8e-95:205:83//BOS TAURUS (BOVINE).//P53620
 F-Y79AA1000349//ANTIFREEZE PEPTIDE 4 PRECURSOR.//0.036:37:54//PSEUODOLEURORECTA AMERICANUS (WINTER FLOUNDER).//P02734
 F-Y79AA1000355//HYPOTHETICAL 18.2 KD PROTEIN ZK632.13 IN CHROMOSOME E 111.//0.0031:106:28//CAENORHABDITIS ELEGANS.//Q10120
 F-Y79AA1000368//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.4e-16:208:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P25343
 F-Y79AA1000405//LIGHT-HARVESTING PROTEIN 8-800-850, ALPHA CHAIN C (ANTENNA PIGMENT PROTEIN, ALPHA CHAIN C) (LH 11-C ALPHA).//0.98:50:30//RHODOSPIRIDIUM PALUSTRI.//P35103
 F-Y79AA1000410//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//7.9e-20:62:79//HOMO SAPIENS (HUMAN).//P39194
 F-Y79AA1000420//HYPOTHETICAL 27.7 KD PROTEIN IN UME3-HDA1 INTERGENIC REGION.//1.4e-06:86:38//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53970
 F-Y79AA1000469//HYPOTHETICAL 48.4 KD PROTEIN F4489.5 IN CHROMOSOME 111.//2.8e-34:211:40//CAENORHABDITIS ELEGANS.//P34426
 F-Y79AA1000480//HYPOTHETICAL 63.2 KD PROTEIN CIF3.09 IN CHROMOSOME 1.//3.9e-15:90:32//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//Q10414
 F-Y79AA1000538//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.37:41:48//HOMO SAPIENS (HUMAN).//P39195
 F-Y79AA1000539//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.8e-21:190:37//HOMO SAPIENS (HUMAN).//Q08170
 F-Y79AA1000540//SPERM PROTEIN P1.//0.00045:66:45//DASTYRUS VIVER RINUS (SOUTHEASTERN QUOLL), AND DASTYRUS HALLUCATUS.//P42135
 F-Y79AA1000560//ALPHA-ADAPTIN C (CLATHRIN ASSEMBLY PROTEIN COMPLEX 2 ALPHA-C LARGE CHAIN) (100 KD COATED VESICLE PROTEIN C) (PLASMA MEMBRANE ADAPTOR HA2/AP2 ADAPTIN ALPHA C SUBUNIT).//1.6e-79:186:87//MUS MUSCULUS (MOUSE).//P17427
 F-Y79AA1000574//AKLAVINONE C-11 HYDROXYLASE (EC 1.-.-.-) (FRAGMENT).//0.010:35:60//STREPTOMYCES PUCETIUS.//P32009
 F-Y79AA1000589//32.3 KD PROTEIN IN CWP1-MBR1 INTERGENIC REGION.//4.5e-27:197:36//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P28320
 F-Y79AA1000627//ZINC FINGER PROTEIN 134.//1.6e-34:191:35//HOMO SAPIENS (HUMAN).//P52741
 F-Y79AA1000705//HYPOTHETICAL 128.5 KD HELICASE IN ATSI-TPD3 INTERGENIC REGION.//8.7e-36:250:40//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P31380
 F-Y79AA1000734//PEROXISOMAL MEMBRANE PROTEIN PMP30A (PMP31) (PEROXIN-11A).//0.00037:108:27//CANDIDA BODINII (YEAST).//Q00316
 F-Y79AA1000748//HYPOTHETICAL 61.3 KD PROTEIN F2585.5 IN CHROMOSOME 111.//1.0e-23:210:34//CAENORHABDITIS ELEGANS.//Q00316
 F-Y79AA1000752//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//1.4e-53:156:68//MUS MUSCULUS (MOUSE).//Q61990
 F-Y79AA1000774//HYPOTHETICAL 77.9 KD PROTEIN IN RRN10-MCM2 INTERGENIC REGION.//1.2e-11:231:26//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38205
 F-Y79AA1000782//CUTICLE COLLAGEN 2.//0.012:56:35//CAENORHABDITIS ELEGANS.//P17656
 F-Y79AA1000784//HISTIDINE-RICH GLYCOPROTEIN PRECURSOR.//1.3e-08:82:39//PLASMODIUM LOPHURAE.//P04929
 F-Y79AA1000794//DNA-BINDING P52/P100 COMPLEX, 100 KD SUBUNIT (FRAGMENTS).//0.043:13:53//HOMO SAPIENS (HUMAN).//P30808
 F-Y79AA1000800//PRIA PROTEIN PRECURSOR.//0.031:94:34//LENTINULA EDODES (SHIITAKE MUSHROOM) (LENTINUS EDODES).//Q01200
 F-Y79AA1000802//HYPOTHETICAL 67.4 KD PROTEIN IN RPS3-PSD1 INTERGENIC REGION.//0.26:186:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P53882
 F-Y79AA1000805//AMP DEAMINASE (EC 3.5.4.6) (MYOADENYLATE DEAMINASE).//0.99:78:35//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST).//P50998
 F-Y79AA1000824//HYPOTHETICAL 81.7 KD PROTEIN IN MOLI-NAT2 INTERGENIC REGION.//3.4e-44:111:49//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P48234
 F-Y79AA1000827//HYPOTHETICAL BHLF1 PROTEIN.//0.0046:187:33//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
 F-Y79AA1000833//TUBULIN ALPHA-1 CHAIN.//1.0e-75:239:66//CRICETULUS GRISEUS (CHINESE HAMSTER).//P05209
 F-Y79AA1000850//SMALL PROLINE-RICH PROTEIN 11 (SPR-11) (CLONE 174 N).//0.0078:57:31//HOMO SAPIENS (HUMAN).//P22532
 F-Y79AA1000962//MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE.//8.5e-11:241:26//GALLUS GALLUS (CHICKEN).//P10587
 F-Y79AA1000966//ATP SYNTHASE A CHAIN (EC 3.6.1.34) (PROTEIN 6).//0.69:122:31//TRYPAANOSOMA BRUCEI BRUCEI.//P24499
 F-Y79AA1000968//TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GTP-GDP EXCHANGE FACTOR).//3.3e-102:211:93//RATTUS NORVEGICUS (RAT).//P70541
 F-Y79AA1000969//PROCOLLAGEN ALPHA 1(I) CHAIN PRECURSOR.//1.0:67:38//GALLUS GALLUS (CHICKEN).//P02457
 F-Y79AA1000976//INVOLUCRIN.//0.99:66:31//CEBUS ALBIFRONS (WHITE-FRONTED CAPUCHIN).//P24709
 F-Y79AA1000985//PERICENTRIN.//1.1e-24:116:59//MUS MUSCULUS (MOUSE).//P48725
 F-Y79AA1001023//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION.//0.37:79:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38250
 F-Y79AA1001041//SPERMATID-SPECIFIC PROTEIN T1 [CONTAINS: SPERM PROTEIN SPI].//0.93:43:39//SEPIA OFFICINALIS (COMMON CUTTLEFISH).//P80001
 F-Y79AA1001048//ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC P RECURSOR (EC 1.3.99.-) (VLCAD).//1.5e-51:211:52//BOS TAURUS (BOVINE).//P48818
 F-Y79AA1001061//!!!! ALU SUBFAMILY SQ WARNING ENTRY !!!!!//3.8e-25:85:69//HOMO SAPIENS (HUMAN).//P39194
 F-Y79AA1001068//PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN].//0.0015:207:33//MUS MUSCULUS (MOUSE).//P28481
 F-Y79AA1001077//ADULT-SPECIFIC RIGID CUTICULAR PROTEIN 11.9 (ACP 11.9).//0.99:36:41//ARANEUS DIADEMATUS (SPIDER).//P80515
 F-Y79AA1001078//HYPOTHETICAL 88.1 KD PROTEIN K02D10.1 IN CHROMOSOME E 111.//1.0e-06:197:23//CAENORHABDITIS ELEGANS.//P34492
 F-Y79AA1001105//HOMEBOX PROTEIN OTX2.//2.9e-62:163:79//MUS MUSCULUS (MOUSE).//P80206
 F-Y79AA1001145//!!!! ALU SUBFAMILY SX WARNING ENTRY !!!!!//0.024:42:59//HOMO SAPIENS (HUMAN).//P39195
 F-Y79AA1001167//HYPOTHETICAL 7.1 KD PROTEIN IN IAP2-VLF1 INTERGENIC REGION.//0.96:20:50//AUTOGRAPHIA CALIFORNICA NUCLEAR POLYHEDROSIS VIRUS (ACNPV).//P41471
 F-Y79AA1001177//HYPOTHETICAL BHLF1 PROTEIN.//3.9e-05:135:34//EPSTEIN-BARR VIRUS (STRAIN B95-8) (HUMAN HERPESVIRUS 4).//P03181
 F-Y79AA1001185//PUTATIVE CUTICLE COLLAGEN C09G5.5.//0.00017:93:38//CAENORHABDITIS ELEGANS.//Q09456
 F-Y79AA1001211
 F-Y79AA1001216//TENSIN.//0.012:134:32//GALLUS GALLUS (CHICKEN).//Q04205
 F-Y79AA1001228//MUCIN 2 PRECURSOR (INTESTINAL MUCIN 2).//0.088:75:34//HOMO SAPIENS (HUMAN).//Q02817
 F-Y79AA1001233//ESTRADIOL 17 BETA-DEHYDROGENASE 1 (EC 1.1.1.62) (17-BETA-HSD 1) (17-BETA-HYDROXYSTEROID DEHYDROGENASE 1).//1.1e-40:139:51//RATTUS NORVEGICUS (RAT).//P51657
 F-Y79AA1001236//HYPOTHETICAL 34.7 KD PROTEIN IN ORC2-TIP1 INTERGENIC REGION.//2.0e-22:108:53//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST).//P38238
 F-Y79AA1001281
 F-Y79AA1001299//PROLINE-RICH PROTEIN MP-3 (FRAGMENT).//0.0022:49:44//MUS MUSCULUS (MOUSE).//P05143
 F-Y79AA1001312//50S RIBOSOMAL PROTEIN L24, CHLOROPLAST PRECURSOR.//0.98:117:25//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS).//P92959
 F-Y79AA1001323//CORNIFIN (SMALL PROLINE-RICH PROTEIN 1) (SPR-1) (SMALL PROLINE-RICH SQUAMOUS CELL MARKER) (SRP).//0.082:44:40//SUS SCROFA (PIG).//P35323
 F-Y79AA1001384//APOLIPOPROTEIN C-III PRECURSOR (APO-CIII).//0.99:74:7:40//MUS MUSCULUS (MOUSE).//P33622
 F-Y79AA1001391//HOMEBOX PROTEIN HOX-A13 (HOX-13).//9.8e-58:157:62//HOMO SAPIENS (HUMAN).//P31271
 F-Y79AA1001394//TRICHOHYALIN.//4.7e-08:121:36//HOMO SAPIENS (HUMAN).//Q07283
 F-Y79AA1001402//ETS-DOMAIN TRANSCRIPTION FACTOR ERF.//0.0087:81:33//MUS MUSCULUS (MOUSE).//P70459
 F-Y79AA1001493//HYPOTHETICAL 48.1 KD PROTEIN B0403.2 IN CHROMOSOME X.//4.5e-21:125:44//CAENORHABDITIS ELEGANS.//Q11076
 F-Y79AA1001511//HYPOTHETICAL 86.6 KD PROTEIN IN PFK1-TDS4 INTERGENIC REGION.//0.00017:93:38//CAENORHABDITIS ELEGANS.//Q09456

【0697】

【表399】

IC REGION. //2.3e-17:249:31//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P53313
 F-Y79AA1001533//DNA-DIRECTED RNA POLYMERASE 1 49 KD POLYPEPTIDE (EC 2.7.7.6) (A49). //0.0099:155:23//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //Q01080
 F-Y79AA1001541
 F-Y79AA1001548//!!!! ALU SUBFAMILY SC WARNING ENTRY !!!!!//1.1e-17:53:83//HOMO SAPIENS (HUMAN). //P39192
 F-Y79AA1001555//MAJOR SURFACE ANTIGEN. //0.046:62:29//HEPATITIS B VIRUS. //P31873
 F-Y79AA1001581//ACETYL-COENZYME A SYNTHETASE (EC 6.2.1.1) (ACETATE-COA LIGASE) (ACTL- ACTIVATING ENZYME). //8.6e-11:144:31//ESCHERICHIA COLI. //P27550
 F-Y79AA1001585//SPERM MITOCHONDRIAL CAPSULE SELENOPROTEIN (MCS). //0.012:64:40//MUS MUSCULUS (MOUSE). //P15265
 F-Y79AA1001594//CORNIFIN BETA. //0.61:88:31//MUS MUSCULUS (MOUSE). //Q09116
 F-Y79AA1001603//TRANSCRIPTION INITIATION FACTOR TFIID 135 KD SUBUNIT (TAF11-135) (TAF11-130) (TAF11-130). //0.024:170:30//HOMO SAPIENS (HUMAN). //Q00268
 F-Y79AA1001613//ZINC FINGER PROTEIN 42 (MYELOID ZINC FINGER 1) (MZ F-1). //4.5e-09:136:27//HOMO SAPIENS (HUMAN). //P28698
 F-Y79AA1001647//HYPOTHETICAL 23.1 KD PROTEIN CY277.20C. //0.093:94:26//MYCOBACTERIUM TUBERCULOSIS. //P17179
 F-Y79AA1001665//HOMEBOX PROTEIN DLX-2 (HOMEBOX PROTEIN TES-1). //0.79:90:26//MUS MUSCULUS (MOUSE). //P40764
 F-Y79AA1001679//LAMBDA-CRYSTALLIN. //1.6e-95:224:81//ORYZOLAGUS CUMICULUS (RABBIT). //P14755
 F-Y79AA1001692//GERM CELL-LESS PROTEIN. //3.5e-08:78:38//DROSOPHILA MELANOGASTER (FRUIT FLY). //Q01820
 F-Y79AA1001696//INSULIN. //1.0:33:27//ANGUILLA ROSTRATA (AMERICAN EEL). //P42633
 F-Y79AA1001705//HYPOTHETICAL BHLF1 PROTEIN. //0.0013:192:33//EPSTEIN-BARR VIRUS (STRAIN 895-8) (HUMAN HERPESVIRUS 4). //P03181
 F-Y79AA1001711//PARATHYROIDIN (ZINC-BINDING 11.5 KD PROTEIN). //0.032:38:34//RATTUS NORVEGICUS (RAT). //P04550
 F-Y79AA1001781
 F-Y79AA1001805//VASODILATOR-STIMULATED PHOSPHOPROTEIN (VASP). //0.063:128:30//HOMO SAPIENS (HUMAN). //P50552
 F-Y79AA1001827//SPERM PROTAMINE P1. //0.015:45:40//DIDELPHIS MARSUPIALIS VIRGINIANA (NORTH AMERICAN OPOSSUM), AND MONODELPHIS DOMESTICA (SHORT-TAILED GREY OPOSSUM). //P35305
 F-Y79AA1001846//!!!! ALU SUBFAMILY J WARNING ENTRY !!!!!//2.4e-09:42:73//HOMO SAPIENS (HUMAN). //P39188
 F-Y79AA1001848//KRUEPPEL PROTEIN (FRAGMENT). //1.8e-10:63:44//PSYCHODA CINEREA. //Q02035
 F-Y79AA1001866//ZINC FINGER PROTEIN 90 (ZFP-90) (ZINC FINGER PROTEIN NK10). //0.00036:108:37//MUS MUSCULUS (MOUSE). //Q61967
 F-Y79AA1001874//OX40L RECEPTOR PRECURSOR (ACT35 ANTIGEN) (TAX-TRANSCRIPTIONALLY ACTIVATED GLYCOPROTEIN 1 RECEPTOR) (CD134 ANTIGEN). //3.2e-07:100:35//HOMO SAPIENS (HUMAN). //P43489
 F-Y79AA1001875//B-CELL GROWTH FACTOR PRECURSOR (BCGF-12 KD). //0.020:25:64//HOMO SAPIENS (HUMAN). //P20931
 F-Y79AA1001923//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE K) [CONTAINS: PEPTIDE P-D] (FRAGMENT). //0.016:83:36//HOMO SAPIENS (HUMAN). //P10162
 F-Y79AA1001963//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C. //8.1e-13:94:47//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //Q42643
 F-Y79AA1002027//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.1) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PUB42). //9.8e-39:143:52//ARABIDOPSIS THALIANA (MOUSE-EAR CRESS). //P42743
 F-Y79AA1002083//DNA-BINDING P52/P100 COMPLEX. 100 KD SUBUNIT (FRAGMENTS). //0.036:53:45//HOMO SAPIENS (HUMAN). //P30808
 F-Y79AA1002089//HYPOTHETICAL 49.1 KD PROTEIN F02A.4 IN CHROMOSOME III. //0.12:171:22//CAENORHABDITIS ELEGANS. //P34384
 F-Y79AA1002093//MAX PROTEIN. //3.1e-07:111:29//BRACHYDANIO RERIO (ZEBRAFISH) (ZEBRA DANIO). //P52161
 F-Y79AA1002103//SHORT NEUROTOXIN C. //0.040:21:47//AIPYSURUS LAEVIS (OLIVE SEA SNAKE). //P19958
 F-Y79AA1002115//HYPOTHETICAL PROTEIN MJ0827. //0.84:68:30//METHANOCoccus JANNASCHII. //Q58237
 F-Y79AA1002125//HYPOTHETICAL 24.7 KD PROTEIN IN POM152-REC114 INTERGENIC REGION. //3.4e-29:197:39//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P40206
 F-Y79AA1002139//DNAJ PROTEIN HOMOLOG 1 (DROJ1). //1.9e-19:120:45//DROSOPHILA MELANOGASTER (FRUIT FLY). //Q24133
 F-Y79AA1002204//TBX6 PROTEIN (T-BOX PROTEIN 6). //0.0011:162:32//MUS MUSCULUS (MOUSE). //P70327
 F-Y79AA1002208//ANKYRIN. //2.9e-08:231:29//MUS MUSCULUS (MOUSE). //Q2357
 F-Y79AA1002209//TYROSYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR (EC 6.1.1.1) (TYROSINE--TRNA LIGASE) (TYRS). //3.7e-23:170:32//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P48527
 F-Y79AA1002210//CORNIFIN A (SMALL PROLINE-RICH PROTEIN 1A) (SPR-1A) (SPRK). //0.0061:69:31//HOMO SAPIENS (HUMAN). //P35321
 F-Y79AA1002211//!!!! ALU SUBFAMILY SP WARNING ENTRY !!!!!//9.2e-10:43:62//HOMO SAPIENS (HUMAN). //P39193
 F-Y79AA1002220
 F-Y79AA1002229//HYPOTHETICAL 60.7 KD PROTEIN C56F8.17C IN CHROMOSOME I. //1.9e-21:147:40//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //Q10264
 F-Y79AA1002234
 F-Y79AA1002246//MYOSIN IC HEAVY CHAIN. //0.00066:131:34//ACANTHAMOEBA CASTELLANII (AMOEBA). //P10569
 F-Y79AA1002258//HYPOTHETICAL 103.9 KD PROTEIN ZK370.3 IN CHROMOSOME III. //4.3e-45:164:48//CAENORHABDITIS ELEGANS. //Q02328
 F-Y79AA1002298//SALIVARY PROLINE-RICH PROTEIN PO (ALLELE M) [CONTAINS: PEPTIDE P-D] (FRAGMENT). //0.0063:99:31//HOMO SAPIENS (HUMAN). //P10161
 F-Y79AA1002307
 F-Y79AA1002311//HYPOTHETICAL 105.3 KD PROTEIN C01G6.5 IN CHROMOSOME III. //0.75:198:24//CAENORHABDITIS ELEGANS. //P46012
 F-Y79AA1002351//CUTICLE COLLAGEN 34. //0.74:128:35//CAENORHABDITIS ELEGANS. //P34687
 F-Y79AA1002361//GLC7-INTERACTING PROTEIN 2. //0.050:71:29//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P40036
 F-Y79AA1002399//NEUROMODULIN (AXONAL MEMBRANE PROTEIN GAP-43) (PP46) (B-50) (PROTEIN F1) (CALMODULIN-BINDING PROTEIN P-57). //1.0:89:30//CARASSIUS AURATUS (GOLDFISH). //P17691
 F-Y79AA1002407//HYPOTHETICAL 31.5 KD PROTEIN IN YGP1-YCK2 INTERGENIC REGION. //3.7e-16:232:28//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P53899
 F-Y79AA1002416//CTP SYNTHASE (EC 6.3.4.2) (UTP--AMMONIA LIGASE) (CTP SYNTHETASE). //6.7e-72:162:84//HOMO SAPIENS (HUMAN). //P17812
 F-Y79AA1002431//SMALL PROLINE RICH PROTEIN II (SPR-11) (CLONE 930). //0.81:34:41//HOMO SAPIENS (HUMAN). //P22531
 F-Y79AA1002433//CELL DIVISION CONTROL PROTEIN 68. //0.00024:85:27//SACCHAROMYCES CEREVISIAE (BAKER'S YEAST). //P32558
 F-Y79AA1002472//ZINC FINGER PROTEIN 35 (ZFP-35). //2.3e-60:217:44//MUS MUSCULUS (MOUSE). //P15620
 F-Y79AA1002482//ZINC FINGER PROTEIN 141. //2.0e-31:90:55//HOMO SAPIENS (HUMAN). //Q15928
 F-Y79AA1002487//HYPOTHETICAL 67.1 KD TRP-ASP REPEATS CONTAINING PROTEIN C57A10.05C IN CHROMOSOME I. //0.18:41:36//SCHIZOSACCHAROMYCES POMBE (FISSION YEAST). //P87053

【0698】

5'末端クローン配列に対するESTとSTSを除いたGenBank相同性検索結果データ

各データは

クローン配列名、

トップヒットデータのDefinition、

P値:比較配列の長さ (base):相同性(%)、

トップヒットデータのAccession No.の順に//で区切って記載した。

なお、相同性のスコアのP値が1より大であった場合はデータは示さない。

【0699】

【表400】

F-HEMBA1000005//Mouse tumor cell dnaJ-like protein 1 mRNA, complete cds.//3.4e-106:695:86//L16953
 F-HEMBA1000012//Caenorhabditis elegans cosmid C16C10, complete sequence.//1.5e-24:374:66//Z46787
 F-HEMBA1000020//Homo sapiens beta 2 gene.//3.5e-112:529:90//X02344
 F-HEMBA1000030//Rattus norvegicus G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein (G11) mRNA, complete cds.//5.6e-124:743:88//AF085693
 F-HEMBA1000042//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-25:529:65//AC004581
 F-HEMBA1000046//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 12513, WORKING DRAFT SEQUENCE.//3.2e-11:330:63//AL033528
 F-HEMBA1000050//Homo sapiens DNA sequence from PAC 172K10 on chromosome 6q24. Contains STS, GSS and chromosome 6 fragment, complete sequence.//0.32:407:59//AL024777
 F-HEMBA1000076//Homo sapiens full length insert cDNA clone ZB97G06.//6.2e-135:594:98//AF086182
 F-HEMBA1000111//CIT-HSP-2291M18, TF CIT-HSP Homo sapiens genomic clone 2291M18, genomic survey sequence.//2.8e-15:132:79//AQ004134
 F-HEMBA1000129//Homo sapiens chromosome 17, clone HC1748C15, complete sequence.//8.6e-98:230:93//AC003104
 F-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds.//2.1e-167:791:98//AB018340
 F-HEMBA1000150//Homo sapiens mRNA for KIAA0788 protein, partial cds.//2.2e-44:242:96//AB018331
 F-HEMBA1000156//Rattus norvegicus scaffold attachment factor B mRNA, complete cds.//1.1e-10:409:60//AF056324
 F-HEMBA1000158//Homo sapiens CAGH44 mRNA, partial cds.//1.6e-35:365:73//U80741
 F-HEMBA1000168//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 32102, WORKING DRAFT SEQUENCE.//0.99:290:61//AL031033
 F-HEMBA1000180//rat u2 small nuclear rna gene and flanks.//3.7e-18:112:98//X00034
 F-HEMBA1000185
 F-HEMBA1000193//Human FMR1 gene, 5' end.//0.0012:191:67//L19476
 F-HEMBA1000201//Human Inr1 mRNA, complete cds.//2.0e-73:440:92//U04847
 F-HEMBA1000213//Plasmodium falciparum MAL3P7, complete sequence.//0.90:332:59//AL034559
 F-HEMBA1000216//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//4.8e-117:585:83//AF060194
 F-HEMBA1000227//H. sapiens CpG island DNA genomic Msa1 fragment, clone 179h6, reverse read cpg179h6.rta.//1.9e-14:95:98//Z64921
 F-HEMBA1000231//H. sapiens CpG island DNA genomic Msa1 fragment, clone 90a5, reverse read cpg90a5.rta.//5.1e-34:186:97//Z56144
 F-HEMBA1000243//Human DNA sequence from PAC 440021 on chromosome X contains ESTs and STS.//4.1e-67:291:82//Z84481
 F-HEMBA1000244//M. musculus Ank-1 mRNA for erythroid ankyrin.//0.029:316:59//X69065
 F-HEMBA1000251//Homo sapiens PAC clone DJ0988L12 from Tq11.23-q21.1, complete sequence.//0.35:467:60//AC004454
 F-HEMBA1000264
 F-HEMBA1000280//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//8.9e-20:218:78//AC004825
 F-HEMBA1000282//Homo sapiens chromosome Y, clone 264.M.20, complete sequence.//4.2e-08:134:77//AC004617
 F-HEMBA1000288//345L5, TPB CIT978SKA1 Homo sapiens genomic clone A-345L05, genomic survey sequence.//1.1e-06:152:73//B17459
 F-HEMBA1000290//Human ornithine decarboxylase gene, complete cds.//3.2e-11:507:62//W33764
 F-HEMBA1000302//CIT-HSP-2169N13, TF CIT-HSP Homo sapiens genomic clone 2169N13, genomic survey sequence.//5.4e-06:86:88//B90730
 F-HEMBA1000303//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.//7.9e-111:701:86//AF030131
 F-HEMBA1000304//HS_3006_A1_A09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=17 Row=A, genomic survey sequence.//5.2e-40:240:92//AQ118226
 F-HEMBA1000307//Mus musculus mRNA for CDV-IR protein.//7.9e-127:815:84//Y10495
 F-HEMBA1000327//HS_3124_B2_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence.//1.4e-11:87:96//AQ187492
 F-HEMBA1000333
 F-HEMBA1000338//Homo sapiens chromosome X, PAC 67109, complete sequence.//4.0e-66:271:84//AF031078
 F-HEMBA1000351//Homo sapiens PAC clone DJ0649P17 from Tq11.23-q21, complete sequence.//0.64:334:60//AC004848
 F-HEMBA1000355//Pseudorabies virus serine/threonine kinase (ULPK) gene, partial cds and alkaline nuclease (AN) gene, complete cds.//0.017:313:63//U25056
 F-HEMBA1000356//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds.//0.87:198:61//L40178
 F-HEMBA1000357//HS_3194_A1_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=G, genomic survey sequence.//6.5e-90:436:98//AQ173748
 F-HEMBA1000366//HS_3027_B2_G06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=12 Row=N, genomic survey sequence.//0.0074:192:64//AQ128843
 F-HEMBA1000369//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//4.2e-106:133:99//AL031587
 F-HEMBA1000376//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.6e-22:659:63//AC006116
 F-HEMBA1000387//Homo sapiens chromosome 12p13.3 clone RPC111-264F23, WORKING DRAFT SEQUENCE, 90 unordered pieces.//3.2e-06:136:75//AC006122
 F-HEMBA1000390//Homo sapiens BAC clone RG119C02 from Tpl5, complete sequence.//3.5e-111:284:95//AC004520
 F-HEMBA1000392//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 173D1, WORKING DRAFT SEQUENCE.//1.8e-39:332:80//AL031984
 F-HEMBA1000396//Human Xq13 3' end of PAC 92E23 containing the X in activation transcript (XIST) gene, complete sequence.//9.5e-35:364:73//U80460
 F-HEMBA1000411//Human Xp22 contig of 3 PACS (R7-39D12, R7-134G1, R7-185L21) from the Roswell Park Cancer Institute, complete sequence.//8.1e-18:424:64//U96409
 F-HEMBA1000418//Drosophila melanogaster Oregon-R mitochondrial A+T region.//0.0026:564:59//U11584
 F-HEMBA1000422//Human DNA from chromosome 19 specific cosmid R30292, genomic sequence, complete sequence.//9.2e-14:232:70//AC003112
 F-HEMBA1000428//Homo sapiens Xp22 BAC GSHB-59D16 (Genome Systems Human BAC library) complete sequence.//3.8e-37:408:69//AC004554
 F-HEMBA1000434//Caenorhabditis elegans cosmid Y48E1B, complete sequence.//0.73:454:57//Z93393
 F-HEMBA1000442
 F-HEMBA1000456//RPC111-30J5, TV RPC111 Homo sapiens genomic clone RPC111-30J5, genomic survey sequence.//6.3e-06:62:96//B85188
 F-HEMBA1000459//Mus musculus hemin-sensitive initiation factor 2 alpha kinase mRNA, complete cds.//6.8e-70:580:79//AF028808
 F-HEMBA1000460//Homo sapiens PAC clone DJ0593H12 from Tpl31, complete sequence.//2.8e-154:746:98//AC004839
 F-HEMBA1000464//Homo sapiens, clone hRPK.15_A.1, complete sequence.//4.8e-25:397:72//AC006213
 F-HEMBA1000469//CIT-HSP-2167P21, TF CIT-HSP Homo sapiens genomic clone 2167P21, genomic survey sequence.//4.0e-83:406:99//B94160
 F-HEMBA1000488//Homo sapiens Chromosome 22q11.2 PAC Clone p_m11 in BCL2-GGT Region, complete sequence.//4.2e-53:312:93//AC004033
 F-HEMBA1000490//Campylobacter jejuni groES, groEL genes.//0.59:451:62//Y13334
 F-HEMBA1000491//Murine sarcoma virus (Harvey-strain) H-ras transfecting p21 gene.//8.6e-06:338:58//X00740
 F-HEMBA1000501//Homo sapiens chromosome 17, clone hRPK.264_B.14, complete sequence.//9.4e-41:591:69//AC005884
 F-HEMBA1000504//Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os).//4.0e-07:57:100//D13666
 F-HEMBA1000505
 F-HEMBA1000508//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0135005: HTGS phase 1, WORKING DRAFT SEQUENCE, 23 unordered pieces.//0.035:329:61//AC004661
 F-HEMBA1000518//Caenorhabditis elegans cosmid CITH12.//0.96:425:58//AF045642
 F-HEMBA1000519//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence.//1.6e-53:300:89//AC004616
 F-HEMBA1000520//Homo sapiens clone DJ0813F11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.7e-10:117:86//AC006006
 F-HEMBA1000523
 F-HEMBA1000531//Mus musculus Hsp70-related NST-1 (hsp.1) mRNA, complete cds.//3.9e-35:290:80//U08215
 F-HEMBA1000534//Homo sapiens chromosome 17, clone hRPK.177_H.5, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.7e-36:328:77//AC005973
 F-HEMBA1000540//Arabidopsis thaliana DNA chromosome 4, BAC clone F7K2 (CESSAII project).//0.057:265:63//AL033545
 F-HEMBA1000542//Rattus norvegicus mRNA for dipeptidyl peptidase II 1, complete cds.//1.2e-110:572:88//D89340
 F-HEMBA1000545//Human DNA from cosmid L27h9, Huntington's Disease Region, chromosome 4p16.3 contains CpG island.//7.5e-130:780:89//Z

【0700】

【表401】

49237
F-HEMBA1000555//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 134019, WORKING DRAFT SEQUENCE. //3.2e-175:838:98//AL034555
F-HEMBA1000557//CIT-HSP-2369F15. TF CIT-HSP Homo sapiens genomic clone 2369F15, genomic survey sequence. //2.8e-32:315:78//AQ074611
F-HEMBA1000561//Rattus norvegicus Olf-1/EBF associated Zn finger protein Roaz mRNA, alternatively spliced form, complete cds. //3.4e-69:665:72//U92564
F-HEMBA1000563//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces. //0.59:261:61//AC005504
F-HEMBA1000568//HS_3243_B2_A12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3243 Col=24 Row=8, genomic survey sequence. //3.1e-54:323:91//AQ219628
F-HEMBA1000569//M. musculus mRNA for GPI-anchored protein. //1.4e-19:440:61//X89571
F-HEMBA1000575//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces. //0.0016:557:57//AC005506
F-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds. //1.7e-11:132:79//AF045573
F-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein. //7.3e-43:228:97//AJ007509
F-HEMBA1000592//Mus musculus clone OST7314, genomic survey sequence. //7.3e-07:68:94//AF046733
F-HEMBA1000594//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs. //8.7e-71:553:79//Z83822
F-HEMBA1000604//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 237J2, WORKING DRAFT SEQUENCE. //2.9e-21:158:75//AL021394
F-HEMBA1000608//Homo sapiens mRNA for KIAA0456 protein, partial cds. //1.1e-118:561:99//AB007925
F-HEMBA1000622//Homo sapiens Chromosome 16 BAC clone CIT9875X-A-15 ZE5, complete sequence. //2.2e-28:426:70//AC004382
F-HEMBA1000636//Human CpG island sequence, clone Q2888. //1.0e-15:274:68//D85773
F-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds. //6.7e-137:639:99//AB014590
F-HEMBA1000655//, complete sequence. //5.1e-83:685:80//AC005815
F-HEMBA1000657//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds. //1.1e-91:597:84//U035776
F-HEMBA1000662//Homo sapiens clone DJ0853H20, WORKING DRAFT SEQUENCE, 5 unordered pieces. //0.019:695:57//AC004907
F-HEMBA1000673//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 229A8, WORKING DRAFT SEQUENCE. //1.5e-48:325:85//Z86090
F-HEMBA1000682//Homo sapiens (subclone 5_g5 from P1 H25) DNA sequence. //7.7e-61:615:74//L43411
F-HEMBA1000686
F-HEMBA1000702
F-HEMBA1000705//Plasmodium falciparum 3D7 chromosome 12 PFYAC88-62 8 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces. //0.0037:569:57//AC005507
F-HEMBA1000719//Streptomyces coelicolor cosmid 1C2. //2.0e-09:483:62//AL031124
F-HEMBA1000722//Toxoplasma gondii chloroplast, complete genome. //0.00058:762:57//U87145
F-HEMBA1000726//H. sapiens HLA-DRB1*15 gene. //9.8e-49:189:89//X88791
F-HEMBA1000727//CIT-HSP-387P22. TRB CIT-HSP Homo sapiens genomic clone 387P22, genomic survey sequence. //0.0054:206:67//B60158
F-HEMBA1000747
F-HEMBA1000749//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence. //3.3e-05:124:75//AL024509
F-HEMBA1000752//Human Chromosome X, complete sequence. //5.9e-48:502:75//AC004073
F-HEMBA1000759//Homo sapiens clone RH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces. //0.011:179:67//AC005043
F-HEMBA1000773//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS ***
from clone Y59A8, WORKING DRAFT SEQUENCE. //0.070:231:63//Z98870
F-HEMBA1000774//Homo sapiens PAC clone DJ1059W17 from 7q21-q31.1, complete sequence. //6.2e-40:385:75//AC004953
F-HEMBA1000791
F-HEMBA1000817//Myrmecia pilosula H187-135 mitochondrion cytochrome b gene, partial cds. //0.99:244:58//U15678
F-HEMBA1000822//Human DNA sequence from PAC 179D3, between markers DXS6791 and DXS8038 on chromosome X contains S10 GTP-binding protein, ESTs and CpG island. //0.033:294:62//Z81370
F-HEMBA1000827//Borrelia burgdorferi (section 50 of 70) of the complete genome. //9.7e-05:463:58//AE001164
F-HEMBA1000843//Homo sapiens DNA sequence from clone 511824 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-11, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. C contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence. //3.0e-153:732:98//AL022394
F-HEMBA1000851//Rattus norvegicus glucocorticoid modulatory element binding protein 2 mRNA, complete cds. //1.6e-31:386:72//AF059273
F-HEMBA1000852//Homo sapiens Xp22 bins 3-5 PAC RPC14-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence. //8.5e-115:455:98//AC005295
F-HEMBA1000867
F-HEMBA1000869//Human DNA sequence from cosmid J138017, between markers DXS6791 and DXS8038 on chromosome X contains EST CA repeat and an endogenous retroviral like element. //6.6e-41:424:75//Z72519
F-HEMBA1000870//Cnaphodotus pumilio cytochrome oxidase II gene, partial cds: and tRNA-Asp, tRNA-His, and tRNA-Lys genes, complete sequence, mitochondrial genes for mitochondrial products. //0.0049:211:66//AF034598
F-HEMBA1000872//CIT-HSP-2355D20. TF CIT-HSP Homo sapiens genomic clone 2355D20, genomic survey sequence. //3.7e-33:180:98//AQ059583
F-HEMBA1000876//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 473B4, WORKING DRAFT SEQUENCE. //5.6e-37:262:72//Z83826
F-HEMBA1000908//Triticum aestivum low-affinity cation transporter (LCT1) mRNA, complete cds. //1.0:304:59//AF015523
F-HEMBA1000910//M. musculus necdin mRNA, complete cds. //6.1e-08:256:61//M80840
F-HEMBA1000918//Tetrahymena thermophila micronuclear developmentally eliminated sequence region. //0.13:232:63//U88158
F-HEMBA1000919//Gallus domesticus filamin mRNA, complete cds. //1.0:213:65//U00147
F-HEMBA1000934//CIT-HSP-2053H24. TR CIT-HSP Homo sapiens genomic clone 2053H24, genomic survey sequence. //5.5e-11:275:64//B69224
F-HEMBA1000942//Homo sapiens clone DJ0754G14, WORKING DRAFT SEQUENCE, 15 unordered pieces. //9.7e-05:78:83//AC004878
F-HEMBA1000943//Homo sapiens chromosome 17, clone hRPK.540_1_15, complete sequence. //5.8e-140:661:99//AC005324
F-HEMBA1000946
F-HEMBA1000960//Homo sapiens clone DJ1111F22, WORKING DRAFT SEQUENCE, 12 unordered pieces. //8.3e-16:181:75//AC004967
F-HEMBA1000968//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 69M21, WORKING DRAFT SEQUENCE. //4.4e-117:398:86//AL031735
F-HEMBA1000971//H. sapiens CpG island DNA genomic MseI fragment, clone 18214, forward read cpgl8214.1tla. //1.5e-20:126:96//Z57528
F-HEMBA1000972//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 1/11. //0.34:642:59//AB020858
F-HEMBA1000974//Homo sapiens clone DA0091H08, complete sequence. //5.1e-183:865:98//AC004817
F-HEMBA1000975//Orf virus homologue of retroviral pseudoprotease gene, complete cds. //0.00065:391:62//M30023
F-HEMBA1000985//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence. //3.4e-05:243:65//Z93929
F-HEMBA1000986//Homo sapiens DNA from chromosome 19-cosmid R31491, genomic sequence. //6.6e-06:508:61//AD000813
F-HEMBA1000991//Homo sapiens mRNA for Hrs, complete cds. //1.2e-22:193:84//D84064
F-HEMBA1001007
F-HEMBA1001008//Human DNA sequence from clone 391022 on chromosome 6p21.2-21.31 Contains pseudogenes similar to ribosomal protein, ESTs, GSSs, complete sequence. //7.8e-46:532:73//AL031577
F-HEMBA1001009//Human mRNA for IgM heavy chain complete sequence. //0.97:369:59//X17115
F-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds. //4.4e-139:661:98//AB007937
F-HEMBA1001019//Homo sapiens, clone hRPK.15_A.1, complete sequence. //1.1e-16:521:64//AC005213
F-HEMBA1001020//Homo sapiens chromosome 17, clone hRPK.178_C.3, complete sequence. //3.8e-50:367:72//AC005702
F-HEMBA1001022

【0701】

【表402】

F-HEMBA1001024//Homo sapiens T-cell receptor alpha delta locus from bases 1 to 250529 (section 1 of 5) of the Complete Nucleotide Sequence.//5.0e-23:378:69//AE000658	F-HEMBA1001310//HS_3252_B2_B12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=24 Row=D, genomic survey sequence.//1.2e-16:166:82//AQ217054
F-HEMBA1001026//Homo sapiens DNA sequence from PAC 41501 on chromosome 1q25. Contains ESTs and STS.//7.6e-19:867:60//Z86064	F-HEMBA1001319//CIT-HSP-2034J6.TF CIT-HSP Homo sapiens genomic clone 2034J6, genomic survey sequence.//0.33:256:59//B79408
F-HEMBA1001043//HS_2219_B1_A10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=19 Row=B, genomic survey sequence.//3.0e-15:124:88//AQ301521	F-HEMBA1001323//Homo sapiens proto-oncogene (Wnt-5a) mRNA, complete cds.//7.8e-30:165:99//L20861
F-HEMBA1001051//Human Chromosome X clone bWXD342, complete sequence.//4.8e-79:308:84//AC004072	F-HEMBA1001326//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glycerinaldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//5.4e-19:347:68//AL021368
F-HEMBA1001052//Homo sapiens chromosome 17, clone hRPK.146_P.2, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.53:384:61//AC005341	F-HEMBA1001327//CIT-HSP-2354E10.TR CIT-HSP Homo sapiens genomic clone 2354E10, genomic survey sequence.//0.012:152:65//AQ075713
F-HEMBA1001059//Human N-acetylgalactosamine 6-sulphatase (GALNS) gene, exon 10.//2.8e-26:397:71//U06084	F-HEMBA1001330//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-103, complete sequence.//0.0037:254:62//AL010208
F-HEMBA1001060//Homo sapiens chromosome 17, clone hRPK.855_D.21, complete sequence.//0.98:280:62//AC006079	F-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VAP-33) mRNA, complete cds.//1.1e-103:516:97//AF057358
F-HEMBA1001071//Human mRNA for pro alpha 1 (Ii) collagen C-terminal propeptide.//1.1e-31:181:96//X01742	F-HEMBA1001361//Homo sapiens chromosome 9, clone hRPK.202_M.3, complete sequence.//1.7e-150:706:99//AC006241
F-HEMBA1001077//nuclear protein TIF1 [mice, mRNA, 3951 nt].//3.6e-13:338:65//S78219	F-HEMBA1001375//Streptomyces coelicolor cosmid 1E6.//1.0:375:59//AL033505
F-HEMBA1001080//Streptomyces coelicolor cosmid 1A9.//0.00012:364:63//AL034446	F-HEMBA1001377//HS_3020_B1_D12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3020 Col=23 Row=H, genomic survey sequence.//0.00022:63:77//AQ105297
F-HEMBA1001085//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, tes, and alpha mannosidase IIa genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//8.5e-134:476:96//AC004586	F-HEMBA1001383//Plasmodium falciparum chromosome 2, section 68 of 73 of the complete sequence.//0.00035:317:60//AE001431
F-HEMBA1001088//Sequence 1 from patent US 5552529.//2.2e-71:303:78//125863	F-HEMBA1001387//HS_3039_B1_D01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=1 Row=H, genomic survey sequence.//5.0e-90:437:98//AQ155035
F-HEMBA1001094//Homo sapiens clone RG491N20, complete sequence.//8.9e-119:609:96//AC005105	F-HEMBA1001388//Homo sapiens clone RG189J21, WORKING DRAFT SEQUENCE, 15 unordered pieces.//4.2e-47:159:89//AC005073
F-HEMBA1001099	F-HEMBA1001391//Human DNA sequence from clone 409010 on chromosome 20q12 Contains CA repeat, GSS, STS, complete sequence.//2.0e-06:495:60//AL031256
F-HEMBA1001109//Homo sapiens BAC clone RG318M05 from Tq22-q31.1, complete sequence.//2.4e-58:347:87//AC005250	F-HEMBA1001398//H. sapiens CpG island DNA genomic MseI fragment, clone 70d11, forward read cpg70d11.f1b.//0.018:46:97//Z62591
F-HEMBA1001121//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 90G24, WORKING DRAFT SEQUENCE.//3.4e-21:226:65//AL008723	F-HEMBA1001405//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.//2.3e-74:623:71//AL034380
F-HEMBA1001122//Plasmodium falciparum chromosome 2, section 20 of 73 of the complete sequence.//9.2e-07:732:57//AE001383	F-HEMBA1001407//Mus musculus domesticus Torino (Sry) gene, complete cds.//0.36:363:57//U03645
F-HEMBA1001123//Homo sapiens full length insert cDNA clone ZD38E1.2.//1.1e-11:231:68//AF086247	F-HEMBA1001411//Homo sapiens genomic DNA, 21q region, clone: S39BG29, genomic survey sequence.//8.4e-12:516:60//AG001050
F-HEMBA1001133//Homo sapiens clone DJ0856024, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.011:163:69//AC004909	F-HEMBA1001413
F-HEMBA1001137//Homo sapiens mRNA for KIAA0798 protein, complete cds.//6.9e-72:527:17//AB018341	F-HEMBA1001415//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 41018, WORKING DRAFT SEQUENCE.//0.98:177:64//AL031732
F-HEMBA1001140//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.3e-120:578:98//AC005077	F-HEMBA1001432//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//8.0e-177:859:97//AC006146
F-HEMBA1001172//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.010:520:59//AC005507	F-HEMBA1001433//Homo sapiens clone DJ0892G19, complete sequence.//2.0e-35:376:64//AC004917
F-HEMBA1001174//R. norvegicus (Sprague Dawley) ARL5 mRNA for ARF-like protein 5.//1.0e-59:565:73//X78604	F-HEMBA1001435//Homo sapiens chromosome 17, clone hRPK.63_A.1, complete sequence.//1.2e-74:284:84//AC005670
F-HEMBA1001197//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0037:151:70//AC004815	F-HEMBA1001442//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-66, complete sequence.//0.056:194:63//AL010138
F-HEMBA1001208//Human BAC clone RC264L19 from 7p15-p21, complete sequence.//7.4e-35:195:81//AC002410	F-HEMBA1001446//Homo sapiens chromosome 4 clone B150J4 map 4q25, complete sequence.//0.96:328:61//AC004047
F-HEMBA1001213//Homo sapiens clone DJ0892G19, complete sequence.//1.9e-171:826:98//AC004917	F-HEMBA1001450
F-HEMBA1001226//Homo sapiens clone DJ0850101, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.00010:557:57//AC006009	F-HEMBA1001454//Human DNA sequence from clone 598A24 on chromosome Xp11.1-11.23 Contains zinc finger X-linked proteins ZXDA, ZXDB, ESTs and STS, complete sequence.//2.0e-47:468:73//AL031115
F-HEMBA1001235//Homo sapiens chromosome 17, clone hRPK.601_M.13, complete sequence.//0.0086:372:58//AC005389	F-HEMBA1001455//CIT978SK-32J2.TV CIT978SK Homo sapiens genomic clone 32J2, genomic survey sequence.//1.5e-05:223:65//B78859
F-HEMBA1001247//H. sapiens CpG island DNA genomic MseI fragment, clone 11b11, reverse read cpg11b11.r1a.//2.0e-24:154:93//Z64441	F-HEMBA1001463//cSRL-69d1-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-69d1, genomic survey sequence.//5.1e-66:564:77//B05652
F-HEMBA1001257//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.9e-88:559:81//AF047020	F-HEMBA1001476//Homo sapiens mRNA for KIAA0572 protein, partial cds.//1.9e-102:489:99//AB011144
F-HEMBA1001265//Human 18S ribosomal RNA.//1.0e-32:180:97//X03205	F-HEMBA1001478//HS_2228_A2_B03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=6 Row=C, genomic survey sequence.//4.5e-40:275:88//AQ032041
F-HEMBA1001281	F-HEMBA1001497//Human DNA sequence from clone 281H8 on chromosome 6q25.1-25.3. Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene). Contains ESTs, STSs, GSSs, a putative CpG island and genomic marker D6S155
F-HEMBA1001286//B. taurus mRNA for RF-36-DNA-binding protein.//7.7e-26:236:81//X15543	
F-HEMBA1001289//Homo sapiens Chromosome 15 BAC clone CIT987SK-A-69 G12, complete sequence.//5.5e-28:530:64//AC004131	
F-HEMBA1001294//Yeast mitochondrial aspl gene for ATPase subunit 8.//2.8e-15:722:60//X00960	
F-HEMBA1001299//Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS, CpG island, complete sequence.//4.2e-24:288:76//AL031003	
F-HEMBA1001302//cDNA encoding a human homologue of a mouse novel polypeptide derived from stromal cell.//7.2e-121:439:96//E12260	
F-HEMBA1001303//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.011:637:56//AC005505	

【表403】

3, complete sequence.//7.7e-47:311:85//AL031133
 F-HEMBA1001510//Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//2.0e-130:69 9:93//J89337
 F-HEMBA1001515//Homo sapiens chromosome 19, cosmid F24866, complete sequence.//4.1e-114:711:85//ACD05794
 F-HEMBA1001517//Homo sapiens BAC clone RG459N13 from 7p15, complete sequence.//5.7e-162:769:98//ACD04549
 F-HEMBA1001522//Caenorhabditis elegans cosmid ZK328.//8.6e-17:498:61//U50193
 F-HEMBA1001526//Human DNA sequence from cosmid 444G9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG islands.//0.31:120:69//Z98258
 F-HEMBA1001533
 F-HEMBA1001557//Chionoecetes opilio (clone COP41) DNA microsatellite repeat regions.//7.0e-25:303:72//L49136
 F-HEMBA1001566//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing monooxygenase 2 and Flavin-containing monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO 11, FMO 3), and a gene for another, unknown, Flavin-containing monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//7.2e-18:805:60//AL021026
 F-HEMBA1001569//Homo sapiens mRNA for vesicle associated membrane protein 2 (VAMP2).//1.1e-64:338:95//AJ225044
 F-HEMBA1001570//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//2.1e-148:698:99//ACD04453
 F-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.2e-173:678:99//AJ012449
 F-HEMBA1001581//Homo sapiens clone DJ1158BD1, WORKING DRAFT SEQUENCE. 23 unordered pieces.//0.30:484:59//ACD04980
 F-HEMBA1001585
 F-HEMBA1001589//Human BAC clone RG317G18 from 7q31, complete sequence.//0.98:197:63//ACD02432
 F-HEMBA1001595//Human mRNA for KIAA0128 gene, partial cds.//8.2e-109:855:78//D50918
 F-HEMBA1001608//RPC111-72E2.TJ RPC111 Homo sapiens genomic clone R-72E2, genomic survey sequence.//3.8e-05:235:64//AQ267131
 F-HEMBA1001620//Oryza sativa RIND1 mRNA for myo-inositol phosphate synthase, complete cds.//3.8e-40:719:64//AB012107
 F-HEMBA1001635//HS_3208_A1_D07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3208 Col=13 Row=G, genomic survey sequence.//1.4e-15:120:90//AQ176944
 F-HEMBA1001636//Homo sapiens 12q24 PAC RPC11-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.15:221:64//ACD04216
 F-HEMBA1001640//HS_3253_B2_D03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3253 Col=6 Row=H, genomic survey sequence.//9.1e-52:278:95//AQ216058
 F-HEMBA1001647//H. sapiens gene for plectin.//0.00052:629:61//Z54367
 F-HEMBA1001651//Salmo salar DNA for a cryptic repeat.//7.9e-08:27 0:64//AJ012206
 F-HEMBA1001655//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//5.9e-164:802:97//ACD05368
 F-HEMBA1001658//M. musculus COL3A1 gene for collagen alpha-1.//2.4e-30:742:62//X52046
 F-HEMBA1001661//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.2e-144:682:99//ACD05740
 F-HEMBA1001672//Homo sapiens methyl-CpG binding protein MB03 (MBD 3) mRNA, complete cds.//6.1e-152:725:98//AF072247
 F-HEMBA1001675//RPC111-54F8.TV RPC111 Homo sapiens genomic clone R-54F8, genomic survey sequence.//5.3e-75:341:85//AQ082126
 F-HEMBA1001678//Homo sapiens Xp22 PAC RPC11-167A22 (from Roswell Park Cancer Center) complete sequence.//8.4e-54:551:74//ACD02349
 F-HEMBA1001681
 F-HEMBA1001702//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//0.94:676:54//AE001398
 F-HEMBA1001709//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 702J19, WORKING DRAFT SEQUENCE.//0.74:659:58//AL033531
 F-HEMBA1001711//Lysiphlebus melandricicola NADH dehydrogenase I gene, mitochondrial gene encoding mitochondrial protein, partial cds.//3.0e-07:413:60//AF069178
 F-HEMBA1001712//Homo sapiens BAC clone RG041H04 from 7q21-q22, complete sequence.//0.091:315:61//ACD04519
 F-HEMBA1001714//Rattus norvegicus mitochondrial ATPase inhibitor gene, complete cds.//1.6e-28:218:75//U12250
 F-HEMBA1001718//HS_3056_A2_H08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3056 Col=16 Row=0, genomic survey sequence.//2.0e-79:383:99//AQ106367
 F-HEMBA1001723//HS_2188_A2_D02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=4 Row=G, genomic survey sequence.//3.8e-28:174:94//AQ116793
 F-HEMBA1001731//HS_3021_A1_A11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3021 Col=21 Row=A, genomic survey sequence.//2.5e-11:420:62//AQ154658
 F-HEMBA1001734//Homo sapiens chromosome Y, clone 264.M.20, complete sequence.//0.00060:392:60//ACD04617
 F-HEMBA1001744//HS_3194_A1_D05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=G, genomic survey sequence.//5.8e-29:163:97//AQ252295
 F-HEMBA1001745//Homo sapiens chromosome 9q34, clone 280C11, complete sequence.//0.66:627:59//ACD02102
 F-HEMBA1001746//HS_2163_B1_F04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2163 Col=7 Row=L, genomic survey sequence.//1.4e-16:238:70//AQ085995
 F-HEMBA1001761//Genomic sequence from Mouse 9, complete sequence.//3.5e-52:198:86//ACD02109
 F-HEMBA1001781
 F-HEMBA1001784//Genomic sequence from Human 9q34, WORKING DRAFT SEQUENCE. 2 unordered pieces.//5.5e-13:296:65//ACD02099
 F-HEMBA1001791//Homo sapiens DNA from chromosome 19-cosmids R3115.8, R31874, and R28125, genomic sequence, complete sequence.//0.18:534:59//AF038458
 F-HEMBA1001800//CIT-HFP-2049NS.TF CIT-HSP Homo sapiens genomic clone 2049NS, genomic survey sequence.//2.2e-40:335:80//AQ009222
 F-HEMBA1001803//M. musculus (Balb/C) P/L01 mRNA.//1.7e-25:286:74//Z31360
 F-HEMBA1001804//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.9e-58:358:89//M21977
 F-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//7.8e-174:809:98//ABD07969
 F-HEMBA1001809//Bovine herpesvirus 1 complete genome.//9.0e-09:63 9:57//AJ004801
 F-HEMBA1001815
 F-HEMBA1001819//HS_3079_B1_E04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3079 Col=7 Row=J, genomic survey sequence.//1.4e-79:396:97//AQ186616
 F-HEMBA1001820//Homo sapiens BAC clone GS165L15 from 7p15, complete sequence.//0.00026:436:60//ACD05013
 F-HEMBA1001822//Homo sapiens intersectin short form mRNA, complete cds.//1.2e-40:510:65//AF064243
 F-HEMBA1001824//Homo sapiens expanded SCA7 CAG repeat.//6.1e-20:34 4:68//AF020275
 F-HEMBA1001835//Homo sapiens BAC clone RG017K18 from 7q31, complete sequence.//0.0094:553:58//ACD05161
 F-HEMBA1001844//Homo sapiens chromosome Xp22-135-136 clone GSHB-56711, WORKING DRAFT SEQUENCE. 35 unordered pieces.//1.2e-22:316:70//ACD05867
 F-HEMBA1001847//M. musculus Zfp-29 gene for zinc finger protein.//5.3e-27:397:69//X55126
 F-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds.//8.8e-184:865:98//AB014517
 F-HEMBA1001864//Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence.//0.38:337:62//ACD05395
 F-HEMBA1001866//Caenorhabditis elegans cosmid F48E3.//1.4e-10:224:63//U28735
 F-HEMBA1001869//Homo sapiens BAC clone RG114B19 from 7q31, complete sequence.//6.7e-98:288:91//ACD05065
 F-HEMBA1001888//Human Chromosome 11p15.5 PAC clone pDJ915f1 containing KvLQT1 gene, complete sequence.//4.9e-114:476:84//ACD03693
 F-HEMBA1001896//Bos taurus pyruvate dehydrogenase phosphatase regulatory subunit precursor, mRNA, complete cds.//2.2e-137:839:86//AF 026954
 F-HEMBA1001910//Homo sapiens Chromosome 2p13 BAC Clone h173, complete sequence.//0.90:221:63//ACD03065
 F-HEMBA1001912//HS_2237_A1_C10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=19 Row=E, genomic survey sequence.//9.7e-76:364:100//AQ033732
 F-HEMBA1001913//Leishmania major chromosome 3 clone L7777 strain Friedlin, WORKING DRAFT SEQUENCE. 6 unordered pieces.//0.00063:219:65//ACD05766
 F-HEMBA1001915//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 5/10.//0.00011:366:63//ABD020873
 F-HEMBA1001918//Pneumocystis carinii gene for major surface glycoprotein MSG105, exon1-2, complete cds.//0.00024:562:58//D82031
 F-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.//2.1e-184:855:99//AF000145
 F-HEMBA1001939//Human DNA sequence from clone 395P12 on chromosome

omic survey sequence.//2.0e-79:383:99//AQ106367
 F-HEMBA1001723//HS_2188_A2_D02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=4 Row=G, genomic survey sequence.//3.8e-28:174:94//AQ116793
 F-HEMBA1001731//HS_3021_A1_A11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3021 Col=21 Row=A, genomic survey sequence.//2.5e-11:420:62//AQ154658
 F-HEMBA1001734//Homo sapiens chromosome Y, clone 264.M.20, complete sequence.//0.00060:392:60//ACD04617
 F-HEMBA1001744//HS_3194_A1_D05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=G, genomic survey sequence.//5.8e-29:163:97//AQ252295
 F-HEMBA1001745//Homo sapiens chromosome 9q34, clone 280C11, complete sequence.//0.66:627:59//ACD02102
 F-HEMBA1001746//HS_2163_B1_F04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2163 Col=7 Row=L, genomic survey sequence.//1.4e-16:238:70//AQ085995
 F-HEMBA1001761//Genomic sequence from Mouse 9, complete sequence.//3.5e-52:198:86//ACD02109
 F-HEMBA1001781
 F-HEMBA1001784//Genomic sequence from Human 9q34, WORKING DRAFT SEQUENCE. 2 unordered pieces.//5.5e-13:296:65//ACD02099
 F-HEMBA1001791//Homo sapiens DNA from chromosome 19-cosmids R3115.8, R31874, and R28125, genomic sequence, complete sequence.//0.18:534:59//AF038458
 F-HEMBA1001800//CIT-HFP-2049NS.TF CIT-HSP Homo sapiens genomic clone 2049NS, genomic survey sequence.//2.2e-40:335:80//AQ009222
 F-HEMBA1001803//M. musculus (Balb/C) P/L01 mRNA.//1.7e-25:286:74//Z31360
 F-HEMBA1001804//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.9e-58:358:89//M21977
 F-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//7.8e-174:809:98//ABD07969
 F-HEMBA1001809//Bovine herpesvirus 1 complete genome.//9.0e-09:63 9:57//AJ004801
 F-HEMBA1001815
 F-HEMBA1001819//HS_3079_B1_E04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3079 Col=7 Row=J, genomic survey sequence.//1.4e-79:396:97//AQ186616
 F-HEMBA1001820//Homo sapiens BAC clone GS165L15 from 7p15, complete sequence.//0.00026:436:60//ACD05013
 F-HEMBA1001822//Homo sapiens intersectin short form mRNA, complete cds.//1.2e-40:510:65//AF064243
 F-HEMBA1001824//Homo sapiens expanded SCA7 CAG repeat.//6.1e-20:34 4:68//AF020275
 F-HEMBA1001835//Homo sapiens BAC clone RG017K18 from 7q31, complete sequence.//0.0094:553:58//ACD05161
 F-HEMBA1001844//Homo sapiens chromosome Xp22-135-136 clone GSHB-56711, WORKING DRAFT SEQUENCE. 35 unordered pieces.//1.2e-22:316:70//ACD05867
 F-HEMBA1001847//M. musculus Zfp-29 gene for zinc finger protein.//5.3e-27:397:69//X55126
 F-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds.//8.8e-184:865:98//AB014517
 F-HEMBA1001864//Arabidopsis thaliana chromosome II BAC F17H15 genomic sequence, complete sequence.//0.38:337:62//ACD05395
 F-HEMBA1001866//Caenorhabditis elegans cosmid F48E3.//1.4e-10:224:63//U28735
 F-HEMBA1001869//Homo sapiens BAC clone RG114B19 from 7q31, complete sequence.//6.7e-98:288:91//ACD05065
 F-HEMBA1001888//Human Chromosome 11p15.5 PAC clone pDJ915f1 containing KvLQT1 gene, complete sequence.//4.9e-114:476:84//ACD03693
 F-HEMBA1001896//Bos taurus pyruvate dehydrogenase phosphatase regulatory subunit precursor, mRNA, complete cds.//2.2e-137:839:86//AF 026954
 F-HEMBA1001910//Homo sapiens Chromosome 2p13 BAC Clone h173, complete sequence.//0.90:221:63//ACD03065
 F-HEMBA1001912//HS_2237_A1_C10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=19 Row=E, genomic survey sequence.//9.7e-76:364:100//AQ033732
 F-HEMBA1001913//Leishmania major chromosome 3 clone L7777 strain Friedlin, WORKING DRAFT SEQUENCE. 6 unordered pieces.//0.00063:219:65//ACD05766
 F-HEMBA1001915//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 5/10.//0.00011:366:63//ABD020873
 F-HEMBA1001918//Pneumocystis carinii gene for major surface glycoprotein MSG105, exon1-2, complete cds.//0.00024:562:58//D82031
 F-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds.//2.1e-184:855:99//AF000145
 F-HEMBA1001939//Human DNA sequence from clone 395P12 on chromosome

【0703】

【表404】

1a24-25. Contains the TIGP1 gene for tax-transcriptionally activated glycoprotein 1 (34kd) (OX40L) and a G0T2 (Aspartate Aminotransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//1.1e-42:380:80//AL022310	25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (CTR2-2), ESTs and CA repeat.//1.2e-50:319:78//AL008712
F-HEMBA1001940//Homo sapiens clone DJ1093116, WORKING DRAFT SEQUENCE. 5 unordered pieces.//7.5e-175:861:97//AC005629	F-HEMBA1002177//Homo sapiens BAC clone RG293F11 from Tq21-Tq22, complete sequence.//2.5e-18:150:88//AC000066
F-HEMBA1001942//Homo sapiens chromosome 12p13.3 clone RPC11-96H9, WORKING DRAFT SEQUENCE. 66 unordered pieces.//0.097:107:71//AC006057	F-HEMBA1002185//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE. 2 unordered pieces.//0.00066:466:59//AC004825
F-HEMBA1001945//Drosophila F family transposable element F12 3' region.//0.94:140:65//X01934	F-HEMBA1002189//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE. 7 unordered pieces.//3.3e-23:176:77//AC005015
F-HEMBA1001950//H. sapiens CpG island DNA genomic MseI fragment, clone 15b5, forward read cpg15b5.f11q.//1.4e-27:168:95//Z54728	F-HEMBA1002191//Homo sapiens mRNA for KIAA0689 protein, partial cds.//1.0:382:59//AB014589
F-HEMBA1001960//Locusta migratoria mRNA for nAChR alpha subunit.//0.010:108:71//AJ000390	F-HEMBA1002199//Homo sapiens chromosome 4 clone B55B24 map 4q25, complete sequence.//1.8e-20:368:66//AC005150
F-HEMBA1001962//Plasmodium falciparum 3D7 chromosome 12 PFYACB-62 B genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//9.7e-05:494:60//AC005507	F-HEMBA1002204//HS_2055_A1_H09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=17 Row=0, genomic survey sequence.//1.2e-06:178:65//AQ235350
F-HEMBA1001964	F-HEMBA1002212//S. cerevisiae chromosome IV reading frame ORF YDL101c.//0.035:345:60//Z74149
F-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (preliminary isolate of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs, complete sequence.//9.6e-122:373:99//AL031178	F-HEMBA1002215//M. musculus mRNA for testin.//4.6e-80:504:87//X78989
F-HEMBA1001979//HS_3067_B1_A06_M9 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3067 Col=11 Row=B, genomic survey sequence.//0.43:193:64//AQ143506	F-HEMBA1002226//Homo sapiens Xp22 bins 87-93 PAC RPC11-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.7e-63:336:74//AC003035
F-HEMBA1001987//Plasmodium falciparum MAL3P6, complete sequence.//1.0:428:56//Z98551	F-HEMBA1002229//Homo sapiens BAC clone NH0539824 from Tp15.1-p14, complete sequence.//2.6e-39:311:81//AC006044
F-HEMBA1001991//HS_2237_A2_G09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=18 Row=M, genomic survey sequence.//4.3e-05:240:64//AQ067283	F-HEMBA1002237//Homo sapiens PAC clone DJ0696ND1 from Tp21-p22, complete sequence.//1.6e-12:397:64//AC004861
F-HEMBA1002003//protein phosphatase 2C isoform [rats, liver, mRNA, 1950 nt].//2.7e-33:364:74//S90449	F-HEMBA1002241
F-HEMBA1002008//WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00032:214:68//AC005948	F-HEMBA1002253
F-HEMBA1002018	F-HEMBA1002257//Homo sapiens diacylglycerol kinase iota (DGKi) mRNA, complete cds.//3.5e-151:731:97//AF061936
F-HEMBA1002022//Human p37NB mRNA, complete cds.//0.014:58:96//U32907	F-HEMBA1002265//Human DNA sequence from cosmid N28H9 on chromosome 22q11.2-qter contains ESTs, STS and endogenous retrovirus.//1.3e-09:313:62//Z71183
F-HEMBA1002035//Mouse transcriptional control element.//7.8e-07:20:0:69//W17284	F-HEMBA1002267
F-HEMBA1002039//Human DNA sequence from clone 267W20 on chromosome 1q22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//0.31:497:58//AL031053	F-HEMBA1002270//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//0.069:495:58//AC006210
F-HEMBA1002049//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//4.5e-42:532:63//AC005216	F-HEMBA1002321//Homo sapiens PAC clone DJ0991023, complete sequence.//0.019:564:58//AC004944
F-HEMBA1002084//Homo sapiens chromosome 19 cosmid F15386, genomic sequence, complete sequence.//0.81:435:59//AF025422	F-HEMBA1002328//CIT-HSP-2387N15, TF.1 CIT-HSP Homo sapiens genomic clone 2387N15, genomic survey sequence.//1.8e-71:346:99//AQ240836
F-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//7.2e-130:769:87//U92703	F-HEMBA1002337//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence.//0.84:547:57//AB020754
F-HEMBA1002100//Homo sapiens PAC clone DJ0991G20, complete sequence.//1.3e-47:124:96//AC004943	F-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds.//2.4e-185:872:98//AB018314
F-HEMBA1002102//Xenopus laevis mRNA for xSox7 protein, complete cds.//2.7e-13:132:71//D83649	F-HEMBA1002348//CIT-HSP-2372K24, TR CIT-HSP Homo sapiens genomic clone 2372K24, genomic survey sequence.//9.1e-33:230:75//AQ110676
F-HEMBA1002113//F. rubripes GSS sequence, clone 063K10b84, genomic survey sequence.//0.029:142:66//Z88840	F-HEMBA1002349//Plasmodium falciparum histidine-rich protein 11 (HRP11) gene, complete cds.//9.4e-06:504:57//U69551
F-HEMBA1002119//Human Chromosome 11 pac pDJ1173a5, complete sequence.//1.3e-14:515:62//AC000378	F-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//7.3e-188:872:99//AF092563
F-HEMBA1002125//Homo sapiens calcium-activated potassium channel (KCNMB3) mRNA, complete cds.//0.98:222:61//AF031815	F-HEMBA1002381//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11.//2.1e-20:262:72//AB020868
F-HEMBA1002139//Caenorhabditis elegans cosmid F55C9, complete sequence.//0.0081:371:60//Z81549	F-HEMBA1002389//D. discoideum spore coat 60 (sp60) gene, 5' flank.//0.010:95:73//M34546
F-HEMBA1002144//Saccharomyces cerevisiae mitochondrion transfer RNA A-Met (tRNA-Met) gene, oxil gene, and ORF1.//4.9e-06:341:61//L36888	F-HEMBA1002417//Canis familiaris ZO-3 (zo-3) mRNA, complete cds.//6.2e-120:767:85//AF023617
F-HEMBA1002150//Homo sapiens mRNA for KIAA0720 protein, partial cds.//0.00017:353:62//AB018263	F-HEMBA1002419//HS-1047-A1-F01-MF, abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830 Col=1 Row=K, genomic survey sequence.//7.6e-06:111:76//B38165
F-HEMBA1002151	F-HEMBA1002430//HS_3137_B2_F10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3137 Col=20 Row=L, genomic survey sequence.//1.6e-56:367:88//AQ148697
F-HEMBA1002153//CITB1-E1-2519120, TR CITB1-E1 Homo sapiens genomic clone 2519120, genomic survey sequence.//8.5e-61:334:94//AQ277613	F-HEMBA1002439//Dictyostelium discoideum actin 8 gene, 3' UTR.//0.67:129:64//M25216
F-HEMBA1002160//Homo sapiens clone DJ1189D06, complete sequence.//8.5e-44:385:77//AC005232	F-HEMBA1002458//Mus musculus REX-3 mRNA, complete cds.//1.1e-30:274:72//AF051347
F-HEMBA1002161//Coturnix coturnix slow myosin heavy chain 2 (qmyh2) mRNA, partial cds.//2.1e-59:571:74//AF006829	F-HEMBA1002460//Homo sapiens clone DJ1137M13, complete sequence.//4.0e-173:822:98//AC005378
F-HEMBA1002162//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//5.3e-53:698:67//AC006210	F-HEMBA1002462//Sequence 41 from patent US 5708157.//9.8e-51:519:73//180067
F-HEMBA1002166//Human DNA sequence from PAC 84F12 on chromosome 1q	F-HEMBA1002469//Human mRNA for KIAA0122 gene, partial cds.//4.0e-108:603:92//D50912

【0704】

【表405】

omic survey sequence.//1.0:179:67//AQ181410
 F-HEMBA1002498//Homo sapiens full length insert cDNA clone ZD7680
 1.//1.4e-129:619:98//AF086404
 F-HEMBA1002503//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUEN
 CE, 6 unordered pieces.//1.9e-24:306:68//AC004873
 F-HEMBA1002508//Homo sapiens chromosome 19, cosmid R33516, complet
 e sequence.//2.9e-76:464:83//AC004799
 F-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like pro
 tein (JN21).//2.8e-157:738:98//AJ011972
 F-HEMBA1002515//Human DNA sequence *** SEQUENCING IN PROGRESS ***
 from clone 407F11, WORKING DRAFT SEQUENCE.//2.6e-07:307:64//AL0223
 29
 F-HEMBA1002538//HS_2185_B2_B04_MR CIT Approved Human Genomic Sperm
 Library D Homo sapiens genomic clone Plate=2185 Col=8 Row=D, geno
 mic survey sequence.//4.7e-37:339:78//AQ298315
 F-HEMBA1002542//HS_3197_B2_B10_T7 CIT Approved Human Genomic Sperm
 Library D Homo sapiens genomic clone Plate=3197 Col=20 Row=D, gen
 omic survey sequence.//3.2e-70:372:95//AQ188792
 F-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds.//
 3.5e-137:655:98//AF016903
 F-HEMBA1002552//Human Hep27 protein mRNA, complete cds.//8.8e-07:1
 73:68//U31875
 F-HEMBA1002555//*** SEQUENCING IN PROGRESS *** Homo sapiens chromo
 some 4, BAC clone C019D06: HTGS phase 1, WORKING DRAFT SEQUENCE,
 21 unordered pieces.//2.2e-15:628:60//AC004670
 F-HEMBA1002558//Human Xp22 BAC CT-285115 (from CalTech/Research Ge
 netics), PAC RPC11-27C22 (from Roswell Park Cancer Center), and C
 osmid U3585 (from Lawrence Livermore), complete sequence.//2.3e-4
 1:353:76//AC002366
 F-HEMBA1002561//Homo sapiens chromosome 17, clone HRPC29G21, compl
 ete sequence.//1.1e-39:538:66//AC03687
 F-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, com
 plete cds.//1.3e-140:457:99//AF075587
 F-HEMBA1002583//CIT-HSP-2321D3.TR CIT-HSP Homo sapiens genomic clo
 ne 2321D3, genomic survey sequence.//5.1e-79:385:99//AQ038102
 F-HEMBA1002590//Homo sapiens chromosome 17, clone hRPK.167_N20, c
 omplete sequence.//1.9e-35:430:70//AC005940
 F-HEMBA1002592//Human genomic DNA sequence from clone 30801 on chr
 omosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG islan
 d.//4.4e-19:303:71//Z93403
 F-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cd
 s.//4.4e-175:820:99//AB011169
 F-HEMBA1002621//Homo sapiens PAC clone DJ0650P09 from 7q21, comple
 te sequence.//0.14:353:58//AC004413
 F-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete c
 ds.//2.9e-187:632:97//AB018351
 F-HEMBA1002628//Plasmodium falciparum 3D7 chromosome 12 PFYACB12 g
 enomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.5
 e-05:792:58//AC004153
 F-HEMBA1002629//Streptomyces coelicolor cosmid 1A9.//8.4e-08:576:5
 8//AL034446
 F-HEMBA1002645//Human DNA sequence *** SEQUENCING IN PROGRESS ***
 from clone 153G14, WORKING DRAFT SEQUENCE.//5.6e-47:222:86//AL0311
 18
 F-HEMBA1002651//Homo sapiens PAC clone DJ0593H12 from 7p31, comple
 te sequence.//3.8e-182:859:99//AC004839
 F-HEMBA1002659//Z. mobilis alcohol dehydrogenase I (adhA) gene, com
 plete cds.//0.97:144:66//B32100
 F-HEMBA1002661//Homo sapiens PAC clone DJ0698G21 from 7p21-p22, co
 mplete sequence.//1.3e-116:774:84//AC004535
 F-HEMBA1002666
 F-HEMBA1002678//Human DNA sequence *** SEQUENCING IN PROGRESS ***
 from clone 1137F22, WORKING DRAFT SEQUENCE.//5.7e-156:750:98//AL03
 4421
 F-HEMBA1002679//nbxb0002cC12r CUG1 Rice BAC Library Oryza sativa g
 enomic clone nbxb0002F23r, genomic survey sequence.//4.3e-09:517:5
 8//AQ051621
 F-HEMBA1002688//Herpes simplex virus type 2 (strain HG52), complet
 e genome.//8.3e-20:651:61//Z86099
 F-HEMBA1002696//Mus musculus proteasome regulator PA28 beta subuni
 t gene, complete cds.//7.6e-62:306:81//AF060195
 F-HEMBA1002703//Homo sapiens mRNA for KIAA0455 protein, complete c
 ds.//1.9e-10:327:62//AB007924
 F-HEMBA1002712
 F-HEMBA1002716//HS_3064_A1_C10_MF CIT Approved Human Genomic Sperm
 Library D Homo sapiens genomic clone Plate=3064 Col=19 Row=E, gen
 omic survey sequence.//8.4e-97:491:96//AQ142980
 F-HEMBA1002728//Homo sapiens chromosome 5, BAC clone 205e20 (LBML
 H170), complete sequence.//6.1e-21:217:77//AC004782
 F-HEMBA1002730//Human platelet glycoprotein IIIa (GP11a) gene, ex
 on 1.//0.57:125:67//M57481
 F-HEMBA1002742//RPC111-39J10.TP RPC111 Homo sapiens genomic clone
 RPC111-39J10, genomic survey sequence.//1.1e-86:414:99//AQ029102
 F-HEMBA1002746//Mus musculus chromosome 19, clone C1T282B21, compl
 ete sequence.//7.1e-70:303:82//AC003694
 F-HEMBA1002748//Human DNA sequence *** SEQUENCING IN PROGRESS ***
 from clone 41018, WORKING DRAFT SEQUENCE.//0.096:212:62//AL031732
 F-HEMBA1002750//Homo sapiens chromosome 5, PAC clone 170a10 (LBML
 H89), complete sequence.//6.7e-40:232:70//AC004622
 F-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cd
 s.//9.0e-177:834:98//AB011126
 F-HEMBA1002770//cDNA encoding novel rat protein TIP120 which is fo
 rmed of complex with TBP (TATA binding protein).//1.3e-140:840:88/
 E12829
 F-HEMBA1002777//F. rubripes GSS sequence, clone 189C06dB12, genomic
 survey sequence.//1.1e-28:263:77//AL007965
 F-HEMBA1002779//CIT-HSP-233311.TF CIT-HSP Homo sapiens genomic cl
 one 233311, genomic survey sequence.//1.8e-32:180:98//AQ036891
 F-HEMBA1002780//Homo sapiens PAC clone DJ0244J05 from 5q31, comple
 te sequence.//7.0e-06:199:67//AC004592
 F-HEMBA1002794//H.sapiens mRNA for protein kinase C mu.//0.00015:2
 44:67//X75756
 F-HEMBA1002801//Plasmodium falciparum MAL3P2, complete sequence.//
 0.0010:534:57//AL034558
 F-HEMBA1002810//Homo sapiens formin binding protein Z1 mRNA, compl
 ete cds.//1.1e-167:820:97//AF071185
 F-HEMBA1002816//Homo sapiens clone MH0576N21, WORKING DRAFT SEQUEN
 CE, 5 unordered pieces.//3.1e-113:254:90//AC005043
 F-HEMBA1002818//Cricetulus griseus H411 precursor (H411) mRNA, com
 plete cds.//1.2e-122:760:86//AF046870
 F-HEMBA1002826//Human DNA sequence from clone 23K20 on chromosome
 Xq25-26.2 Contains EST, STS, GSS, complete sequence.//0.0055:235:6
 5//AL022153
 F-HEMBA1002833//Homo sapiens chromosome 17, clone hRPC.117_B12, c
 omplete sequence.//1.4e-170:744:99//AC004707
 F-HEMBA1002850//Ephedrus persicae NADH dehydrogenase I gene, mitoc
 hondrial gene encoding mitochondrial protein, partial cds.//1.3e-0
 5:334:59//AF069186
 F-HEMBA1002863//CIT-HSP-2323A16.TF CIT-HSP Homo sapiens genomic cl
 one 2323A16, genomic survey sequence.//2.9e-140:750:93//AQ028419
 F-HEMBA1002876//HS_2270_B1_H03_MF CIT Approved Human Genomic Sperm
 Library D Homo sapiens genomic clone Plate=2270 Col=5 Row=P, geno
 mic survey sequence.//0.44:163:64//AQ164031
 F-HEMBA1002886
 F-HEMBA1002896//Homo sapiens chromosome 5, P1 clone 793CS (LBML HS
 B), complete sequence.//0.00015:277:61//AC005195
 F-HEMBA1002921
 F-HEMBA1002924//CIT-HSP-2171H4.TR CIT-HSP Homo sapiens genomic cl
 one 2171H4, genomic survey sequence.//0.0016:175:66//B89715
 F-HEMBA1002934//Human DNA sequence *** SEQUENCING IN PROGRESS ***
 from clone 862K6, WORKING DRAFT SEQUENCE.//1.2e-169:797:98//AL0316
 81
 F-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cd
 s.//4.9e-173:803:99//AB011148
 F-HEMBA1002937//Human DNA sequence *** SEQUENCING IN PROGRESS ***
 from clone 702J19, WORKING DRAFT SEQUENCE.//1.2e-163:411:99//AL033
 531
 F-HEMBA1002939//RPC111-74014.TJ RPC111 Homo sapiens genomic clone
 R-74014, genomic survey sequence.//1.7e-41:215:99//AQ266676
 F-HEMBA1002944//RPC111-55C2.TV RPC111 Homo sapiens genomic clone
 R-55C2, genomic survey sequence.//1.7e-37:375:74//AQ082240
 F-HEMBA1002951//Homo sapiens chromosome 19, cosmid F20887, complet
 e sequence.//0.00074:683:58//AC005578
 F-HEMBA1002954//RPC111-79F7.TV RPC111 Homo sapiens genomic clone
 R-79F7, genomic survey sequence.//6.1e-24:250:78//AQ284146
 F-HEMBA1002968//HS_2262_B2_G04_T7 CIT Approved Human Genomic Sperm
 Library D Homo sapiens genomic clone Plate=2262 Col=8 Row=N, geno
 mic survey sequence.//0.99:270:60//AQ217059
 F-HEMBA1002970//RPC111-5L24.TV RPC111 Homo sapiens genomic clone
 RPC111-5L24, genomic survey sequence.//1.4e-10:189:71//B49289
 F-HEMBA1002971//CIT-HSP-2363L16.TF CIT-HSP Homo sapiens genomic cl
 one 2363L16, genomic survey sequence.//4.3e-21:181:80//AQ080538
 F-HEMBA1002973//Rattus norvegicus Wistar 3',5'-cyclic AMP phosphod
 iesterase (PDE4-10) gene, exon 10.//2.5e-40:257:89//U01290
 F-HEMBA1002997//CIT-HSP-2387H15.TF.1 CIT-HSP Homo sapiens genomic
 clone 2387H15, genomic survey sequence.//9.5e-17:128:92//AQ240797
 F-HEMBA1002999//Rattus norvegicus lamina associated polypeptide 1C
 (LAP1C) mRNA, complete cds.//3.1e-62:713:73//U20286
 F-HEMBA1003021//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUEN
 CE, 3 unordered pieces.//7.5e-50:331:85//AC005484

【0705】

【表406】

F-HEMBA1003033//Drosophila melanogaster, chromosome 3L, region 62A 10-62B5, P1 clones DS02777, DS03222, DS03345, and DS04808, complete sequence.//2.6e-20:357:66//AC005557	survey sequence.//0.00032:57:96//B46142
F-HEMBA1003034//Human DNA sequence from 4PTEL, Huntington's Disease Region, chromosome 4p16.3.//4.5e-60:415:73//Z95704	F-HEMBA1003257//H.sapiens mRNA for RDC-1 POU domain containing protein.//2.2e-08:531:59//X64624
F-HEMBA1003035//Homo sapiens chromosome Y, clone 264.M.20, complete sequence.//2.3e-05:591:57//AC004617	F-HEMBA1003273//H.sapiens flow-sorted chromosome 6 HindIII fragment, SC6pA19H4.//0.070:267:64//Z78949
F-HEMBA1003037//RPC111-88F2.TJ RPC111 Homo sapiens genomic clone R-88F2, genomic survey sequence.//0.68:230:60//AQ286677	F-HEMBA1003276//CIT-HSP-230184.TF CIT-HSP Homo sapiens genomic clone 230184, genomic survey sequence.//5.2e-08:295:63//AQ015073
F-HEMBA1003041//Homo sapiens PAC clone DJ1163J12 from Tq21.2-q31.1, complete sequence.//8.1e-128:550:94//AC004983	F-HEMBA1003278//HS_3075_A1_G09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=17 Row=M, genomic survey sequence.//0.98:399:58//AQ120599
F-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds.//1.0e-164:777:98//AF054182	F-HEMBA1003281//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//4.8e-101:277:97//AC005840
F-HEMBA1003064//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.5e-07:744:59//AC005505	F-HEMBA1003286//Homo sapiens chromosome 3q13 beta-1,4-galactosyltransferase mRNA, complete cds.//9.0e-145:539:97//AF038662
F-HEMBA1003067//Rat dynorphin gene, exon 3.//1.0:140:63//M32783	F-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds.//5.0e-166:799:98//AB011109
F-HEMBA1003071//Homo sapiens alpha-C4-adrenergic receptor gene, complete cds.//1.5e-20:595:65//U72648	F-HEMBA1003296//CITB1-E1-2507M8.TR CITB1-E1 Homo sapiens genomic clone 2507M8, genomic survey sequence.//1.9e-05:388:63//AQ262551
F-HEMBA1003077//CIT-HSP-2366J21.TF CIT-HSP Homo sapiens genomic clone 2366J21, genomic survey sequence.//4.4e-33:176:99//AQ080257	F-HEMBA1003304//Budworm mitochondrial partial transfer RNA-Met (tRNA-Met) gene; and partial 12S ribosomal RNA (12S rRNA) gene.//8.0e-05:388:62//L17343
F-HEMBA1003078//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CoQ island. Contains ESTs, genomic marker D1S2691 and STSs.//9.4e-43:478:70//Z9297	F-HEMBA1003309//Crassostrea gigas clone CN20 microsatellite sequence.//0.0017:210:64//AF051177
F-HEMBA1003079//Homo sapiens Xp22-132-134 BAC CSHB-590J15 (Genome Systems Human BAC library) complete sequence.//0.96:57:85//AC004673	F-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds.//4.6e-188:865:99//AB001872
F-HEMBA1003083//Homo sapiens PAC clone DJ1182N03 from Tq11.23-q21.1, complete sequence.//8.0e-74:359:81//AC004548	F-HEMBA1003322//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 16915, WORKING DRAFT SEQUENCE.//2.4e-54:316:87//Z93015
F-HEMBA1003086//Homo sapiens chromosome 16 BAC clone CIT987SK-334011 complete sequence.//3.6e-11:734:58//AF001550	F-HEMBA1003327//CIT-HSP-2024C24.TRB CIT-HSP Homo sapiens genomic clone 2024C24, genomic survey sequence.//8.4e-12:166:76//B67147
F-HEMBA1003096//Sequence 4 from patent US 5440017.//5.7e-56:594:71//113750	F-HEMBA1003328//HS_2230_B2_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2230 Col=16 Row=P, genomic survey sequence.//0.026:128:71//AQ153313
F-HEMBA1003098//Human DNA sequence from cosmid SRL11M20, chromosome region 11p13. Contains EST and STS.//1.9e-09:230:69//Z83308	F-HEMBA1003330//Homo sapiens wbscr1 (WBSR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//4.0e-160:745:99//AF045555
F-HEMBA1003117//Mouse T1S1 primary response gene, complete cds.//0.00054:480:60//M58564	F-HEMBA1003348//HS_3194_A1_G05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3194 Col=9 Row=M, genomic survey sequence.//5.0e-79:381:99//AQ173779
F-HEMBA1003129//HS_3139_B2_F05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3139 Col=10 Row=L, genomic survey sequence.//2.3e-100:510:97//AQ187635	F-HEMBA1003369//H.vulgaris GAA-satellite DNA.//0.12:89:71//Z50100
F-HEMBA1003133//Mouse BAC C1bCJ7 219m7, genomic sequence, complete sequence.//1.3e-78:370:90//AC005259	F-HEMBA1003370//Homo sapiens cosmid 123E15, complete sequence.//3.5e-32:199:80//AF024533
F-HEMBA1003136	F-HEMBA1003373//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SEQUENCE.//0.019:117:71//AL034405
F-HEMBA1003142//Homo sapiens full length insert cDNA clone ZC39806.//6.9e-121:563:100//AF086197	F-HEMBA1003376//Human clone HS4.66 Alu-Ya5 sequence.//4.2e-30:196:85//U67229
F-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//6.7e-183:850:99//AJ005670	F-HEMBA1003380//Homo sapiens DNA sequence from clone 394P21 on chromosome 1p36.12-36.13. Contains the PAX7 gene, locus D1S2644, ESTs and STSs, complete sequence.//4.6e-22:206:81//AL021528
F-HEMBA1003166//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-34564 complete genomic sequence, complete sequence.//3.8e-27:229:76//AC002302	F-HEMBA1003384//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00094:72:90//AC006026
F-HEMBA1003175//Homo sapiens genomic DNA for centromeric end of NH C class I region on chromosome 6, WORKING DRAFT SEQUENCE.//9.4e-09:837:58//AB000882	F-HEMBA1003395//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE.//0.00041:826:57//AL031744
F-HEMBA1003179//Homo sapiens DNA sequence from Fosmid 27C3 on chromosome 22q11.2-qter. Contains two possibly alternatively spliced unknown genes, one with homology to a worm protein. Contains ESTs, complete sequence.//5.4e-115:174:98//AL022325	F-HEMBA1003402//CIT-HSP-2339K16.TR CIT-HSP Homo sapiens genomic clone 2339K16, genomic survey sequence.//2.4e-05:265:64//AQ056234
F-HEMBA1003197//Arabidopsis thaliana chromosome 11 BAC F15K20 genomic sequence, complete sequence.//1.1e-05:473:59//AC005824	F-HEMBA1003403//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//4.3e-135:780:90//AC004066
F-HEMBA1003199//Rattus norvegicus Sprague-Dawley thyroid hormone receptor alpha gene, exon 1.//1.6e-05:367:61//U09302	F-HEMBA1003408
F-HEMBA1003202//Homo sapiens BAC clone RC437L15 from 8q21, complete sequence.//9.0e-23:247:73//AC004003	F-HEMBA1003417//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//1.9e-41:239:95//AL031321
F-HEMBA1003204//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 409J21, WORKING DRAFT SEQUENCE.//4.7e-26:141:83//Z83824	F-HEMBA1003418//Rattus norvegicus Wistar polymeric immunoglobulin receptor (PIGR) gene, 3' UTR and trinucleotide repeat microsatellites.//2.2e-06:247:64//U08273
F-HEMBA1003212//Human Chromosome 11 Overlapping Cosmids cSRL72g2 and cSRL140b8, complete sequence.//1.9e-31:158:86//AC002037	F-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds.//1.4e-149:697:99//AF051334
F-HEMBA1003220//Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.4e-24:284:75//AC004150	F-HEMBA1003447//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//1.7e-77:461:90//AC004066
F-HEMBA1003222//RPC111-47P17.TJ RPC111 Homo sapiens genomic clone R-47P17, genomic survey sequence.//0.7e-39:202:99//AQ202885	F-HEMBA1003461//Rhodobacter sphaeroides FliH (fliH) gene, partial cds, FliI (fliI) and FliJ (fliJ) genes, complete cds.//8.6e-08:752:58//U31090
F-HEMBA1003229//Arabidopsis thaliana genomic DNA, chromosome 3, PI clone: NEB5, complete sequence.//0.86:227:62//AB019230	F-HEMBA1003463//Homo sapiens chromosome 17, clone HCIT305D20, complete sequence.//0.089:172:68//AC004098
F-HEMBA1003235//Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence.//0.6e-05:372:61//AE001373	F-HEMBA1003480//Homo sapiens clone NH0523H20, complete sequence.//4.5e-150:562:97//AC005041
F-HEMBA1003250//HS-1063-A1-H02-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 796 Col=3 Row=0, genomic	F-HEMBA1003528//Streptomyces fradiae gene for trypsinogen precursor, complete cds.//4.7e-09:433:60//D16687
	F-HEMBA1003531//Homo sapiens PAC clone DJ1185107 from Tq11.23-q21, complete sequence.//2.3e-48:297:90//AC004990

【0706】

【表407】

F-HEMBA1003538//Human complement C1r mRNA, complete cds.//4.3e-22:474:63//M14058
 F-HEMBA1003545//Rattus norvegicus (clone 1.6kb) islet-2 mRNA, complete cds.//3.5e-143:805:91//L35571
 F-HEMBA1003548
 F-HEMBA1003555//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 447E6, WORKING DRAFT SEQUENCE.//3.4e-58:331:83//AL031724
 F-HEMBA1003556//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome Systems Human BAC Library) complete sequence.//6.0e-99:703:84//AC005913
 F-HEMBA1003560//Bovine GTP-binding regulatory protein gamma-6 subunit mRNA, complete cds.//1.3e-99:587:89//J05071
 F-HEMBA1003568//HS_3149_A1_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3149 Col=7 Row=E, genomic survey sequence.//4.1e-05:389:57//AQ166810
 F-HEMBA1003569//Homo sapiens BAC clone NH0335J18 from 2, complete sequence.//1.6e-102:669:85//AC005539
 F-HEMBA1003571//Dictyostelium discoideum RegA (regA) gene, complete cds.//0.00033:649:58//U60170
 F-HEMBA1003579//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MALIP1, WORKING DRAFT SEQUENCE.//0.00034:623:56//AL031744
 F-HEMBA1003581//Mouse mRNA for talin.//3.3e-41:181:86//X56123
 F-HEMBA1003591//Homo sapiens chromosome 16, BAC clone RPC1-11_192K18, complete sequence.//4.4e-70:273:94//AC006075
 F-HEMBA1003595//Plasmodium falciparum chromosome 2, section 32 of 73 of the complete sequence.//6.0e-17:768:58//AE001395
 F-HEMBA1003597//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//4.0e-09:777:56//AE001398
 F-HEMBA1003598//Homo sapiens PAC clone OJ0537P09 from Tpl1.2-p12, complete sequence.//1.3e-146:692:98//AC005153
 F-HEMBA1003615//HS_2010_A2_A07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2010 Col=14 Row=A, genomic survey sequence.//1.1e-22:137:97//AQ226592
 F-HEMBA1003617//Homo sapiens HRHFB2157 mRNA, partial cds.//2.4e-169:501:97//AB015344
 F-HEMBA1003621//Mus musculus PIAS3 mRNA, complete cds.//4.7e-37:165:92//AF034080
 F-HEMBA1003622//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0024:514:58//AC005139
 F-HEMBA1003630//CIT-HSP-2168N15, TR CIT-HSP Homo sapiens genomic clone 2168N15, genomic survey sequence.//6.5e-15:358:63//B92984
 F-HEMBA1003637//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.0e-21:238:76//AC005077
 F-HEMBA1003640//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 112K5, WORKING DRAFT SEQUENCE.//2.3e-15:371:63//Z85987
 F-HEMBA1003645//A. thaliana 81kb genomic sequence.//1.0:529:57//X98130
 F-HEMBA1003646
 F-HEMBA1003656
 F-HEMBA1003662//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence.//1.6e-175:824:98//AC005746
 F-HEMBA1003667//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces.//1.1e-24:190:87//AC004765
 F-HEMBA1003679//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//1.7e-162:579:99//AC005065
 F-HEMBA1003680//H. sapiens DNA sequence.//7.3e-22:172:87//Z22322
 F-HEMBA1003684//H. sapiens mRNA for Miz-1 protein.//0.0054:146:70//Y09723
 F-HEMBA1003690//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//2.9e-72:606:77//AF039691
 F-HEMBA1003692
 F-HEMBA1003711//Homo sapiens chromosome 17, clone HRP41C23, complete sequence.//0.55:450:60//AC003101
 F-HEMBA1003714
 F-HEMBA1003715//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DIS8098, complete sequence.//3.0e-16:316:68//AL023575
 F-HEMBA1003720//Homo sapiens chromosome 4 clone B227H22 map 4q25, complete sequence.//1.3e-41:483:73//AC004056
 F-HEMBA1003725//CIT-HSP-2351H9, TF CIT-HSP Homo sapiens genomic clone 2351H9, genomic survey sequence.//1.1e-112:532:99//AQ079348
 F-HEMBA1003729//HS_3043_A1_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3043 Col=13 Row=I, genomic survey sequence.//1.6e-12:87:98//AQ129345
 F-HEMBA1003733//Homo sapiens, clone hRPK.15_A_1, complete sequence.//4.7e-104:761:82//AC006213
 F-HEMBA1003742//HS_3027_A2_B02_MR CIT Approved Human Genomic Sperm

Library D Homo sapiens genomic clone Plate=3027 Col=4 Row=C, genomic survey sequence.//3.4e-08:67:97//AQ154731
 F-HEMBA1003758//CIT-HSP-2379D18, TR CIT-HSP Homo sapiens genomic clone 2379D18, genomic survey sequence.//2.9e-10:310:63//AQ113513
 F-HEMBA1003760//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//6.4e-114:714:86//AF060194
 F-HEMBA1003773//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.078:378:58//AC005139
 F-HEMBA1003783//Human DNA sequence from PAC 509L4 on chromosome 6q22.1-6q22.33. Contains SSX3 like pseudogene, EST, STS.//9.0e-135:804:89//Z99496
 F-HEMBA1003784//Caenorhabditis elegans cosmid C5586.//0.054:463:58//U80181
 F-HEMBA1003799//Homo sapiens Chromosome 22q11.2 Cosmid Clone 105a In DCCR Region, complete sequence.//1.9e-44:425:76//AC000070
 F-HEMBA1003803//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds.//0.95:198:62//L40178
 F-HEMBA1003804//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence.//1.2e-138:275:99//AC004596
 F-HEMBA1003805//Mus musculus quaking type 1 (QK1) mRNA, complete cds.//6.6e-148:753:95//U44940
 F-HEMBA1003807//HS-1068-B1-G06-MR, abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 278 Col=11 Row=M, genomic survey sequence.//6.7e-07:241:67//B47212
 F-HEMBA1003827//Homo sapiens mRNA for KIAA0616 protein, partial cds.//1.0e-83:586:87//AB014516
 F-HEMBA1003836//S. cerevisiae chromosome IX cosmid 9150.//5.1e-16:368:63//Z38125
 F-HEMBA1003838//CIT-HSP-384J15, TR CIT-HSP Homo sapiens genomic clone 384J15, genomic survey sequence.//1.4e-45:180:90//B54810
 F-HEMBA1003856//Homo sapiens chromosome 10 clone CIT987SK-1188B12 map 10p12.1, complete sequence.//0.0014:574:58//AC005875
 F-HEMBA1003864//, complete sequence.//2.1e-91:234:95//AC005300
 F-HEMBA1003866//Mus musculus semaphorin 11a mRNA, complete cds.//5.9e-81:853:71//AF030430
 F-HEMBA1003879//H. sapiens CBP80 mRNA.//2.0e-08:87:95//X80030
 F-HEMBA1003880//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//1.7e-180:853:98//AP000036
 F-HEMBA1003885//Homo sapiens PAC clone OJ0167F23 from 7p15, complete sequence.//4.5e-39:376:67//AC004079
 F-HEMBA1003893//H. sapiens CpG island DNA genomic MseI fragment, clone 11b6, forward read cpg11b6.ftla.//3.6e-32:173:99//Z59012
 F-HEMBA1003902//RPC111-26M20, TPB RPC1-11 Homo sapiens genomic clone RPC1-11-26M20, genomic survey sequence.//8.2e-12:422:61//AQ003455
 F-HEMBA1003908//Plasmodium falciparum chromosome 2, section 38 of 73 of the complete sequence.//0.0063:468:58//AE001401
 F-HEMBA1003926//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 310013, WORKING DRAFT SEQUENCE.//3.6e-27:278:76//AL031658
 F-HEMBA1003937//Homo sapiens chromosome 3 subtelomeric region.//1.4e-55:315:81//AF109718
 F-HEMBA1003939//HS-1047-A1-C04-MF, abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830 Col=7 Row=M, genomic survey sequence.//6.1e-09:413:63//B38195
 F-HEMBA1003942//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.42:205:65//AC005140
 F-HEMBA1003950//M. capricolus DNA for CONTIG MC072.//0.029:458:58//Z33058
 F-HEMBA1003953//HS_2268_A1_B04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2268 Col=7 Row=C, genomic survey sequence.//9.0e-07:239:64//AQ085098
 F-HEMBA1003958//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence.//2.8e-57:424:74//AC004894
 F-HEMBA1003959//RPC111-78E8, TV RPC111 Homo sapiens genomic clone R-78E8, genomic survey sequence.//4.3e-86:441:96//AQ285498
 F-HEMBA1003976//HS_3146_A1_H09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3146 Col=17 Row=0, genomic survey sequence.//6.3e-10:129:80//AQ141146
 F-HEMBA1003978
 F-HEMBA1003985//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y10SC5, WORKING DRAFT SEQUENCE.//1.0:258:60//Z98855
 F-HEMBA1003987
 F-HEMBA1003989//Streptomyces coelicolor cosmid 1A9.//0.40:238:61//AL034446
 F-HEMBA1004000//Rattus norvegicus satellite sequence dMco2.//2.0e-07:116:70//U19354

【0707】

【表408】

F-HEMBA1004011//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.09 8:286:60//AC004710

F-HEMBA1004012//Homo sapiens chromosome 17, clone hRPM.63_A_1, complete sequence.//2.8e-185:896:97//AC005670

F-HEMBA1004015//Homo sapiens chromosome 17, clone hRPM.721_K_1, complete sequence.//6.3e-68:417:80//AC005411

F-HEMBA1004024//Homo sapiens Xp22-B3 BAC GSHB-324M7 (Genome Systems Human BAC Library) complete sequence.//2.0e-47:418:77//AC005859

F-HEMBA1004038//Homo sapiens genomic DNA, chromosome 21q11.1, segment 23/28, WORKING DRAFT SEQUENCE.//1.6e-51:564:74//AP000052

F-HEMBA1004042//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//1.2e-05:636:55//AE001398

F-HEMBA1004045//Homo sapiens (subclone 1_g7 from BAC H76) DNA sequence, complete sequence.//1.9e-31:373:76//AC002252

F-HEMBA1004048//Homo sapiens DNA for P35-related protein, exon 2.//0.039:234:63//D63393

F-HEMBA1004049//Homo sapiens Xp22 GS-52411 (Genome Systems Human BAC Library), complete sequence.//4.8e-135:780:89//AC003106

F-HEMBA1004055//Human chromosome 3p21.1 gene sequence.//4.7e-09:45 7:58//L13435

F-HEMBA1004056//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 447C4, WORKING DRAFT SEQUENCE.//3.3e-25:246:77//AL02197 7

F-HEMBA1004074//CIT-HSP-2053J5.TF CIT-HSP Homo sapiens genomic clone 2053J5, genomic survey sequence.//7.8e-24:233:76//B68555

F-HEMBA1004086//Saccharomyces douglasii mitochondrial tRNA-Ser and tRNA-Phe genes, partial sequence, and Var1 (var1) gene, mitochondrial gene encoding mitochondrial protein, complete cds.//4.5e-08: 614:59//U49822

F-HEMBA1004091//Mus musculus putative transcription factor mRNA, complete cds.//5.9e-121:502:85//AF091234

F-HEMBA1004111//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0481P14: HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.0e-36:317:80//AC006160

F-HEMBA1004131//Mus musculus clone OS72067, genomic survey sequence.//8.7e-24:320:71//AF046393

F-HEMBA1004132//HS_3226_B1_D10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3226 Col=19 Row=H, genomic survey sequence.//9.7e-13:232:71//AQ182017

F-HEMBA1004133

F-HEMBA1004138//HS_3036_B1_C11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=21 Row=N, genomic survey sequence.//0.0035:165:64//AQ294763

F-HEMBA1004143

F-HEMBA1004146

F-HEMBA1004150//Human DNA sequence from PAC 5201 on chromosome Xq2 1. Contains CA repeats, STS.//0.00011:618:60//Z96811

F-HEMBA1004164//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome Systems Human BAC Library) complete sequence.//2.9e-30:454:68//AC0 05913

F-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//4.5e-13 3:649:97//AF067855

F-HEMBA1004199

F-HEMBA1004200//HS_2015_A1_B05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2015 Col=9 Row=C, genomic survey sequence.//8.5e-34:236:87//AQ247957

F-HEMBA1004202//Mus musculus chromosome 11, clone mCIT.268_P_23, complete sequence.//7.8e-59:216:83//AC004807

F-HEMBA1004203//Homo sapiens clone MH0313P13, WORKING DRAFT SEQUENCE, 15 unordered pieces.//6.3e-98:173:98//AC005488

F-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//3.2e-166:791:98//U50748

F-HEMBA1004225//Plasmodium falciparum chromosome 2, section 61 of 73 of the complete sequence.//6.5e-08:584:60//AE001424

F-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds.//8.0e-115:713:86//AF095927

F-HEMBA1004238

F-HEMBA1004241//CIC5B11.1 check: 4870 from: 1 to: 167234, complete sequence.//0.57:552:58//AC004708

F-HEMBA1004246//Human DNA sequence from clone 422F24 on chromosome 6q24.1-25.2. Contains a novel gene similar to C. elegans C02C2.5. Contains ESTs, STSs and GSSs, complete sequence.//6.1e-21:254:77//AL031010

F-HEMBA1004248//Rattus rattus insulin-induced growth-response protein in (CL-6) mRNA, complete cds.//1.7e-30:315:74//L13619

F-HEMBA1004264//Homo sapiens cosmid clone LUCA20 from 3p21.3, complete sequence.//4.4e-07:674:60//AC004693

F-HEMBA1004267//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence.//3.1e-78:335:87//AC004707

F-HEMBA1004272//Homo sapiens 12p13.3 PAC RPC15-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.4e-17 6:856:97//AC005831

F-HEMBA1004274//HS_3064_B2_A04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-28:153:100//AQ136993

F-HEMBA1004275//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 501A4, WORKING DRAFT SEQUENCE.//5.2e-17:109:99//Z98051

F-HEMBA1004276//CIT-HSP-2387K6.TF.1 CIT-HSP Homo sapiens genomic clone 2387K6, genomic survey sequence.//5.0e-07:63:98//AQ240477

F-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds.//2.1e-185:868:99//AF022795

F-HEMBA1004289//Arabidopsis thaliana genomic DNA, chromosome 5, PI clone: NQN23, complete sequence.//1.0:387:59//AB013395

F-HEMBA1004295//Homo sapiens DNA, anonymous heat-stable fragment R P11-3A.//7.8e-06:92:89//AB012254

F-HEMBA1004306//Homo sapiens clone DJ0811N16, complete sequence.//0.00037:413:59//AC004897

F-HEMBA1004312//Rickettsia prowazekii strain Madrid E, complete genome: segment 2/4.//0.28:522:57//AJ235271

F-HEMBA1004321//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//7.1e-136:548:92//AC006130

F-HEMBA1004323//Human DNA sequence from PAC 450C20 on chromosome X.//1.3e-32:320:65//Z84720

F-HEMBA1004327//Homo sapiens mRNA for KIAA0522 protein, partial cds.//0.93:222:62//AB011094

F-HEMBA1004330//Homo sapiens clone DJ1196H06, WORKING DRAFT SEQUENCE, 4 unordered pieces.//7.0e-168:895:93//AC004995

F-HEMBA1004334//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC Library) complete sequence.//4.6e-73:713:75//AC002980

F-HEMBA1004335//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 417M14, WORKING DRAFT SEQUENCE.//1.3e-25:121:85//AL0244 98

F-HEMBA1004341

F-HEMBA1004353//***ALU WARNING: Human Alu-Sc subfamily consensus sequence.//6.4e-38:278:85//U14571

F-HEMBA1004354//Human clone C3 CHL1 protein (CHL1) mRNA, alternatively spliced, complete cds.//4.1e-45:190:92//U75968

F-HEMBA1004356

F-HEMBA1004366//P. falciparum complete gene map of plastid-like DNA (IR-A).//2.2e-07:736:57//X95275

F-HEMBA1004372//H. sapiens dystrophin gene intron 44.//1.0:129:62// 177644

F-HEMBA1004389//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//4.7e-42:237:94//M21977

F-HEMBA1004394//Plasmodium falciparum chromosome 2, section 39 of 73 of the complete sequence.//5.2e-05:519:59//AE001402

F-HEMBA1004396//Human BAC clone RG302F04 from 7q31, complete sequence.//4.0e-32:261:76//AC002463

F-HEMBA1004405//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-62 8 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.4e-07:693:58//AC005507

F-HEMBA1004408//Homo sapiens clone MH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-69:195:100//AC005037

F-HEMBA1004429//HS_3193_A1_B06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3193 Col=11 Row=C, genomic survey sequence.//5.1e-67:386:91//AQ172942

F-HEMBA1004433//Human Chromosome 11p11.2 PAC clone pDJ404M15, complete sequence.//3.2e-27:242:82//AC002554

F-HEMBA1004460//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//1.7e-75:590:81//AC004846

F-HEMBA1004461//Human DNA sequence from clone 657J8 on chromosome Xq26.1-26.3 Contains GSS, complete sequence.//0.045:215:66//AL0344 07

F-HEMBA1004479//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//5.2e-43:364:79//AF060194

F-HEMBA1004482//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//6.8 e-17:791:59//AC005505

F-HEMBA1004499//Homo sapiens chromosome 17, clone hRPC.1073_F_15, complete sequence.//4.4e-125:251:94//AC004686

F-HEMBA1004502//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0 12:635:57//AC004709

F-HEMBA1004506//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//2.8e-127:766:88//AC004453

F-HEMBA1004507

F-HEMBA1004509//Arabidopsis thaliana DNA chromosome 4, BAC clone T 10114 (ESSA11 project).//1.0e-13:244:67//AL021712

F-HEMBA1004534//Human mRNA for actin-binding protein (filamin) (AB

【0708】

【表409】

P-280) //1.6e-72:678:74//X53416
 F-HEMBA1004538//Sequence 1 from patent US 5612190. //0.00015:416:59 //136871
 F-HEMBA1004542//Homo sapiens clone NM0486122, WORKING DRAFT SEQUENCE, 5 unordered pieces. //0.95:202:64//AC005038
 F-HEMBA1004554//Arabidopsis thaliana BAC T26D22. //0.45:624:56//AF058826
 F-HEMBA1004560//Human mRNA for KIAA0281 gene, complete cds. //9.1e-10:173:70//D87457
 F-HEMBA1004573//Human BAC clone RG114A06 from 7q31, complete sequence. //6.1e-23:134:73//AC002542
 F-HEMBA1004577//Homo sapiens Chromosome 16 BAC clone CIT987SK-582J 2, complete sequence. //1.6e-15:190:77//AC004525
 F-HEMBA1004586//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces. //3.1e-31:388:76//AC004895
 F-HEMBA1004596//RPC111-81021.TJ RPC111 Homo sapiens genomic clone R-81021, genomic survey sequence. //2.2e-90:458:90//AQ285136
 F-HEMBA1004604//Mus musculus COP9 complex subunit 7a (COPS7a) mRNA, complete cds. //8.6e-105:699:84//AF071316
 F-HEMBA1004610//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence. //5.4e-20:267:72//AC004983
 F-HEMBA1004617//CIT-HSP-2319H15.TF CIT-HSP Homo sapiens genomic clone 2319H15, genomic survey sequence. //6.2e-26:147:99//AQ034944
 F-HEMBA1004629//Plasmodium falciparum 307 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces. //5.6e-06:766:56//AC005504
 F-HEMBA1004631//Human DNA sequence from PAC 368A4 on chromosome X. Contains ESTs, CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP) like gene and STSs. //4.7e-73:412:92//Z83843
 F-HEMBA1004632//Canine herpesvirus DNA for gene homolog of HSV1 UL16, EHVI ORF 46, VZV ORF 44. //0.92:181:61//X90418
 F-HEMBA1004637//G. gallus mRNA for LRP/alpha-2-macroglobulin receptor. //7.8e-47:784:65//X74904
 F-HEMBA1004638//Rattus norvegicus homeodomain protein Nkx6.1 (nkx6.1) mRNA, complete cds. //6.4e-06:458:61//AF004431
 F-HEMBA1004656//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y4703, WORKING DRAFT SEQUENCE. //0.30:733:55//Z98865
 F-HEMBA1004669//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG island s, complete sequence. //7.5e-136:521:98//AL031432
 F-HEMBA1004670//Homo sapiens Chromosome 22q12 Cosmid Clone p90g5, complete sequence. //0.43:365:59//AC000045
 F-HEMBA1004672
 F-HEMBA1004693//Plasmodium falciparum 307 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces. //0.096:651:54//AC005308
 F-HEMBA1004697//CIT-HSP-2326C13.TR CIT-HSP Homo sapiens genomic clone 2326C13, genomic survey sequence. //0.23:238:65//AQ040642
 F-HEMBA1004705//Homo sapiens Xp22 Cosmid U151G1 (from Lawrence Livermore X library) and PAC RPC111-93D11 (from Roswell Park Cancer Center) complete sequence. //2.1e-27:375:72//AC002357
 F-HEMBA1004709//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence. //1.6e-36:191:91//AC006210
 F-HEMBA1004711//Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence. //1.1e-133:639:99//AC005562
 F-HEMBA1004725//RPC111-75013.TJ RPC111 Homo sapiens genomic clone R-75013, genomic survey sequence. //6.2e-32:169:100//AQ266512
 F-HEMBA1004730//Human BAC clone RG035E18 from 7q31, complete sequence. //8.0e-68:732:72//AC004029
 F-HEMBA1004733//CIT-HSP-2305M23.TF CIT-HSP Homo sapiens genomic clone 2305M23, genomic survey sequence. //4.9e-18:209:69//AQ017556
 F-HEMBA1004734//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UBC17) mRNA, complete cds. //1.8e-13:451:62//AF028340
 F-HEMBA1004736//Human DNA sequence from PAC 436M11 on chromosome X p22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the R51 gene for retinosis (X-linked, juvenile) 1 (XLR51). Contains ESTs, an STS and GSSs, complete sequence. //5.0e-87:646:78//Z94056
 F-HEMBA1004748//Human BAC clone RG204116 from 7q31, complete sequence. //0.24:526:57//AC002461
 F-HEMBA1004751//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces. //1.4e-25:268:76//AC004913
 F-HEMBA1004752//R. norvegicus mRNA for leucocyte common antigen-related protein (3941 bp). //1.1e-07:503:61//X83546
 F-HEMBA1004753//Homo sapiens Chromosome 12 Cosmid Clone 6e5, complete sequence. //4.5e-38:314:81//AC000028
 F-HEMBA1004756//Homo sapiens, complete sequence. //1.4e-111:326:84//AC005854
 F-HEMBA1004758//Sequence 29 from patent US 5534410. //3.9e-135:769:91//123472
 F-HEMBA1004763//Homo sapiens apoptosis inhibitor survivin gene, complete cds. //3.6e-47:404:79//U75285
 F-HEMBA1004768//Homo sapiens PAC clone DJ0979P20 from 7q33-q35, complete sequence. //6.7e-107:890:78//AC004941
 F-HEMBA1004770//Plasmodium falciparum 307 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces. //7.9e-09:806:59//AC004709
 F-HEMBA1004771//G. muris ribosomal RNA operon DNA encoding 16S, 23S and 5.8S ribosomal RNA. //0.69:239:61//X65063
 F-HEMBA1004776
 F-HEMBA1004778
 F-HEMBA1004795//Drosophila melanogaster A-kinase anchor protein DA KAP550 mRNA, partial cds. //3.4e-46:778:64//AF003622
 F-HEMBA1004803//Homo sapiens chromosome Y, clone 264.M.20, complete sequence. //4.3e-82:580:82//AC004617
 F-HEMBA1004806//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence. //5.4e-07:642:59//AC005083
 F-HEMBA1004807//Human HIV1 tata element modulatory factor mRNA sequence from chromosome 3. //1.4e-46:171:92//L01042
 F-HEMBA1004816//Homo sapiens calpastatin (CAST) gene, exons 10-14. //3.5e-31:546:66//U86257
 F-HEMBA1004820//C. botulinum progenitor toxin complex genes. //0.0014:343:62//X87972
 F-HEMBA1004847//Canine mRNA for 68kDa subunit of signal recognition particle (SRP68). //1.5e-85:512:88//X53744
 F-HEMBA1004850//Homo sapiens TGF-beta type I receptor (TGFBR1) gene, exon 1. //0.0065:284:61//AF054590
 F-HEMBA1004863//Genomic sequence from Mouse 11, complete sequence. //0.92:250:59//AC000400
 F-HEMBA1004864
 F-HEMBA1004865//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence. //3.6e-12:214:72//AL031120
 F-HEMBA1004880//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence. //1.1e-08:255:69//AC004020
 F-HEMBA1004889//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds. //0.062:155:69//U32943
 F-HEMBA1004900//Plasmodium falciparum unidentified mRNA sequence. //0.00055:323:60//L12043
 F-HEMBA1004909//Homo sapiens chromosome 17, clone 289A8, complete sequence. //9.6e-16:166:80//AC003051
 F-HEMBA1004918//Turritella communis mitochondrial 16S ribosomal RNA gene, partial. //0.81:146:65//M94003
 F-HEMBA1004923//Human DNA from overlapping chromosome 19-specific cosmids R32543, and F15613 containing ZNF gene family member, genomic sequence, complete sequence. //1.4e-36:338:78//AC003006
 F-HEMBA1004929//CIT-HSP-2373116.TR CIT-HSP Homo sapiens genomic clone 2373116, genomic survey sequence. //2.4e-86:443:96//AQ108676
 F-HEMBA1004930//Homo sapiens PAC clone DJ0608H12 from 7q21, complete sequence. //4.6e-20:219:73//AC004109
 F-HEMBA1004933//HS-1003-A1-E10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 497 Col=19 Row=1, genomic survey sequence. //1.4e-28:216:85//B30726
 F-HEMBA1004934//Homo sapiens chromosome 21q22.3 PAC 267010, complete sequence. //0.53:222:61//AF042091
 F-HEMBA1004944//Homo sapiens clone DJ0736H05, WORKING DRAFT SEQUENCE, 5 unordered pieces. //1.2e-58:509:78//AC005482
 F-HEMBA1004954//HS-2033_A2_A08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=16 Row=A, genomic survey sequence. //3.7e-47:243:99//AQ229758
 F-HEMBA1004956//P. falciparum complete gene map of plastid-like DNA (IR-B). //0.048:421:58//X95276
 F-HEMBA1004960//Arabidopsis thaliana DNA chromosome 4, ESSA1 contig fragment No. 8. //0.89:333:58//Z97343
 F-HEMBA1004972
 F-HEMBA1004973//RPC111-66P8.TK RPC111 Homo sapiens genomic clone R-66P8, genomic survey sequence. //3.5e-22:245:77//AQ238471
 F-HEMBA1004977//Homo sapiens full length insert cDNA clone Y283B0.8. //9.0e-11:84:98//AF086080
 F-HEMBA1004978//CIT-HSP-2354E10.TR CIT-HSP Homo sapiens genomic clone 2354E10, genomic survey sequence. //0.0021:152:66//AQ075713
 F-HEMBA1004980//HS-3018_A2_E04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=8 Row=1, genomic survey sequence. //1.9e-77:392:97//AQ071873
 F-HEMBA1004983//Albinaria corrugata isolate cor.Prnl.1 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence. //0.0030:276:61//AF031680
 F-HEMBA1004995//Homo sapiens chromosome 16, cosmid bridge clone 30

【0709】

【表410】

6E6 (LANL), complete sequence.//4.2e-138:640:99//AC005590
 F-HEMBA1005008//Human mariner1 transposase gene, complete consensus sequence.//6.8e-20:160:88//U52077
 F-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds.//2.0e-144:668:99//AF041474
 F-HEMBA1005019//Homo sapiens mRNA for KIAA0548 protein, partial cds.//1.4e-146:693:98//AB014548
 F-HEMBA1005029//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c), H4FFP (H4/f pseudogene), H2AFC (H2A/c), H3FIK (H3.1/K) and a tRNA A-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSs, GSSs and genomic marker D6S464, complete sequence.//2.2e-115:668:90//AL009179
 F-HEMBA1005035//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence.//4.6e-138:591:98//AC004596
 F-HEMBA1005039//CIT-HSP-2338L5.TR CIT-HSP Homo sapiens genomic clone 2338L5, genomic survey sequence.//3.7e-61:271:88//AQ055486
 F-HEMBA1005047//Mus musculus mRNA for Rab24 protein.//3.8e-17:218:73//Z22819
 F-HEMBA1005050//Human Tis1ld gene, complete cds.//0.079:251:63//U07802
 F-HEMBA1005062//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.018:560:56//AC004688
 F-HEMBA1005066//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 774G10, WORKING DRAFT SEQUENCE.//3.4e-97:432:84//AL034410
 F-HEMBA1005075//H. sapiens DNA 3' flanking simple sequence region clone wg2c3.//6.9e-07:176:68//X76589
 F-HEMBA1005079//CIT-HSP-2325M21.TRB CIT-HSP Homo sapiens genomic clone 2325M21, genomic survey sequence.//2.1e-48:274:93//AQ038720
 F-HEMBA1005083//HS_2248_B1_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2248 Col=9 Row=H, genomic survey sequence.//3.4e-06:230:64//AQ129575
 F-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//1.3e-161:762:98//AF080561
 F-HEMBA1005113//L. esculentum microsatellite repeat DNA region.//0.0038:742:57//X90770
 F-HEMBA1005123//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//9.6e-83:479:78//AC004854
 F-HEMBA1005133//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//3.9e-24:576:64//AL023808
 F-HEMBA1005149//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//4.7e-36:283:80//AC004542
 F-HEMBA1005152//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.//5.0e-10:332:64//AC004469
 F-HEMBA1005159//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE.//4.0e-10:734:58//AP000023
 F-HEMBA1005185//H. sapiens CpG island DNA genomic MseI fragment, clone 91b2, forward read cpg91b2.ftt.//2.2e-14:93:100//Z63847
 F-HEMBA1005201//Drosophila melanogaster cosmid 152A3.//4.7e-35:67:9:64//AL009194
 F-HEMBA1005202//Canine mRNA for 68kDa subunit of signal recognition particle (SRP68).//6.7e-138:778:90//X53744
 F-HEMBA1005206//Drosophila melanogaster Su(P) and anon-73B1 genes and partial o25 gene and Pros26 gene.//7.1e-12:376:62//AJ011320
 F-HEMBA1005219//Homo sapiens mRNA for KIAA0445 protein, complete cds.//7.1e-05:411:60//AB007914
 F-HEMBA1005223//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//3.5e-06:212:66//AC004542
 F-HEMBA1005232//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.7e-07:625:57//AC005308
 F-HEMBA1005241//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//8.7e-45:567:72//AC005154
 F-HEMBA1005244//Homo sapiens chromosome X clone U177G4, U152H5, U168D5, 17A46, U172D6, and U186B3 from Xp22, complete sequence.//0.96:298:62//AC002365
 F-HEMBA1005251
 F-HEMBA1005252//Homo sapiens chromosome 17, clone hRPK.318_A_15, complete sequence.//4.5e-160:392:99//AC005837
 F-HEMBA1005274//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence.//2.3e-05:496:60//AF069291
 F-HEMBA1005275//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence.//5.7e-05:220:64//AL033521
 F-HEMBA1005293//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//2.4e-20:338:65//U97018
 F-HEMBA1005296
 F-HEMBA1005304//Human DNA sequence from clone 364122 on chromosome Xq21.31-22.3. Contains an STS and GSSs, complete sequence.//1.6e-51:381:78//AL031012
 F-HEMBA1005311
 F-HEMBA1005314//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE.//0.94:226:63//AP000031
 F-HEMBA1005315//Homo sapiens BAC810, complete sequence.//9.5e-15:684:62//U85198
 F-HEMBA1005318//Human DNA sequence from PAC 394F12 on chromosome X contains EST, STS, CpG island clone.//2.6e-05:472:59//Z83823
 F-HEMBA1005331//Homo sapiens chromosome 17, clone hRPK.214_C_8, complete sequence.//3.3e-90:300:90//AC005803
 F-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial.//1.4e-151:740:97//AJ007581
 F-HEMBA1005353//CIT-HSP-2310N10.TR CIT-HSP Homo sapiens genomic clone 2310N10, genomic survey sequence.//2.1e-86:438:97//AQ016145
 F-HEMBA1005359//Human zinc finger protein ZNF137 mRNA, complete cds.//1.8e-98:500:88//U09414
 F-HEMBA1005367//Mus musculus melastatin mRNA, complete cds.//8.3e-72:577:73//AF047714
 F-HEMBA1005372//Human DNA sequence from PAC 293E14 contains ESTs, STS.//1.3e-07:274:66//Z82900
 F-HEMBA1005374//Homo sapiens clone 277F10, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.9e-48:611:69//AC004813
 F-HEMBA1005382//HS_3063_B2_F11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3063 Col=22 Row=L, genomic survey sequence.//1.6e-27:154:98//AQ103204
 F-HEMBA1005389//Plasmodium falciparum telomere nucleotide sequence.//4.0e-07:443:61//M23175
 F-HEMBA1005394//CIT-HSP-2368B11.TR CIT-HSP Homo sapiens genomic clone 2368B11, genomic survey sequence.//7.6e-17:225:71//AQ076749
 F-HEMBA1005403//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//4.5e-131:278:98//AL034379
 F-HEMBA1005408//HS_3007_B2_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=8 Row=N, genomic survey sequence.//8.0e-06:218:66//AQ294366
 F-HEMBA1005410//Human DNA sequence from cosmid CU120E2, on chromosome X contains Lowe oculocerebrorenal syndrome (OCRL) ESTs and STS.//1.5e-41:432:76//Z73496
 F-HEMBA1005411
 F-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds.//1.0e-169:537:99//AF041248
 F-HEMBA1005426
 F-HEMBA1005443//Homo sapiens chromosome 19, BAC CIT-8-19In6, complete sequence.//7.1e-37:260:76//AC006130
 F-HEMBA1005447//CIT-HSP-2173N7.TR CIT-HSP Homo sapiens genomic clone 2173N7, genomic survey sequence.//5.0e-133:631:98//B93234
 F-HEMBA1005468//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence.//1.5e-118:868:83//AL022576
 F-HEMBA1005469//Homo sapiens chromosome 16, P1 clone 96-4B (LANL), complete sequence.//1.2e-179:838:99//AC005212
 F-HEMBA1005472//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 22B13, WORKING DRAFT SEQUENCE.//3.4e-20:187:74//AL031985
 F-HEMBA1005474//Homo sapiens genomic DNA, chromosome 21q11.1, segment 12/28, WORKING DRAFT SEQUENCE.//4.1e-22:445:65//AP000041
 F-HEMBA1005475//CIT-HSP-2322D14.TR CIT-HSP Homo sapiens genomic clone 2322D14, genomic survey sequence.//6.7e-51:269:97//AQ026941
 F-HEMBA1005497//HS_3097_A2_G05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3097 Col=10 Row=M, genomic survey sequence.//1.4e-66:345:96//AQ103810
 F-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from 7q11.23-q21, complete sequence.//5.4e-178:818:98//AC004957
 F-HEMBA1005506//Mus musculus (clone OEBF17) early B-cell factor (EBF) mRNA, complete cds.//2.6e-06:73:98//L12147
 F-HEMBA1005508//Homo sapiens, clone hRPK.1_A_1, complete sequence.//0.00012:455:60//AC006196
 F-HEMBA1005511//Homo sapiens MHC class I region.//3.3e-43:421:77//AF055066
 F-HEMBA1005513//Drosophila melanogaster males-absent on the first (maf) gene, complete cds.//2.3e-20:352:69//U71219
 F-HEMBA1005517//Homo sapiens DNA for (CCG)n trinucleotide repeat region, isolate ET.//2.5e-08:431:62//AJ001216
 F-HEMBA1005518//M. musculus mRNA for paladin gene.//8.2e-90:651:81//X99384
 F-HEMBA1005520//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE

【0710】

【表4 1 1】

CE, 6 unordered pieces.//7.8e-167:755:99//AC004913
 F-HEMBA1005526//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence.//2.4e-42:475:73//AC006241
 F-HEMBA1005528//Mus musculus mCAF1 protein mRNA, complete cds.//1.2e-94:512:92//U21855
 F-HEMBA1005530
 F-HEMBA1005548//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 970A17, WORKING DRAFT SEQUENCE.//9.4e-87:422:99//AL034431
 F-HEMBA1005552//Homo sapiens PAC clone DJ0807C15 from Tq34-q36, complete sequence.//6.1e-41:486:68//AC004743
 F-HEMBA1005558//Drosophila melanogaster DNA sequence (P1 DS00837 (D87)), complete sequence.//2.9e-19:306:68//AC004377
 F-HEMBA1005566//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0093:345:60//AC004153
 F-HEMBA1005570//Plasmodium falciparum chromosome 2, section 44 of 73 of the complete sequence.//4.2e-09:592:59//AE001407
 F-HEMBA1005576//Homo sapiens mRNA for KIAA0463 protein, partial cds.//5.9e-127:610:98//AB007932
 F-HEMBA1005577//HS-1004-A1-E11-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 498 Col=21 Row=1, genomic survey sequence.//0.00034:254:64//B30971
 F-HEMBA1005581//Rattus norvegicus mRNA for MEGF5, complete cds.//4.0e-57:826:65//AB011531
 F-HEMBA1005582//HS-3242-A1-B07-MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3242 Col=13 Row=C, genomic survey sequence.//1.1e-13:91:98//AQ211275
 F-HEMBA1005583
 F-HEMBA1005588//Homo sapiens PAC clone DJ1188N21 from Tq11.23-q21.1, complete sequence.//8.7e-31:283:75//AC006025
 F-HEMBA1005593//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence.//8.3e-158:748:99//AC005746
 F-HEMBA1005595//CIT-HSP-2309F14.TF CIT-HSP Homo sapiens genomic clone 2309F14, genomic survey sequence.//6.4e-30:194:91//AQ016527
 F-HEMBA1005606//CIT-HSP-232616.TR CIT-HSP Homo sapiens genomic clone 232616, genomic survey sequence.//0.0014:132:70//AQ041484
 F-HEMBA1005609//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.9e-33:249:85//AC005089
 F-HEMBA1005616//Homo sapiens DNA sequence from PAC 43C13 on chromosome 1q21.1-Xq21.3, rab proteins geranylgeranyltransferase component A1 (rab escort protein 1) (REP-1) (choroideremia protein) (TC D protein).//6.5e-29:278:69//AL009175
 F-HEMBA1005621//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 330012, WORKING DRAFT SEQUENCE.//6.4e-90:158:87//AL031731
 F-HEMBA1005627//RPC111-34P9.TJ RPC1-11 Homo sapiens genomic clone RPC1-11-34P9, genomic survey sequence.//0.014:168:67//AQ045110
 F-HEMBA1005631//Homo sapiens PAC clone DJ1086D14, complete sequence.//1.0e-149:736:93//AC004450
 F-HEMBA1005632
 F-HEMBA1005634//Human DNA sequence from PAC 187N21 on chromosome 6p21.2-6p21.33, Contains ESTs.//6.6e-38:452:67//Z98036
 F-HEMBA1005666
 F-HEMBA1005670//Homo sapiens PAC clone DJ066SC04 from Tq14-p13, complete sequence.//5.1e-59:687:74//AC004850
 F-HEMBA1005679//Homo sapiens clone DJ0425102, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.0e-47:357:85//AC005478
 F-HEMBA1005680
 F-HEMBA1005685//RPC111-23D19.TKBR RPC1-11 Homo sapiens genomic clone RPC1-11-23D19, genomic survey sequence.//0.99:228:63//AQ013742
 F-HEMBA1005699//Human ligand for sph-related receptor tyrosine kinases (EPLCA) mRNA, complete cds.//1.4e-72:406:92//U57001
 F-HEMBA1005705//Human (D21S172) DNA segment containing (CA) repeat.//0.00040:190:66//X56513
 F-HEMBA1005717//Plasmodium falciparum MAL3P1, complete sequence.//0.0099:260:63//Z97348
 F-HEMBA1005732//Human mRNA for KIAA0003 gene, complete cds.//8.1e-19:151:88//D14697
 F-HEMBA1005737//Homo sapiens PAC clone DJ1099C19 from Tq21-q22, complete sequence.//5.6e-15:157:79//AC005156
 F-HEMBA1005746//RPC111-63N8.TX RPC111 Homo sapiens genomic clone R-63N8, genomic survey sequence.//1.3e-18:113:100//AQ238535
 F-HEMBA1005755//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4, Contains STSs and the DXS7 locus with GT and GTG repeat polymorphisms, complete sequence.//3.6e-56:764:70//Z97181
 F-HEMBA1005765//Human DNA sequence from PAC 288L1 on chromosome 22q12-qter contains ESTs and polymorphic CA repeat (D22S1152).//1.1e-30:275:77//Z82196
 F-HEMBA1005780//RPC111-74E19.TJ RPC111 Homo sapiens genomic clone R-74E19, genomic survey sequence.//0.0011:283:62//AQ268432
 F-HEMBA1005813//Homo sapiens PAC clone DJ0167F23 from Tq15, complete sequence.//0.14:326:61//AC004079
 F-HEMBA1005815//M.musculus mRNA for skeletal muscle-specific calpain.//6.3e-10:706:59//X92523
 F-HEMBA1005822//Mouse Bac 291C16, WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.87:417:56//AC003020
 F-HEMBA1005829//Homo sapiens Chromosome 22q11.2 FOSMID Clone f39e1 in DCCR Region, complete sequence.//8.8e-42:370:79//AC000094
 F-HEMBA1005834//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.1e-42:690:67//AL022577
 F-HEMBA1005852//F.rubripes GSS sequence, clone 163A22aE9, genomic survey sequence.//4.3e-07:253:59//AL018749
 F-HEMBA1005853//CIT-HSP-2289L23.TR CIT-HSP Homo sapiens genomic clone 2289L23, genomic survey sequence.//2.2e-68:333:99//B98952
 F-HEMBA1005884//Homo sapiens chromosome 5, BAC clone 78c6 (LBNL HI 91), complete sequence.//1.9e-57:331:87//AC005351
 F-HEMBA1005891//Homo sapiens PAC clone DJ097N05 from Tq11.23-q21.1, complete sequence.//5.1e-182:864:98//AC004945
 F-HEMBA1005894//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//3.0e-44:340:80//AC004086
 F-HEMBA1005909//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylamine Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylamine Oxidase 3, FMO II, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//8.3e-12:828:57//AL021026
 F-HEMBA1005911//Human DNA sequence from clone 1158E12 on chromosome Xp11.23-11.4 Contains EST, STS, GSS, CpG island, complete sequence.//1.0e-44:328:77//AL031584
 F-HEMBA1005921//Homo sapiens chromosome 17, clone hRPK.112_H_10, complete sequence.//1.3e-41:431:77//AC005666
 F-HEMBA1005931//Homo sapiens chromosome 12p13.3 clone RPC14-761J1, WORKING DRAFT SEQUENCE, 60 unordered pieces.//1.1e-29:394:70//AC006086
 F-HEMBA1005934//Homo sapiens PAC clone DJ1140G11 from 14q24.3, complete sequence.//8.1e-06:115:80//AC004974
 F-HEMBA1005962//RPC111-17015.TY RPC1-11 Homo sapiens genomic clone RPC1-11-17015, genomic survey sequence.//9.5e-36:315:84//B82821
 F-HEMBA1005963//HS-3055-A1-E08-MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=15 Row=1, genomic survey sequence.//9.3e-73:372:97//AQ147357
 F-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//1.3e-149:697:99//AF082516
 F-HEMBA1005991//Plasmodium falciparum chromosome 2, section 45 of 73 of the complete sequence.//6.3e-07:423:60//AE001408
 F-HEMBA1005999//Homo sapiens chromosome 4 clone C0026P05 map 4P16, complete sequence.//3.8e-09:360:64//AC005599
 F-HEMBA1006002
 F-HEMBA1006005//Homo sapiens NLL (NLL) gene, exons 1-3, and partial cds.//4.5e-83:495:90//AF036405
 F-HEMBA1006031
 F-HEMBA1006035
 F-HEMBA1006036//Human (lambda) DNA for immunoglobulin light chain.//2.4e-59:652:74//D87009
 F-HEMBA1006042//Homo sapiens chromosome 10 clone CIT987SK-1057L21 map 10q25, complete sequence.//2.1e-43:330:70//AC005386
 F-HEMBA1006067//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.11:433:59//AC004153
 F-HEMBA1006081
 F-HEMBA1006090//, complete sequence.//4.5e-139:748:92//AC005500
 F-HEMBA1006091//Homo sapiens gene encoding telethonin, exons 1 to 2, partial.//0.0091:346:62//AJ011098
 F-HEMBA1006100//Homo sapiens chromosome 10 clone CIT987SK-1143A11 map 10q25, complete sequence.//2.8e-18:180:78//AC005880
 F-HEMBA1006108//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte Marker CTX, the possibly alternatively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//0.26:84:71//AL031177
 F-HEMBA1006121//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 601N24, WORKING DRAFT SEQUENCE.//5.2e-18:147:87//AL0316

【0 7 1 1】

【表412】

72	F-HEMBA1006124//CIT-HSP-2355817.TF CIT-HSP Homo sapiens genomic clone 2355817, genomic survey sequence.//0.044:225:61//AQ058966	known putative gene, a pseudogene with high similarity to part of a ntigen K1-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055, complete sequence.//1.2e-39:752:63//AL022165
	F-HEMBA1006130//CIT-HSP-386A20.TF CIT-HSP Homo sapiens genomic clone 386A20, genomic survey sequence.//8.8e-07:173:69//B55085	F-HEMBA1006421//Homo sapiens chromosome 14q24.3 clone BAC270M14 transforming growth factor-beta 3 (TGF-beta 3) gene, complete cds: a nd unknown genes.//2.4e-41:438:76//AF107885
	F-HEMBA1006138//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//7.5e-22:164:75//AL022162	F-HEMBA1006424//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//0.027:293:64//AL031781
	F-HEMBA1006142//, complete sequence.//7.9e-125:586:99//AC005500	F-HEMBA1006426//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 292E10, WORKING DRAFT SEQUENCE.//1.7e-50:310:80//Z93930
	F-HEMBA1006155//H.sapiens CpG island DNA genomic MseI fragment, clone 119b6, forward read cpg119b6.ftla.//1.0:85:72//Z64428	F-HEMBA1006438//Liverwort Marchantia polymorpha chloroplast genome DNA.//0.051:440:59//X04465
	F-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.//1.1e-185:852:99//AF048693	F-HEMBA1006445//Felis catus ras p21 (H-ras) mRNA, partial cds.//1.0:238:59//U62088
	F-HEMBA1006173//striatum enriched phosphatase=protein-tyrosine-phosphatase [rat, striata, mRNA, 2815 nt].//8.4e-50:642:73//S49400	F-HEMBA1006446//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P6, WORKING DRAFT SEQUENCE.//2.4e-05:702:58//AL031749
	F-HEMBA1006182//Homo sapiens Chromosome 15q26.1 PAC clone pDJ105i19, complete sequence.//1.4e-22:194:74//AC005318	F-HEMBA1006461//Homo sapiens chromosome 19, cosmid R30676, complete sequence.//8.6e-55:409:83//AC004560
	F-HEMBA1006198	F-HEMBA1006467//Homo sapiens chromosome 17, clone hRPK.346_K10, complete sequence.//1.0:293:59//AC006120
	F-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//2.6e-175:836:98//AF070557	F-HEMBA1006471//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.4e-05:731:59//AC004709
	F-HEMBA1006248//Pinctada fucata mRNA for insoluble protein, complete cds.//8.2e-05:359:61//D86074	F-HEMBA1006474//CIT-HSP-2017H3.TF CIT-HSP Homo sapiens genomic clone 2017H3, genomic survey sequence.//5.2e-60:435:83//B54247
	F-HEMBA1006252//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 531H16, WORKING DRAFT SEQUENCE.//0.98:397:58//AL031664	F-HEMBA1006483//Homo sapiens chromosome 5, BAC clone 8e5 (LBML H167), complete sequence.//2.9e-48:286:84//AC004752
	F-HEMBA1006253	F-HEMBA1006485//Homo sapiens BAC clone MHD044G14 from Tq11.23-21.1, complete sequence.//0.96:283:59//AC006031
	F-HEMBA1006259//HS_2231_A1_D10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2231 Col=19 Row=G, genomic survey sequence.//1.2e-11:233:68//AQ152722	F-HEMBA1006486//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//1.8e-14:259:67//AL022577
	F-HEMBA1006268//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//5.2e-27:156:85//AC004673	F-HEMBA1006489//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 467K16, WORKING DRAFT SEQUENCE.//6.6e-11:595:61//AL031283
	F-HEMBA1006272//Human endogenous retrovirus gag mRNA.//8.1e-115:847:80//X72791	F-HEMBA1006492//Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.//6.0e-122:337:100//AC005828
	F-HEMBA1006278//Mus musculus poly(A) polymerase VI mRNA, complete cds.//2.1e-57:665:70//U58134	F-HEMBA1006494//Homo sapiens chromosome 7qtel0 BAC E3, complete sequence.//3.8e-23:459:68//AF093117
	F-HEMBA1006283	F-HEMBA1006497//HS_3023_B2_H03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=6 Row=P, genomic survey sequence.//2.3e-81:433:95//AQ093846
	F-HEMBA1006284//Streptomyces fradiae tylosone synthase, starter module and modules 1-7, (tylG) gene, complete cds.//9.6e-06:623:60//U78289	F-HEMBA1006502//H.sapiens TSL repeat (clones 2-19b).//1.6e-13:86:87//X62364
	F-HEMBA1006291//HS_2208_A1_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=5 Row=E, genomic survey sequence.//1.2e-13:105:92//AQ091804	F-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds.//2.3e-139:470:98//AB014566
	F-HEMBA1006293//Sequence 8 from patent US 5721351.//5.6e-77:580:75//I89415	F-HEMBA1006521//Human BAC clone RC167B05 from Tq21, complete sequence.//4.3e-27:406:71//AC003991
	F-HEMBA1006309//Caenorhabditis elegans cosmid F01F1.//1.1e-21:420:63//U13070	F-HEMBA1006530//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE.//2.9e-27:408:65//AL031650
	F-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1 (PACS-1) mRNA, complete cds.//6.8e-120:748:85//AF076183	F-HEMBA1006535//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//0.028:599:60//AL034557
	F-HEMBA1006328//Homo sapiens fragile X mental retardation protein (FMR-1) gene (6 alternative splices), complete cds.//1.5e-46:485:73//L29074	F-HEMBA1006540//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds.//1.4e-171:654:98//AF093419
	F-HEMBA1006334//HS-1051-B2-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 773 Col=2 Row=L, genomic survey sequence.//0.0032:61:91//B40563	F-HEMBA1006546//Human DNA sequence from cosmid 232L22, between markers DXS366 and DXS87 on chromosome X contains ESTs glycerol kinase pseudogene.//3.8e-104:811:80//Z73986
	F-HEMBA1006344//HS-1009-A2-802-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 331 Col=4 Row=C, genomic survey sequence.//3.3e-09:218:66//B31420	F-HEMBA1006559//Mus musculus PRAJ1 (Praj1) mRNA, complete cds.//4.8e-99:386:82//U06944
	F-HEMBA1006347//Drosophila melanogaster males-absent on the first (mot) gene, complete cds.//1.6e-31:484:68//U71219	F-HEMBA1006562//Human fructose-1,6-bisphosphatase (FBP1) gene, exon 1.//0.012:322:60//U21925
	F-HEMBA1006349//HS-1054-A1-G06-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 776 Col=11 Row=M, genomic survey sequence.//5.4e-15:95:100//B41671	F-HEMBA1006566//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.026:540:58//AC005504
	F-HEMBA1006359//Human ZNF43 mRNA.//1.4e-115:823:81//X59244	F-HEMBA1006569//Ovis aries beta actin mRNA, complete cds.//6.3e-08:231:70//U39357
	F-HEMBA1006364//Mouse mRNA for transforming growth factor-beta2.//2.7e-10:247:71//X57413	F-HEMBA1006579//CIT-HSP-2380A22.TR CIT-HSP Homo sapiens genomic clone
	F-HEMBA1006377//Mus musculus chromosome 7, clone 19K5, complete sequence.//3.0e-57:401:81//AC002327	
	F-HEMBA1006380//CIT-HSP-217K18.TF CIT-HSP Homo sapiens genomic clone 217K18, genomic survey sequence.//1.3e-110:525:99//B92570	
	F-HEMBA1006381//HS-1045-B2-F10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 828 Col=20 Row=L, genomic survey sequence.//4.4e-05:163:70//B37813	
	F-HEMBA1006398//Homo sapiens 12q24.2 BAC RPC111-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//3.8e-62:370:86//AC004806	
	F-HEMBA1006416//Homo sapiens chromosome 5, P1 clone 1041F10 (LBML H88), complete sequence.//3.7e-15:157:78//AC005179	
	F-HEMBA1006419//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo)gene, an unk	

【0712】

【表413】

one 2380A22, genomic survey sequence.//0.036:250:62//AQ197107	F-HEMBA1006824//Homo sapiens chromosome 19, cosmid R29368, complete sequence.//0.40:159:66//AC004262
F-HEMBA1006583//Mycobacterium tuberculosis H37Rv complete genome: segment 143/162.//1.0:225:63//AL021841	F-HEMBA1006832//Homo sapiens (subclone 3_g8 from P1 H25) DNA sequence, complete sequence.//1.8e-24:323:71//AC002196
F-HEMBA1006595//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30A23, WORKING DRAFT SEQUENCE.//3.6e-50:689:69//AL022156	F-HEMBA1006849//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 4/10.//0.15:403:60//AB020872
F-HEMBA1006597//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.9e-42:253:84//AC004166	F-HEMBA1006865//Plasmodium falciparum chromosome 2, section 6 of 7 of the complete sequence.//0.20:472:57//AE001369
F-HEMBA1006612//RPC111-88F20, TJ RPC111 Homo sapiens genomic clone R-88F20, genomic survey sequence.//1.1e-51:266:98//AQ286726	F-HEMBA1006877//Mus musculus clone OST9241, genomic survey sequence.//3.4e-79:641:76//AF046757
F-HEMBA1006617//HS_2193_B2_H07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=14 Row=P, genomic survey sequence.//1.1e-59:413:85//AQ299685	F-HEMBA1006885//HS_2208_B2_G06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=12 Row=N, genomic survey sequence.//4.9e-18:206:76//AQ089246
F-HEMBA1006624//Human DNA sequence from clone 406A7 on chromosome 6q23-24. Contains three pseudogenes similar to Elongation Factor 1-Alpha (EF-1-ALPHA, Statin S1), 60S Acidic Ribosomal Protein P1 and NADH-Ubiquinone Oxidoreductase 15 kDa subunit, and part of the Microtubule Associated Protein E-MAP-115 gene. Contains ESTs, STSs and GSSs, complete sequence.//1.4e-35:257:89//AL023284	F-HEMBA1006900//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//5.4e-07:298:65//AL031321
F-HEMBA1006631//Homo sapiens Chromosome 11q23 PAC clone pDJ3566, complete sequence.//9.6e-112:800:83//AC002036	F-HEMBA1006914//S.pombe chromosome 11 cosmid c16H5.//0.00040:194:66//AL022104
F-HEMBA1006635//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MALIP2, WORKING DRAFT SEQUENCE.//0.15:393:58//AL031745	F-HEMBA1006921//Homo sapiens BAC clone GS114109 from Tpl4-p15, complete sequence.//1.1e-174:813:99//AC006027
F-HEMBA1006639//Petrocyon marinus polyadenylate binding protein (PABP) mRNA, complete cds.//9.6e-15:318:68//AF032896	F-HEMBA1006926//Caenorhabditis elegans cosmid ZK185.//0.0075:183:65//AF036704
F-HEMBA1006643//Homo sapiens clone DJ0902E20, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.58:254:65//AC006148	F-HEMBA1006929//P.falciparum complete gene map of plastid-like DNA (IR-A).//4.0e-06:739:57//X95275
F-HEMBA1006648//Mus musculus integrin binding protein kinase mRNA, complete cds.//1.5e-37:108:88//U94479	F-HEMBA1006936
F-HEMBA1006652//Homo sapiens chromosome 5, BAC clone 343g16 (LBML H180), complete sequence.//1.3e-154:671:96//AC005601	F-HEMBA1006938//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MALIP4, WORKING DRAFT SEQUENCE.//1.1e-05:733:57//AL031747
F-HEMBA1006653	F-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein.//1.3e-90:437:98//AJ010841
F-HEMBA1006659//Homo sapiens PAC clone DJ0905J08 from Tpl2-pl4, complete sequence.//5.2e-110:254:93//AC005189	F-HEMBA1006949//Human DNA sequence from PAC 363L9 on chromosome X, contains STS and polymorphic CA repeat.//0.67:217:62//Z82205
F-HEMBA1006665//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC library) complete sequence.//1.4e-14:177:76//AC004554	F-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//5.6e-143:740:94//AF004828
F-HEMBA1006674//Homo sapiens mRNA for nucleolar protein hNop56.//5.5e-15:122:90//Y12065	F-HEMBA1006976//cDNA encoding alpha 2 to 3 sialyltransferase.//2.8e-101:338:89//E06058
F-HEMBA1006676//Homo sapiens chromosome 19, fosmid 37502, complete sequence.//0.098:218:63//AC004755	F-HEMBA1006993//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//7.1e-31:536:66//AC003071
F-HEMBA1006682//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 668J24, WORKING DRAFT SEQUENCE.//1.4e-05:719:57//AL034346	F-HEMBA1006996//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//9.5e-07:285:60//Z82209
F-HEMBA1006695//Homo sapiens clone DJ0935K16, complete sequence.//3.1e-22:151:78//AC006011	F-HEMBA1007002//Genomic sequence for Arabidopsis thaliana BAC F20N 2, complete sequence.//0.99:388:58//AC002328
F-HEMBA1006696//CITBI-E1-2522D16, TF CITBI-E1 Homo sapiens genomic clone 2522D16, genomic survey sequence.//5.6e-17:324:66//AQ280738	F-HEMBA1007017//Sequence 3 from Patent W09416067.//0.96:220:62//A39358
F-HEMBA1006708	F-HEMBA1007018//G.gallus mRNA for dynein light chain-A.//1.3e-124:838:83//X79088
F-HEMBA1006709	F-HEMBA1007045
F-HEMBA1006717//Homo sapiens clone GS308H05, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.3e-08:136:79//AC005537	F-HEMBA1007051//Caenorhabditis elegans cosmid Y57G11C, complete sequence.//0.17:343:60//Z99281
F-HEMBA1006737//Homo sapiens chromosome 17, clone hRPK.269_G_24, complete sequence.//5.8e-162:497:98//AC005828	F-HEMBA1007052//Homo sapiens FSHD-associated repeat DNA, proximal region.//4.3e-67:659:74//U85056
F-HEMBA1006744//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g 4, complete sequence.//7.4e-48:320:87//AC004796	F-HEMBA1007062//Tubulin gene.//1.0:113:67//A18572
F-HEMBA1006754//Human DNA sequence from PAC 82J11 and cosmid U134E 6 on chromosome Xq22. Contains NIK like and Thyroxin-binding globulin precursor (T4-binding globulin, TBG) genes, ESTs and STSs.//4.1e-129:804:85//Z83850	F-HEMBA1007066//HS_3116_A2_A03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3116 Col=6 Row=A, genomic survey sequence.//0.80:214:62//AQ140467
F-HEMBA1006758//Homo sapiens chromosome 5, BAC clone 182a8 (LBML H161), complete sequence.//2.2e-162:766:99//AC005752	F-HEMBA1007073//Homo sapiens 12q13 PAC RPC11-316M24 (Roswell Park Cancer Institute Human PAC library) complete sequence.//9.3e-54:519:68//AC004242
F-HEMBA1006767//Human Xq28 cosmid U247A3 from LLOXNC01 X chromosome library, complete sequence.//1.2e-19:326:69//U73465	F-HEMBA1007078//CIT-HSP-2318N6, TF CIT-HSP Homo sapiens genomic clone 2318N6, genomic survey sequence.//8.7e-80:387:98//AQ044076
F-HEMBA1006779//Human DNA sequence from clone 80119 on chromosome 6p21.31-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence.//1.4e-103:355:87//AL022727	F-HEMBA1007080
F-HEMBA1006780//CIT-HSP-2359P7, TR CIT-HSP Homo sapiens genomic clone 2359P7, genomic survey sequence.//0.072:147:68//AQ077208	F-HEMBA1007085//Streptomyces coelicolor cosmid 7A1.//3.5e-06:496:59//AL034447
F-HEMBA1006789//nxb0037113r CUG1 Rice BAC Library Oryza sativa genomic clone nxb0037113r, genomic survey sequence.//0.00011:288:63//AQ290474	F-HEMBA1007087//Plasmodium falciparum MAL3P6, complete sequence.//7.4e-07:553:56//Z98551
F-HEMBA1006795//CIT-HSP-2307E3, TF CIT-HSP Homo sapiens genomic clone 2307E3, genomic survey sequence.//5.1e-80:420:96//AQ020511	F-HEMBA1007112//HS_2171_A1_B01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=1 Row=C, genomic survey sequence.//1.0:172:61//AQ091865
F-HEMBA1006796//Human clone 23803 mRNA, partial cds.//4.5e-06:202:68//U79298	F-HEMBA1007113//Human DNA sequence from clone 1044017 on chromosome Xp11.3-11.4 Contains GSS and STS, complete sequence.//0.54:502:56//AL023875
F-HEMBA1006807//Homo sapiens mRNA for SPDP.//1.2e-66:651:73//AJ000644	F-HEMBA1007121//Caenorhabditis elegans cosmid ZK430.//1.4e-08:265:64//U42833
F-HEMBA1006821//Homo sapiens chromosome 17, clone hRPC.62_0_9, complete sequence.//6.0e-116:541:99//AC004797	F-HEMBA1007129//CITBI-E1-2504A5, TF CITBI-E1 Homo sapiens genomic clone 2504A5, genomic survey sequence.//0.97:267:62//AQ264035

【0713】

【表4 1 4】

F-HENBA1007151//CITBI-E1-2522H6.TF CITBI-E1 Homo sapiens genomic clone 2522H6, genomic survey sequence.//2.0e-20:157:87//AQ280780
 F-HENBA1007174//Homo sapiens epsilon 2a mRNA, complete cds.//2.0e-6 2:318:97//AF062085
 F-HENBA1007178//Homo sapiens chromosome 12p13.3 clone RPC111-372B 4, WORKING DRAFT SEQUENCE, 129 ordered pieces.//1.6e-21:205:80//AC 005911
 F-HENBA1007194//HS_3124_82_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, genomic survey sequence.//1.3e-11:87:96//AQ187492
 F-HENBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds.//1.7e-156:478:98//AB06987
 F-HENBA1007206//Homo sapiens chromosome 17, clone HRPB37J1, complete sequence.//0.024:342:63//AC004223
 F-HENBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds.//5.0e-176:839:98//AB018340
 F-HENBA1007243//Chinese hamster hprt mRNA, complete cds.//4.3e-58:687:68//100060
 F-HENBA1007251//Rabbit troponin T messenger fragment (aa 49 to 129).//0.084:177:62//Y00899
 F-HENBA1007256//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 32E19, WORKING DRAFT SEQUENCE.//1.3e-75:490:88//AL022240
 F-HENBA1007267//HS_3218_A1_F07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=13 Row=K, genomic survey sequence.//2.9e-62:393:87//AQ181128
 F-HENBA1007273//CIT-HSP-2171B10.TF CIT-HSP Homo sapiens genomic clone 2171B10, genomic survey sequence.//1.1e-63:314:99//B95401
 F-HENBA1007279//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-11 6A10, complete sequence.//3.1e-31:401:72//AC004638
 F-HENBA1007281//HS_3115_A1_A11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3115 Col=21 Row=A, genomic survey sequence.//5.0e-70:372:96//AQ186691
 F-HENBA1007288//Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS, CpG island, complete sequence.//1.2e-152:727:98//AL031003
 F-HENBA1007300//Canis familiaris PDE5 mRNA for 3', 5'-Cyclic GMP Phosphodiesterase, complete cds.//2.1e-21:542:63//AB008467
 F-HENBA1007301//COL1A1-type I collagen pro alpha 1(I) chain propeptide (3' region) [human, fetal cells 86-237, 86-146, 88-251, mRNA Partial Mutant, 855 nt].//1.7e-08:388:61//S64596
 F-HENBA1007319//Genomic sequence from Mouse 9, complete sequence.//6.0e-84:390:75//AC000399
 F-HENBA1007320
 F-HENBA1007322//Homo sapiens BAC clone RG118E13 from 7p15-p21, complete sequence.//0.091:260:64//AC004485
 F-HENBA1007327//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-42 0 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.12:472:59//AC005140
 F-HENBA1007341//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//1.5e-18:408:64//AC006120
 F-HENBA1007342//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.7e-25:500:62//AC005377
 F-HENBA1007347//Homo sapiens chromosome 5, BAC clone 7g12 (LBNL H1 26), complete sequence.//0.75:269:61//AC005738
 F-HENBB1000005//Homo sapiens chromosome Y, clone 264.M.20, complete sequence.//5.0e-05:441:60//AC004617
 F-HENBB1000008//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//1.0e-44:417:77//AC004491
 F-HENBB1000018//HS_2179_B2_E04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=8 Row=J, genomic survey sequence.//0.012:87:77//AQ023250
 F-HENBB1000024//Human DNA sequence from PAC 106120 on chromosome 2 2q12-qter contains NADH pseudogene, ESTs, STS.//8.1e-11:461:61//Z81369
 F-HENBB1000025//CIT-HSP-2348F3.TR CIT-HSP Homo sapiens genomic clone 2348F3, genomic survey sequence.//0.95:198:62//AQ062938
 F-HENBB1000030//Homo sapiens DNA sequence from PAC 32F7 on chromosome X. Contains NUCLEOSOME ASSEMBLY PROTEIN 1-LIKE 3, ESTs.//0.00049:276:64//AL009173
 F-HENBB1000036//H. sapiens chromosome 22 CpG island DNA genomic Mse I fragment, clone 302e2, reverse read 302e2.r.//0.0057:66:81//Z79857
 F-HENBB1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//1.9e-100:450:98//AF084928
 F-HENBB1000039//HS_2167_B1_F12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2167 Col=23 Row=L, genomic survey sequence.//0.022:108:69//AQ092404
 F-HENBB1000044//Borrelia burgdorferi (section 50 of 70) of the complete genome.//1.0e-07:486:61//AE001164
 F-HENBB1000048//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-62 8 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//5.3e-05:585:58//AC005507
 F-HENBB1000050//Homo sapiens DNA sequence from clone 501N12 on chromosome 6p22.1-22.3 Contains a gene almost identical to four genes of unknown function, a pseudogene, three (pseud?) genes similar to genes of unknown function, an unknown gene similar to a rat EST, a PX19 LIKE pseudogene and another unknown gene. Contains ESTs, STSs and GSSs, complete sequence.//5.8e-38:549:67//AL022170
 F-HENBB1000054//Homo sapiens Xp22 PAC RPC11-167A22 (from Roswell Park Cancer Center) complete sequence.//7.0e-98:328:83//AC002349
 F-HENBB1000055//Homo sapiens genomic DNA for centromeric end of MC class I region on chromosome 6, cosmid clone: TY2F10, WORKING DRAFT SEQUENCE.//3.7e-05:600:58//AB000880
 F-HENBB1000059//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE, 10 unordered pieces.//1.3e-48:472:78//AC005096
 F-HENBB1000083
 F-HENBB1000089//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE.//0.0035:679:56//AL031744
 F-HENBB1000099//Homo sapiens chromosome 18 BAC RPC111-128D14 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.1e-15:312:68//AC005909
 F-HENBB1000103//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.0e-37:316:74//AC006210
 F-HENBB1000113//Homo sapiens chromosome 21q22.3 cosmid Q11M15, complete sequence.//3.1e-25:259:76//AF045450
 F-HENBB1000119//Homo sapiens ASMTL gene.//1.2e-137:654:98//Y15521
 F-HENBB1000136//Mycobacterium tuberculosis H37Rv complete genome: segment 127/162.//0.59:217:66//Z74697
 F-HENBB1000141//Homo sapiens DNA from chromosome 19q13.1 cosmid t14121 containing ATP4A and GADPH-2 genes, genomic sequence.//8.4e-31:113:88//AD000090
 F-HENBB1000144//Human BAC clone RG114A06 from 7q31, complete sequence.//4.4e-58:339:87//AC002542
 F-HENBB1000173//Homo sapiens 12q24 BAC RPC111-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//9.4e-160:562:93//AC002996
 F-HENBB1000175
 F-HENBB1000198//HS_3071_A2_A10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=20 Row=A, genomic survey sequence.//0.99:261:61//AQ137388
 F-HENBB1000215//Homo sapiens chromosome 17, clone hRPK.481_C_4, complete sequence.//6.7e-17:138:86//AC005839
 F-HENBB1000217//Arabidopsis thaliana ubiquitin activating enzyme (UBA1) gene, complete cds.//0.00083:287:60//U80808
 F-HENBB1000218//Caenorhabditis elegans cosmid C52A11, complete sequence.//0.90:337:56//Z46792
 F-HENBB1000226//Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16 p13.3. Contains ESTs and CpG island.//1.7e-90:175:92//Z69890
 F-HENBB1000240//Human G-protein-coupled inwardly rectifying potassium channel (KCNJ3) gene, polymorphic repeat sequence.//0.16:171:62//U07918
 F-HENBB1000244//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.8e-08:355:63//AC005522
 F-HENBB1000250//Homo sapiens protein associated with Myc mRNA, complete cds.//6.6e-155:735:98//AF075587
 F-HENBB1000258//Human adenosine monophosphate deaminase 1 (AMPD1) gene, exons 1-16.//0.58:396:59//M88818
 F-HENBB1000264//Human clone C3 CHL1 protein (CHL1) mRNA, alternatively spliced, complete cds.//4.4e-32:100:100//U75968
 F-HENBB1000266//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence.//3.8e-16:176:78//AC004470
 F-HENBB1000272//Plasmodium falciparum chromosome 2, section 6 of 7 3 of the complete sequence.//0.011:379:58//AE001369
 F-HENBB1000274//Arabidopsis thaliana DNA chromosome 4, BAC clone T5K18 (ESSA11 project).//0.92:272:61//AL022580
 F-HENBB1000284//Human Xp22 BAC CT-285115 (from CalTech/Research Genetics), PAC RPC11-27C22 (from Roswell Park Cancer Center), and Cosmid U35B5 (from Lawrence Livermore), complete sequence.//0.00071:568:57//AC002366
 F-HENBB1000307//Human DNA sequence from PAC 29K1 on chromosome 6p21.3-22.2. Contains glutathione peroxidase-like: zinc finger, ESTs, mRNA, STS, tRNAs, olfactory receptor pseudogene.//3.0e-13:439:65//Z98745
 F-HENBB1000312//Homo sapiens clone GS051M12, complete sequence.//0.031:252:65//AC005007
 F-HENBB1000317//Fugu rubripes GSS sequence, clone 060J22aE10, genomic

【0 7 1 4】

【表415】

mic survey sequence.//0.0033:173:65//AL025242
 F-HEMBB1000318//HS_3244_B2_H10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=20 Row=P, genomic survey sequence.//3.9e-85:438:95//AQ252951
 F-HEMBB1000335//Homo sapiens chromosome 18, clone hRPK.24_A_23, complete sequence.//0.63:285:61//AC005968
 F-HEMBB1000336
 F-HEMBB1000337//Homo sapiens chromosome 4 clone B208G5 map 4q25, complete sequence.//0.0014:309:64//AC004051
 F-HEMBB1000338//HS_3108_A2_F07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=14 Row=K, genomic survey sequence.//3.8e-09:331:63//AQ140356
 F-HEMBB1000339//Homo sapiens 12q24 PAC RPC11-46F2 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.2e-52:295:77//AC002351
 F-HEMBB1000341
 F-HEMBB1000343//Plasmodium falciparum MAL3P3, complete sequence.//0.00081:397:61//Z98547
 F-HEMBB1000354//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmalipin, ESTs and GSSs, complete sequence.//9.1e-34:596:66//AL020989
 F-HEMBB1000369//Genomic sequence from Human 17, complete sequence.//0.012:298:60//AC002090
 F-HEMBB1000374//Human Xp22 contig of 3 PACS (R7-39012, R7-134G1, R7-185L21) from the Roswell Park Cancer Institute, complete sequence.//9.3e-69:294:89//U96409
 F-HEMBB1000376//Human DNA sequence from clone 751H9 on chromosome 6q13. Contains part of an unknown gene, ESTs, STSs and GSSs, complete sequence.//3.5e-54:352:88//AL034377
 F-HEMBB1000391//Trichothecium roseum internal transcribed spacer 1, 5.8S ribosomal RNA gene; and internal transcribed spacer 2, complete sequence.//0.011:168:67//U51982
 F-HEMBB1000399//Homo sapiens Rad17-like protein (RAD17) mRNA, complete cds.//2.6e-163:762:98//AF076838
 F-HEMBB1000402//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//7.7e-15:466:63//AC002368
 F-HEMBB1000404//Homo sapiens mRNA for myosin-IXA.//3.5e-65:324:98//AJ001714
 F-HEMBB1000420//244Kb Contig from Human Chromosome 11p15.5 spanning D1S1 through D1S25, complete sequence.//0.013:399:62//AC001228
 F-HEMBB1000434//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//6.1e-83:571:84//AC004263
 F-HEMBB1000438//RPC111-21E14.TP RPC11-11 Homo sapiens genomic clone RPC11-11-21E14, genomic survey sequence.//0.0030:295:63//B83110
 F-HEMBB1000441//Homo sapiens Chromosome 22q12 Cosmid Clone 1147g1, complete sequence.//2.5e-33:372:72//AC000035
 F-HEMBB1000449//Human DNA sequence from PAC 296K21 on chromosome X contains cytochrome P-450, delta-aminolevulinic synthase (erythroid): 5-aminolevulinic acid synthase. (EC 2.3.1.37), 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.//1.3e-51:534:72//Z83821
 F-HEMBB1000455//Saccharomyces cerevisiae mitochondrion origin of replication (ori6) and oli1 gene, complete cds.//0.016:522:58//L36899
 F-HEMBB1000472
 F-HEMBB1000480
 F-HEMBB1000487//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 12803, WORKING DRAFT SEQUENCE.//0.00013:314:64//Z98742
 F-HEMBB1000490//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE.//4.1e-110:529:98//AL034423
 F-HEMBB1000491//Plasmodium falciparum chromosome 2, section 25 of 73 of the complete sequence.//0.10:187:65//AE001388
 F-HEMBB1000493//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SMN2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//3.7e-06:637:58//AL022577
 F-HEMBB1000510//Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence.//3.1e-96:737:81//AC005553
 F-HEMBB1000518//Homo Sapiens Chromosome X clone bNXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.00014:163:68//AC004676
 F-HEMBB1000523//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-105, complete sequence.//0.41:349:56//AL010212
 F-HEMBB1000530//H.sapiens mRNA for extracellular matrix protein collagen type XIV, C-terminus.//6.6e-37:138:96//Y11710
 F-HEMBB1000550//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//3.9e-56:683:71//AB020860
 F-HEMBB1000554//Homo sapiens *** SEQUENCING IN PROGRESS *** WORKING DRAFT SEQUENCE.//2.2e-51:282:84//AJ011929
 F-HEMBB1000556//Homo sapiens mRNA for KIAA0750 protein, complete cds.//6.1e-32:537:65//AB018293
 F-HEMBB1000564
 F-HEMBB1000573//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//8.2e-33:268:73//AC005077
 F-HEMBB1000575//Human DNA sequence from clone 323M22 on chromosome 22q13.1-13.2. Contains the 5' part of the human ortholog of chicken PS2 and mouse H74, and a novel gene coding for a protein similar to KIAA0173 and worm Tubulin Tyrosine Ligase. Contains ESTs, STSs, GSSs, genomic marker D22S418 and putative CpG islands, complete sequence.//5.8e-47:734:66//AL022476
 F-HEMBB1000586//H.sapiens highly polymorphic microsatellite DNA.//0.030:147:67//X79883
 F-HEMBB1000589//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//6.3e-41:278:83//AC002300
 F-HEMBB1000591//Homo sapiens Xp22 bins 45-47 BAC GSHB-665M22 (Genome Systems Human BAC Library) complete sequence.//1.1e-182:871:98//AC005184
 F-HEMBB1000592//Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence, clone #19.//0.012:185:64//AF009074
 F-HEMBB1000593//Homo sapiens chromosome 7q22 sequence, complete sequence.//1.2e-131:353:93//AF053356
 F-HEMBB1000598//Homo sapiens 12p13.3 BAC RPC13-488H23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//9.1e-58:600:72//AC006207
 F-HEMBB1000623//cDNA encoding Colliolus manganese peroxidase.//0.89:284:62//E12284
 F-HEMBB1000630//Mus musculus clone NSAT47 nonsatellite RNA sequence.//1.9e-15:129:87//U26231
 F-HEMBB1000631//Sequence 26 from patent US 5708157.//3.2e-27:180:88//180057
 F-HEMBB1000632//Human mRNA for KIAA0351 gene, complete cds.//1.6e-48:811:65//AB002349
 F-HEMBB1000637//Homo sapiens clone DJ0425102, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.1e-58:649:73//AC005478
 F-HEMBB1000638//HS_3051_A1_C01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=M, genomic survey sequence.//0.0032:497:56//AQ155234
 F-HEMBB1000643//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.4e-50:791:68//AC005077
 F-HEMBB1000649//Homo sapiens Chromosome 16 BAC clone CIT987-SK502C, complete sequence.//5.2e-64:775:69//AC003009
 F-HEMBB1000652//Homo sapiens chromosome 10 clone CR1-JC2048 map 10q22.1, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.7e-52:334:89//AC006186
 F-HEMBB1000665//Human DNA sequence from clone 452W16 on chromosome Xq21.1-21.33 Contains capping protein alpha subunit isoform 1 pseudogene, STS, GSS, and CA repeat, complete sequence.//0.0062:426:60//AL024493
 F-HEMBB1000671//Human DNA sequence from PAC 93H18 on chromosome 6 contains ESTs heterochromatin protein HP1h-gamma pseudogene, STS and CpG island.//9.6e-95:399:78//Z84488
 F-HEMBB1000673//HS_3039_A2_C08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=16 Row=E, genomic survey sequence.//3.8e-50:293:92//AQ155121
 F-HEMBB1000684//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 222E13, WORKING DRAFT SEQUENCE.//8.0e-65:282:83//Z93241
 F-HEMBB1000693//Homo sapiens neuroanl mRNA, complete cds.//1.6e-11:575:97//AF040723
 F-HEMBB1000705//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//8.6e-07:251:61//AC005507
 F-HEMBB1000706//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 153G14, WORKING DRAFT SEQUENCE.//2.9e-20:434:64//AL031118
 F-HEMBB1000709//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 99AL9, WORKING DRAFT SEQUENCE.//0.26:184:65//AL034554
 F-HEMBB1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//1.8e-129:692:93//U53475
 F-HEMBB1000726//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//2.7e-40:304:80//U91321
 F-HEMBB1000738//Human Xq28 cosmids U126G1, U142F2, U69B6, U145C10, U169A5, U84H1, U24D12, U80A7, U153E6, L35485, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete sequence.//8.9e-35:582:63//AF011889
 F-HEMBB1000749//Homo sapiens chromosome 11 clone CIT-HSP-1337H24,

【0715】

【表416】

WORKING DRAFT SEQUENCE. 9 unordered pieces. //6.2e-46:262:89//AC005849
 F-HEMBB1000763//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SEQUENCE. //1.6e-99:316:98//AL034405
 F-HEMBB1000770//Human DNA sequence from clone 80119 on chromosome 6p21.31-22.2. Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence. //0.044:325:60//AL022727
 F-HEMBB1000774
 F-HEMBB1000781//Sequence 3 from patent US 5753446. //1.2e-92:599:86//AR008277
 F-HEMBB1000789//Homo sapiens mRNA for KIAA0677 protein, complete cds. //9.3e-64:672:71//AB014577
 F-HEMBB1000790//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence. //2.4e-41:460:74//AC004801
 F-HEMBB1000810//HS_3034_B2_D12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3034 Col=24 Row=H, genomic survey sequence. //1.8e-74:378:97//AQ117099
 F-HEMBB1000807//H. sapiens CoG island DNA genomic MseI fragment, clone 39d7, reverse read cpg39d7.r11a. //8.5e-14:95:97//Z58412
 F-HEMBB1000810//H. sapiens chromosome 22 CoG island DNA genomic MseI fragment, clone 303a8, complete read. //3.2e-05:138:71//Z79983
 F-HEMBB1000821//HS_2168_B1_A12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2168 Col=23 Row=B, genomic survey sequence. //0.85:208:60//AQ086361
 F-HEMBB1000822//Human BAC clone GS113M23 from 5p15.2, complete sequence. //3.0e-06:361:60//AC003015
 F-HEMBB1000826//Human BAC clone RG180F08 from 7q31, complete sequence. //1.1e-27:360:69//AC002431
 F-HEMBB1000827
 F-HEMBB1000831
 F-HEMBB1000835//Human DNA sequence from clone 4514 on chromosome 6q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence. //0.00098:234:63//AL023581
 F-HEMBB1000840//Human Chromosome 11 Cosmid cSRL97a6, complete sequence. //4.5e-61:328:79//U73649
 F-HEMBB1000848//Homo sapiens DNA sequence from PAC 206D15 on chromosome 1q24. Contains a Reduced Folate Carrier protein (RFC) LIKE gene, a mitochondrial ATP Synthetase protein 8 (ATP8, MITATP8) LIKE pseudogene, an unknown gene and the last exon of the JEM1 gene coding for the Basic-Leucine Zipper nuclear factor JEM-1. Contains ESTs, an STS and a BAC end sequence (GSS), complete sequence. //9.7e-144:809:87//AL021068
 F-HEMBB1000852//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE. 9 unordered pieces. //0.12:492:58//AC004157
 F-HEMBB1000870//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE. 9 unordered pieces. //0.0024:212:67//AC004157
 F-HEMBB1000876//Homo sapiens ELIS-1 mRNA, partial cds. //1.5e-32:200:94//AF085351
 F-HEMBB1000883//HS_3065_B2_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3065 Col=8 Row=F, genomic survey sequence. //0.0017:152:66//AQ137687
 F-HEMBB1000887
 F-HEMBB1000888//CIT-HSP-2329A10. TR CIT-HSP Homo sapiens genomic clone 2329A10, genomic survey sequence. //1.5e-31:172:98//AQ044369
 F-HEMBB1000890
 F-HEMBB1000893//Plasmodium falciparum MAL3P2, complete sequence. //9.5e-06:768:56//AL034558
 F-HEMBB1000908//Homo sapiens clone DJ1119N05, complete sequence. //4.5e-21:199:82//AC004968
 F-HEMBB1000910//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE. //0.72:366:59//AL034557
 F-HEMBB1000913//HS_3078_B1_C02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=3 Row=F, genomic survey sequence. //9.9e-12:221:63//AQ144507
 F-HEMBB1000915//Homo sapiens DNA for (CGG)n trinucleotide repeat region, isolate P4. //1.2e-49:252:99//AJ001215
 F-HEMBB1000917//Homo sapiens chromosome 5, P1 clone 254f11 (LBNL H 62), complete sequence. //2.3e-42:316:76//AC006077
 F-HEMBB1000927//Human BDR-2 mRNA for hippocalcin, complete cds. //3.6e-30:528:65//D16593
 F-HEMBB1000947//CpG08568 Cp10WAGDNA1 Cryptosporidium parvum genomic, genomic survey sequence. //0.81:262:62//AQ254493
 F-HEMBB1000959//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 34606, WORKING DRAFT SEQUENCE. //1.2e-43:454:75//Z84487
 F-HEMBB1000973//Mus musculus schlafen2 (Slfn2) mRNA, complete cds. //8.3e-42:458:72//AF099973
 F-HEMBB1000975//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MBKS, complete sequence. //0.98:196:63//AB005234
 F-HEMBB1000981
 F-HEMBB1000985//Homo sapiens chromosome 19, cosmid R29388, complete sequence. //2.9e-06:566:57//AC004476
 F-HEMBB1000991//Human DNA sequence from PAC 238J17 on chromosome 6q22. Contains EST and STS. //0.089:391:57//Z98753
 F-HEMBB1000996//Human DNA sequence from BAC 999D10 on chromosome 2q13.3. Contains two BAC end-sequences (GSSs). //6.2e-33:227:80//Z94802
 F-HEMBB1001004
 F-HEMBB1001008//Human Chromosome 16 BAC clone CIT987SK-A-951C11, complete sequence. //4.0e-13:164:79//AC002551
 F-HEMBB1001011//Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence. //7.5e-13:229:69//AC002310
 F-HEMBB1001014//Homo sapiens chromosome 16, BAC clone 375G12 (LAN L), complete sequence. //0.32:474:58//AC005751
 F-HEMBB1001020//Homo sapiens BAC clone 255A7 from Bq21 containing NBS1 gene, complete sequence. //2.6e-39:218:80//AF069291
 F-HEMBB1001024//Homo sapiens BAC clone 393122 from Bq21, complete sequence. //5.3e-05:656:59//AF070717
 F-HEMBB1001037//CIT-HSP-2358K16. TF CIT-HSP Homo sapiens genomic clone 2358K16, genomic survey sequence. //6.6e-05:228:64//AQ080539
 F-HEMBB1001047//Homo sapiens cosmids Qc14E2, Qc12H12, Qc11F9, Qc10G9, LA1733 and Qc17B8 from Xq28, complete sequence. //4.0e-27:385:71//U82671
 F-HEMBB1001051//H. sapiens mRNA for FAN protein. //1.2e-27:160:98//X95586
 F-HEMBB1001056//Homo sapiens clone DJ0953A04, WORKING DRAFT SEQUENCE. 5 unordered pieces. //2.3e-89:180:91//AC006014
 F-HEMBB1001058//Homo sapiens 3p22-8 PAC RPC14-736H12 (Roswell Park Cancer Institute Human PAC Library) complete sequence. //1.2e-41:468:74//AC006060
 F-HEMBB1001060//Human Tigger1 transposable element, complete consensus sequence. //4.3e-122:785:86//U49973
 F-HEMBB1001063//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 523G1, WORKING DRAFT SEQUENCE. //7.1e-162:770:99//AL03475
 F-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds. //3.1e-146:736:95//AF034803
 F-HEMBB1001096//Buchnera aphidicola genomic fragment containing (c haperone Hsp60) groEL, DNA biosynthesis initiating protein (dnaA), ATP operon (atpCDGAHFEB), and putative chromosome replication protein (gidA) genes, complete cds; and termination factor Rho (rho) gene, partial cds. //0.00088:690:57//AF008210
 F-HEMBB1001102//Homo sapiens huntingtin interacting protein HYPH mRNA, partial cds. //2.1e-76:368:99//AF049612
 F-HEMBB1001105//CIT-HSP-2185N1. TR CIT-HSP Homo sapiens genomic clone 2185N1, genomic survey sequence. //1.0e-09:136:76//AQ002987
 F-HEMBB1001112//Rattus rattus sec61 homologue mRNA, complete cds. //1.0e-108:909:76//M96630
 F-HEMBB1001114//Homo sapiens chromosome 17, clone hRPK.795_F_17, complete sequence. //7.2e-07:459:59//AC005284
 F-HEMBB1001117//HS_2178_B1_E12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=23 Row=J, genomic survey sequence. //7.8e-50:331:86//AQ068244
 F-HEMBB1001119//Human collagen type X11 alpha-1 precursor (COL12A1) mRNA, complete cds. //1.6e-25:150:98//U73778
 F-HEMBB1001126
 F-HEMBB1001133//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence. //2.8e-24:228:80//AC004673
 F-HEMBB1001137
 F-HEMBB1001142//Homo sapiens chromosome Y, clone 264.M.20, complete sequence. //1.0e-40:231:76//AC004617
 F-HEMBB1001151//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds. //2.9e-47:640:67//AF015264
 F-HEMBB1001153//CIT-HSP-2359K11. TR CIT-HSP Homo sapiens genomic clone 2359K11, genomic survey sequence. //0.76:136:67//AQ075724
 F-HEMBB1001169//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2), ESTs and CA repeat. //9.9e-63:259:79//AL008712
 F-HEMBB1001175//Human mRNA for ankyrin motif, complete cds. //2.2e-34:509:66//D78334
 F-HEMBB1001177//CIT-HSP-2321117. TR CIT-HSP Homo sapiens genomic clone 2321117, genomic survey sequence. //5.9e-27:320:75//AQ036473
 F-HEMBB1001182//RPC111-30J5.TV RPC11-11 Homo sapiens genomic clone RPC11-11-30J5, genomic survey sequence. //5.7e-06:62:96//B85188
 F-HEMBB1001199

【0716】

【表417】

F-HEMBB1001208//HS_2026_B1_C07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=13 Row=F, genomic survey sequence.//0.00018:134:70//AQ229237	F-HEMBB1001394//Homo sapiens BAC clone GS421103 from Xq25-q26, complete sequence.//4.0e-129:788:88//AC005023
F-HEMBB1001209//CITB1-E1-2521F23.TF CITB1-E1 Homo sapiens genomic clone 2521F23, genomic survey sequence.//1.4e-95:464:98//AQ278357	F-HEMBB1001410//Homo sapiens wbscr1 (WBSR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//4.8e-11:632:59//AF045555
F-HEMBB1001210//HS_3102_A2_F09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3102 Col=18 Row=K, genomic survey sequence.//2.6e-90:446:98//AQ119196	F-HEMBB1001424//Mus musculus Chromosome 4 BAC clone Bac86, complete sequence.//0.0012:435:59//AC003019
F-HEMBB1001218//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796F18, WORKING DRAFT SEQUENCE.//1.0e-31:315:72//AL031291	F-HEMBB1001426//Homo sapiens clone DJ0736H05, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.8e-17:360:64//AC005482
F-HEMBB1001221//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.7e-17:770:59//AC005504	F-HEMBB1001429//leucine aminopeptidase [cattle, kidney, mRNA, 2056 nt].//4.1e-114:668:88//S65367
F-HEMBB1001234//H.sapiens CpG island DNA genomic MseI fragment, clone 3919, forward read cpg3919.ftt.//4.0e-30:171:97//Z65435	F-HEMBB1001436//Homo sapiens FUT2 gene, intron 1, complete sequence.//2.3e-37:438:74//AB000931
F-HEMBB1001242//Homo sapiens mRNA for LAK-1, complete cds.//3.8e-30:458:67//AB005754	F-HEMBB1001443//Bos taurus pyruvate dehydrogenase phosphatase mRNA, complete cds.//9.1e-92:550:88//L18966
F-HEMBB1001249//CIT-HSP-2375N19.TF CIT-HSP Homo sapiens genomic clone 2375N19, genomic survey sequence.//0.0076:250:63//AQ109087	F-HEMBB1001449//Homo sapiens chromosome 5, PAC clone 228g9 (LBNL H142), complete sequence.//0.00024:385:62//AC004768
F-HEMBB1001253//Homo sapiens genomic DNA, chromosome 21q11.1, segment 3/28, WORKING DRAFT SEQUENCE.//0.0097:89:80//AP000032	F-HEMBB1001454//Homo sapiens chromosome 19, cosmid R34169, complete sequence.//0.84:577:57//AC005790
F-HEMBB1001254//CIT-HSP-2320E5.TF CIT-HSP Homo sapiens genomic clone 2320E5, genomic survey sequence.//3.7e-54:284:97//AQ037173	F-HEMBB1001458//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//8.0e-40:377:78//AC000382
F-HEMBB1001267//Homo sapiens chromosome 17, clone hRPC.488_L1, complete sequence.//3.5e-30:236:78//AC005303	F-HEMBB1001463//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//0.011:482:59//AF001549
F-HEMBB1001271//HS_3011_A1_G02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3011 Col=3 Row=M, genomic survey sequence.//5.2e-07:364:62//AQ214217	F-HEMBB1001464//Human chromosome 16p13 BAC clone CIT987SK-3H8 complete sequence.//0.019:263:61//U91320
F-HEMBB1001282//CIT-HSP-2356J20.TF CIT-HSP Homo sapiens genomic clone 2356J20, genomic survey sequence.//1.8e-16:109:97//AQ060969	F-HEMBB1001482//Rattus norvegicus Olf-1/EBF associated Zn finger protein Roaz mRNA, alternatively spliced form, complete cds.//1.0e-30:521:66//U92564
F-HEMBB1001288//R.norvegicus mRNA for gephyrin.//3.4e-18:194:77//X66366	F-HEMBB1001500//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.3e-31:479:71//AC004873
F-HEMBB1001289//Genomic sequence from Human 9q34, complete sequence.//4.8e-66:434:74//AC000387	F-HEMBB1001521//Homo sapiens clone RG269P13, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.7e-51:680:70//AC005080
F-HEMBB1001294//HS_3039_B1_D01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=1 Row=H, genomic survey sequence.//2.0e-90:437:99//AQ155035	F-HEMBB1001527
F-HEMBB1001302	F-HEMBB1001531//Homo sapiens Chromosome 22q11.2 Cosmid Clone 89h1 n DCCR Region, complete sequence.//1.3e-79:696:79//AC000089
F-HEMBB1001304//CIT-HSP-2053E15.TF CIT-HSP Homo sapiens genomic clone 2053E15, genomic survey sequence.//2.2e-07:370:61//B69144	F-HEMBB1001535//O.aries DNA for polymorphic marker 'OVINRA01' (339 bp).//0.00034:217:62//X89268
F-HEMBB1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//5.7e-116:663:85//U92703	F-HEMBB1001536//Homo sapiens PAC clone DJ1182N03 from 7q11.23-q21.1, complete sequence.//0.54:266:60//AC004548
F-HEMBB1001315//Homo sapiens chromosome 10 clone LA10NC01_0_G_3 map 10q26.1-10q26.2, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.5e-33:328:77//AC006096	F-HEMBB1001537//Homo sapiens chromosome 19, cosmid R29368, complete sequence.//4.6e-25:784:61//AC004262
F-HEMBB1001317//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.4e-122:680:91//AC006210	F-HEMBB1001555//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-248F7, complete sequence.//6.9e-50:213:80//AC004605
F-HEMBB1001325//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence.//2.8e-09:518:60//AC004129	F-HEMBB1001562//Homo sapiens clone NH0523H20, complete sequence.//0.46:269:60//AC005041
F-HEMBB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain:BALB/c.//3.7e-56:458:79//D63850	F-HEMBB1001564//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmalogen, ESTs and GSSs, complete sequence.//1.7e-107:620:83//AL020989
F-HEMBB1001335//HS_3055_A1_H10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=19 Row=O, genomic survey sequence.//1.0:222:63//AQ147384	F-HEMBB1001565//Homo sapiens BAC clone RG437L15 from 8q21, complete sequence.//2.4e-50:734:67//AC004003
F-HEMBB1001337//Human PAC clone DJ0093103 from Xq23, complete sequence.//1.0e-74:319:85//AC003983	F-HEMBB1001585//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence.//1.4e-16:816:97//AL031677
F-HEMBB1001339//Homo sapiens FSHD-associated repeat DNA, proximal region.//4.0e-135:856:87//U85056	F-HEMBB1001586
F-HEMBB1001346//Human familial Alzheimer's disease (STM2) gene, complete cds.//3.3e-44:481:74//U50871	F-HEMBB1001588//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.6e-21:419:65//AC005261
F-HEMBB1001348//Homo sapiens BAC clone NH0491B03 from 7p21-p15, complete sequence.//1.8e-17:210:73//AC006041	F-HEMBB1001603
F-HEMBB1001350//Homo sapiens clone RG252P22, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:386:59//AC005079	F-HEMBB1001618//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connective tissue growth factor (NOV, GIG) LIKE gene, a predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence.//4.5e-29:422:72//Z99289
F-HEMBB1001364//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence.//0.97:349:61//AC004662	F-HEMBB1001619//HS_3079_B1_A04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3079 Col=7 Row=B, genomic survey sequence.//0.0010:77:79//AQ123388
F-HEMBB1001366//Homo sapiens chromosome 10 clone CIT987SK-118815 map 10p11.2-10p12.1, complete sequence.//5.5e-161:766:98//AC005876	F-HEMBB1001630//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.2e-12:667:59//AC005089
F-HEMBB1001367//Homo sapiens chromosome 17, clone hRPC.906_A_24, complete sequence.//3.0e-55:510:76//AC004408	F-HEMBB1001635//Plasmodium falciparum MAL3P7, complete sequence.//3.8e-05:475:57//AL034559
F-HEMBB1001369//Homo sapiens BAC clone RG163K11 from 7q31, complete sequence.//0.048:244:64//AC005192	F-HEMBB1001637//Homo sapiens DNA sequence from PAC 934G17 on chromosome 1p36.21. Contains the alternatively spliced CLCN6 gene for chloride channel proteins CLC-6A (KIAA0046) -B, -C and -D, the alternatively spliced NPPA gene coding for Atrial Natriuretic Factor ANP precursor (Atrial Natriuretic peptide ANP, Prepronatriuretic), the NPPB gene for Brain Natriuretic Protein BNP, and a pseudogene similar to SBF1 (and other Myotubularin-related protein genes). Contains ESTs, STSs and the genomic marker D1S2740, complete sequence.//9.2e-13:168:76//AL021155
F-HEMBB1001380//Homo sapiens clone DJ1102B04 from 7q11.23-7q21, complete sequence.//2.5e-26:257:78//AC006204	F-HEMBB1001641//Arabidopsis thaliana genomic DNA, chromosome 5, PI
F-HEMBB1001384//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//5.1e-99:571:89//AF071314	
F-HEMBB1001387//Leishmania tarentolae mitochondrial 12S ribosomal RNA gene.//7.1e-05:546:58//X02354	

【0717】

【表418】

clone: MPO12, complete sequence.//0.00097:721:58//AB006702	F-HEM8B1001872
F-HEM8B1001653//Homo sapiens chromosome 2 clone 10186 map 2p11, complete sequence.//0.15:276:63//AC002038	F-HEM8B1001874//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.4e-14:631:61//AC005000
F-HEM8B1001665//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.43:393:61//L14320	F-HEM8B1001875//Human DNA sequence from clone J42BA131, WORKING DRAFT SEQUENCE.//0.93:415:57//Z82209
F-HEM8B1001668//F16C15-T7 IGF Arabidopsis thaliana genomic clone F16C15, genomic survey sequence.//0.040:275:60//B12308	F-HEM8B1001880//Human genomic DNA sequence from clone 30801 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//1.0e-18:729:60//Z93403
F-HEM8B1001673//Homo sapiens mRNA for KIAA0646 protein, complete cds.//7.2e-171:803:98//AB014546	F-HEM8B1001899//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-10, complete sequence.//0.0038:425:58//AL010216
F-HEM8B1001684//Sequence 1 from patent US 5700927.//7.5e-124:883:81//186429	F-HEM8B1001905//S.pombe chromosome III cosmid c330.//1.1e-23:520:62//AL031603
F-HEM8B1001685//CIT-HSP-228709.TF CIT-HSP Homo sapiens genomic clone 228709, genomic survey sequence.//2.3e-34:191:97//B99261	F-HEM8B1001906
F-HEM8B1001695//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog); translocated to 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STSs, GSSs, and a putative CpG island, complete sequence.//0.0091:334:63//AL009178	F-HEM8B1001908//Human monocytic leukemia zinc finger protein (MZF2) mRNA, complete cds.//3.7e-82:672:81//U47742
F-HEM8B1001704//Human DNA sequence from clone 931E15 on chromosome 1q25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//1.2e-17:144:87//AL023575	F-HEM8B1001910//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0033:566:55//AC005505
F-HEM8B1001706	F-HEM8B1001911//Arabidopsis thaliana chromosome II BAC F26C24 genomic sequence, complete sequence.//1.0:581:58//AC004705
F-HEM8B1001707//Guinea pig CD19 mRNA, complete cds.//0.57:232:62//M62543	F-HEM8B1001915//Caenorhabditis elegans cosmid T05H10, complete sequence.//1.2e-16:283:67//Z47812
F-HEM8B1001717//Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes.//1.1e-13:723:58//AJ223323	F-HEM8B1001921//Homo sapiens chromosome 17, clone hCIT.123_J_14, complete sequence.//3.4e-07:803:58//AC003950
F-HEM8B1001735//Human PAC clone DJ0596009 from Tpl5, complete sequence.//1.3e-36:427:73//AC003074	F-HEM8B1001922//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete sequence.//5.0e-06:756:56//AE001391
F-HEM8B1001736//S.pombe chromosome II cosmid c484.//0.0085:479:57//AL023706	F-HEM8B1001925//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-p35. Contains delta opiate receptor, CpG island, CA repeat.//3.1e-45:609:73//AL009181
F-HEM8B1001747//Homo sapiens PAC clone DJ1002N02 from Tp21-p22, complete sequence.//4.0e-112:532:84//AC005376	F-HEM8B1001930//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 10/11.//3.2e-158:745:99//AB020867
F-HEM8B1001749//Homo sapiens chromosome 17, clone hRPK.259_G_18, complete sequence.//1.3e-98:395:82//AC005829	F-HEM8B1001944//, complete sequence.//4.1e-60:638:73//AC005815
F-HEM8B1001753//S.maximus repeat region, 342bp.//4.2e-11:69:85//Z78099	F-HEM8B1001945//HS_3185_B1_G05_MIR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=9 Row=N, genomic survey sequence.//1.0:280:58//AQ188882
F-HEM8B1001756//Homo sapiens full length insert cDNA clone ZD86A11.//0.0015:302:62//AF080664	F-HEM8B1001947//Human mRNA for KIAA0392 gene, partial cds.//5.6e-20:333:66//AB002390
F-HEM8B1001760//P.falciparum complete gene map of plastid-like DNA (IR-A).//0.011:615:56//X95275	F-HEM8B1001950//Human lipocortin (LIP) 2 gene, upstream region.//0.0094:180:63//M62899
F-HEM8B1001762//CIT-HSP-2290J16.TF CIT-HSP Homo sapiens genomic clone 2290J16, genomic survey sequence.//0.84:208:64//AQ005184	F-HEM8B1001952//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 101A4, WORKING DRAFT SEQUENCE.//5.4e-19:329:70//Z93341
F-HEM8B1001785//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MALIP3, WORKING DRAFT SEQUENCE.//0.0019:469:60//AL031746	F-HEM8B1001953//Homo sapiens chromosome 17, clone hRPK.795_F_17, complete sequence.//0.11:589:58//AC005284
F-HEM8B1001797//Human heterogeneous nuclear RNA W16W.//0.00012:83:86//X17272	F-HEM8B1001957//Human DNA sequence from PAC 204E5 on chromosome 12. Contains exon similar to Wilms' Tumour-related protein QM-like P2X-like receptor, ATP ligand gated ion channel, ESTs, CpG island.//9.8e-25:446:67//Z98941
F-HEM8B1001802//Plasmodium falciparum MAL3P7, complete sequence.//1.8e-11:538:60//AL034559	F-HEM8B1001962//Homo sapiens chromosome 16, BAC clone 462G18 (LAN L), complete sequence.//2.8e-147:727:97//AC005736
F-HEM8B1001812//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 356B8, WORKING DRAFT SEQUENCE.//1.0e-56:304:84//Z98882	F-HEM8B1001967//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces.//3.2e-56:650:71//AC004963
F-HEM8B1001816//Homo sapiens chromosome 19, cosmid F24083, complete sequence.//3.6e-75:300:87//AC005204	F-HEM8B1001973//Homo sapiens chromosome 12p13.3 clone RPC111-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces.//1.2e-42:327:84//AC005844
F-HEM8B1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds.//2.3e-162:763:98//AF056209	F-HEM8B1001983//CIT-HSP-2315M4.TF CIT-HSP Homo sapiens genomic clone 2315M4, genomic survey sequence.//8.8e-35:198:96//AQ028071
F-HEM8B1001834//CIT-HSP-2291012.TF CIT-HSP Homo sapiens genomic clone 2291012, genomic survey sequence.//7.6e-08:73:94//AQ004168	F-HEM8B1001988//D.polychroa microsatellite sequence (clone Dp 1C e 12).//4.5e-07:337:62//X92189
F-HEM8B1001836//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.7e-30:297:79//AC004801	F-HEM8B1001990//HS_3234_A1_G08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3234 Col=15 Row=M, genomic survey sequence.//0.039:279:59//AQ020469
F-HEM8B1001839//Human Chromosome X, complete sequence.//0.016:293:63//AC004073	F-HEM8B1001996//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191J18, WORKING DRAFT SEQUENCE.//0.18:392:58//AL024507
F-HEM8B1001850//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.027:812:58//AC005504	F-HEM8B1001997//Homo sapiens clone RC140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.3e-43:446:71//AC005069
F-HEM8B1001863//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.3e-43:520:72//AC004581	F-HEM8B1002002//Plasmodium falciparum 3D7 chromosome 12 PFYAC312 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.077:444:58//AC004153
F-HEM8B1001867//Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.//1.7e-56:399:86//U07563	F-HEM8B1002005//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 963K23, WORKING DRAFT SEQUENCE.//3.4e-16:173:78//AL031685
F-HEM8B1001868//Rattus norvegicus clone 923 polymeric immunoglobulin receptor mRNA 3' untranslated region, CA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats.//6.1e-08:234:67//U01145	F-HEM8B1002009//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.0033:790:56//AC005506
F-HEM8B1001869//Homo sapiens full length insert cDNA clone YT86F01.//7.4e-87:432:97//AF085974	F-HEM8B1002015//Homo sapiens genomic DNA, chromosome 21q11.1, segment 27/28, WORKING DRAFT SEQUENCE.//6.7e-05:126:76//AP000056
	F-HEM8B1002042//Oncorhynchus mykiss cytochrome P450 (CYP4V1) mRNA, partial cds.//6.4e-33:402:69//AF046012

【0718】

【表419】

F-HEM81002043	F-HEM81002371//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.9 e-05:674:56//AC004153
F-HEM81002044//Homo sapiens chromosome 5p, BAC clone 50g21 (LBML H154), complete sequence.//3.0e-167:809:97//AC005740	F-HEM81002381//Homo sapiens chromosome 16, cosmid clone RT163 (LA NL), complete sequence.//0.34:238:61//AC005222
F-HEM81002045	F-HEM81002383
F-HEM81002049//Homo sapiens chromosome 17, clone hRPC.161_P_9, complete sequence.//0.87:177:65//AC006237	F-HEM81002387//CIT-HSP-2173E20, TR CIT-HSP Homo sapiens genomic clone 2173E20, genomic survey sequence.//5.2e-17:434:66//B91052
F-HEM81002050//Streptomyces coelicolor cosmid 078.//8.5e-08:644:58//AL034355	F-HEM81002409//Human DNA sequence from PAC 84F12 on chromosome Xq 25-Xq26.3. Contains glypican-3 precursor (intestinal protein OC1-5) (GTR2-2), ESTs and CA repeat.//1.2e-56:324:88//AL008712
F-HEM81002068//Homo sapiens mRNA for KIAA0612 protein, partial cds.//2.5e-05:402:61//AB014512	F-HEM81002415//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 36411, WORKING DRAFT SEQUENCE.//8.9e-35:334:75//AL031319
F-HEM81002069	F-HEM81002425//Chromosome 22q13 BAC Clone CIT987SK-38408 complete sequence.//1.0e-36:317:76//U62317
F-HEM81002092//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B3108: HTCS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//7.8e-104:550:83//AC004064	F-HEM81002442//Rattus norvegicus lin-10 protein homolog (lin-10) mRNA, complete cds.//4.3e-88:296:92//U92010
F-HEM81002094//Homo sapiens genomic DNA, 21q region, clone: 125H6 N2, genomic survey sequence.//2.9e-49:302:83//AC001476	F-HEM81002453//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 86D1, WORKING DRAFT SEQUENCE.//2.7e-43:419:78//AL034349
F-HEM81002115//Homo sapiens chromosome 16, cosmid clone 378E2 (LA NL), complete sequence.//0.00023:542:61//AC004035	F-HEM81002457//Homo sapiens clone DJ0982E09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.3e-27:542:68//AC005534
F-HEM81002134//Human h-neuro-d4 protein mRNA, complete cds.//7.3 e-43:533:70//U43843	F-HEM81002458//HS_3246_A2_G05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3246 Col=10 Row=M, genomic survey sequence.//3.2e-51:257:99//AQ217993
F-HEM81002139//HS-1048-A2-802-MR, abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 831 Col=4 Row=C, genomic survey sequence.//0.055:228:66//B38714	F-HEM81002477//Human Grb2-associated binder-1 mRNA, complete cds.//1.9e-87:493:92//U43885
F-HEM81002142//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P5, WORKING DRAFT SEQUENCE.//0.0095:276:64//AL031748	F-HEM81002489
F-HEM81002152//Human Chromosome X, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.055:520:57//AC002421	F-HEM81002492//Arabidopsis thaliana BAC T15B16.//0.028:516:57//AF104919
F-HEM81002189//Homo sapiens cosmid ICRF10410935Q8 from Xq28, complete sequence.//2.6e-05:311:63//AF002998	F-HEM81002495//Homo sapiens chromosome 17, clone hRPK.421_E_14, complete sequence.//1.1e-16:297:68//AC006141
F-HEM81002190//Plasmodium falciparum 3D7 chromosome 12 PFYAC88-42 0 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//5.4e-05:647:59//AC005140	F-HEM81002502//Homo sapiens clone DJ1163L11, complete sequence.//1.1e-91:675:82//AC005230
F-HEM81002193//Sequence 5 from patent US 5709858.//1.8e-34:179:100//I0346	F-HEM81002509//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-24 8FT, complete sequence.//2.7e-11:648:60//AC004605
F-HEM81002217//Homo sapiens mRNA for zinc finger protein 10.//1.2 e-23:405:67//X52332	F-HEM81002510//HS_3236_B1_H1_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3236 Col=21 Row=P, genomic survey sequence.//1.2e-06:67:94//AQ205992
F-HEM81002218//HS_2056_B1_C09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=17 Row=F, genomic survey sequence.//3.3e-45:245:97//AQ244711	F-HEM81002520//Homo sapiens BAC clone AH0004N07 from Y, complete sequence.//1.2e-70:580:72//AC006152
F-HEM81002232//Human chromosome 11 72g7 cosmid, complete sequence.//1.9e-21:314:70//U73648	F-HEM81002522//Homo sapiens Xp22 bin 150 clone GSHB-223P11 (Genome Systems Human BAC library) complete sequence.//5.6e-22:516:64//AC004553
F-HEM81002247	F-HEM81002531
F-HEM81002249//Homo sapiens DNA sequence from BAC 3418 on chromosome 5p21.3-22.1. Contains ZNF184 gene coding for Kruppel related Zinc Finger protein 184, a hnRNP core protein A1 (mouse Fli-2, rat helix stabilizing protein, mouse Topoisomerase-inhibitor suppressor gene TIS) LIKE pseudogene, a HB15 (CD83 antigen precursor) LIX E pseudogene, Ser-tRNA, Glu-tRNA and Met-tRNA (Met-tRNA-i gene) genes. Contains ESTs, STSs and GSSs, complete sequence.//4.1e-45:327:83//AL021918	F-HEM81002534//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 668J24, WORKING DRAFT SEQUENCE.//6.9e-62:265:87//AL034346
F-HEM81002254//Human chromosome 16 BAC clone LAML cosmid-440E5, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.8e-40:315:82//AC002506	F-HEM81002545//Human BAC clone RG128M16 from Tq21-Tq22, complete sequence.//2.7e-44:200:82//AC000059
F-HEM81002255//Plasmodium falciparum MAL3P3, complete sequence.//0.0035:312:62//Z98547	F-HEM81002550//Homo sapiens PAC clone DJ0910117 from Tq11.21-q11.23, complete sequence.//0.22:161:68//AC004927
F-HEM81002266//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.013:469:59//AC005504	F-HEM81002556//Homo sapiens PAC clone DJ0696N01 from Tq21-p22, complete sequence.//7.5e-43:306:77//AC004851
F-HEM81002280//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-25 9H10, complete sequence.//5.3e-18:527:61//AC004682	F-HEM81002579
F-HEM81002300//Human Chromosome 11 Cosmid cSRL30H11, complete sequence.//8.6e-139:818:88//U73642	F-HEM81002582//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 349A12, WORKING DRAFT SEQUENCE.//0.00018:431:61//AL033520
F-HEM81002306//HS_3109_A2_H01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3109 Col=2 Row=0, genomic survey sequence.//1.3e-75:371:98//AQ148164	F-HEM81002590//Yeast (S.cerevisiae) mitochondrial apocytochrome b gene, 3' flank.//0.78:147:64//J01471
F-HEM81002327//HS_3235_B2_G10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=20 Row=M, genomic survey sequence.//3.3e-83:418:97//AQ209752	F-HEM81002596//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 9E21, WORKING DRAFT SEQUENCE.//3.6e-50:692:69//AL008639
F-HEM81002329//CITB1-E1-2503J7, TR CITB1-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//3.3e-31:220:88//AQ263402	F-HEM81002600//Homo sapiens tetraspan NET-5 mRNA, complete cds.//9.1e-151:710:98//AF089749
F-HEM81002340	F-HEM81002601//Human BAC clone RG020D02 from Tq22, complete sequence.//1.5e-07:416:60//AC002381
F-HEM81002342//Homo sapiens mRNA for putative thioredoxin-like protein.//4.1e-154:724:98//A010841	F-HEM81002603//Human BAC clone G5552A01 from Tq21-q22, complete sequence.//0.40:341:60//AC002454
F-HEM81002358//Human thymidylate kinase (CDC8) mRNA, complete cds.//3.3e-36:192:98//L16991	F-HEM81002607//Mus musculus homeobox containing nuclear transcriptional factor Hmx1 (Hmx1) gene, complete cds.//0.0042:460:60//AF009614
F-HEM81002359//Human Rev interacting protein Rip-1 mRNA, complete cds.//1.8e-13:96:96//U55766	F-HEM81002610//Homo sapiens Chromosome 12q24 PAC RPC13-462E2 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.3e-23:559:63//AC003029
F-HEM81002364//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 376D21, WORKING DRAFT SEQUENCE.//7.5e-24:202:71//Z98946	F-HEM81002613//Homo sapiens Chromosome 22q12 BAC Clone 566c1, complete sequence.//4.2e-17:441:63//AC000025
	F-HEM81002614//Plasmodium falciparum chromosome 2, section 54 of 73 of the complete sequence.//0.013:324:56//AE001417
	F-HEM81002617//Homo sapiens chromosome 16 BAC clone CIT987SK-3340 11 complete sequence.//2.1e-07:441:60//AF001550

【表420】

F-HM8B1002623//C. hyalina microsatellite marker DNA (id ATCC4).//0.57:106:66//Z95304
 F-HM8B1002635//Human JNK3 alpha2 protein kinase (JNK3A2) mRNA, complete cds.//4.8e-22:127:100//U34819
 F-HM8B1002664//HS_2265_A1_H06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2265 Col=11 Row=D, genomic survey sequence.//0.54:115:67//AQ101557
 F-HM8B1002677//Homo sapiens (subclone 3_d1 from P1 H25) DNA sequence, complete sequence.//2.2e-49:784:68//L81774
 F-HM8B1002683//Homo sapiens type IV collagen 5a chain (COL4A5) gene, exon 23.//1.0:112:63//U04492
 F-HM8B1002684//HS-1050-A2-G06-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 772 Col=12 Row=M, genomic survey sequence.//4.4e-07:86:84//B39748
 F-HM8B1002686//HS-1023-B2-F10-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 802 Col=20 Row=L, genomic survey sequence.//0.98:183:61//B34077
 F-HM8B1002692//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1108H3, WORKING DRAFT SEQUENCE.//0.00039:408:60//AL033525
 F-HM8B1002697//Homo sapiens clone DJ1087M19, WORKING DRAFT SEQUENCE, 7 unordered pieces.//7.3e-35:323:74//AC004955
 F-HM8B1002699//Mus musculus D5Mm5e protein (D5Mm5e) and DOK protein (Dok) genes, complete cds: and LOR2 protein (Lor2) gene, partial cds.//0.031:325:62//AF084363
 F-HM8B1002702//HS-1025-A2-D01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 804 Col=2 Row=G, genomic survey sequence.//1.8e-25:158:95//B34720
 F-HM8B1002705//Homo sapiens DNA, chromosome 21q22.2, PAC clone 25 P16 complete sequence, encoding carbonyl reductase and carbonyl reductase 3 (complete cds).//1.7e-137:534:96//AB003151
 F-HM8B1002712//Human DNA sequence from cosmid CU115G11, between markers DXS6791 and DXS8038 on chromosome X contains ESTs and STS.//0.0019:612:58//Z71187
 F-HM8B1000009//Human chromosome 1 BAC 308G1 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//6.1e-43:354:81//AC003117
 F-HM8B1000019
 F-HM8B1000020//H. sapiens mRNA for flavin-containing monooxygenase 5 (FMO5).//2.0e-40:185:97//Z47553
 F-HM8B1000025//Homo sapiens PAC clone DJ0806A17 from Tpl3-p14, complete sequence.//1.0:211:65//AC005483
 F-HM8B1000043//Human angiotensin I-converting enzyme (ACE) gene, intron 12.//0.075:204:65//M73275
 F-HM8B1000045//Human DNA sequence from clone 142F18 on chromosome Xq26.3-27.2 Contains part of a gene similar to melanoma-associated antigen, EST, GSS and an inverted repeat, complete sequence.//4.1e-122:495:79//AL031073
 F-HM8B1000055//M. musculus mRNA for testin.//2.1e-35:559:66//X78989
 F-HM8B1000057//Homo sapiens chromosome 17, clone hRPK.259_G_18, complete sequence.//5.5e-121:703:89//AC005829
 F-HM8B1000069//Homo sapiens minisatellite ccb1 repeat region.//0.00013:329:60//AF048727
 F-HM8B1000084//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//2.1e-53:445:79//Z93023
 F-HM8B1000085//Caenorhabditis elegans cosmid Y23H5A.//0.0017:164:64//AF077541
 F-HM8B1000092//Homo sapiens BAC clone GS465M13 from Tpl5-p21, complete sequence.//1.2e-70:598:78//AC004744
 F-HM8B1000103//Homo sapiens chromosome 17, clone hCIT.91_J_4, complete sequence.//1.1e-156:857:92//AC003976
 F-HM8B1000117//HS_3223_B2_D08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=16 Row=H, genomic survey sequence.//5.4e-100:527:94//AQ221160
 F-HM8B1000129//ryanodine receptor.//0.055:492:59//A20359
 F-HM8B1000133
 F-HM8B1000134//HS_3078_B1_C02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=3 Row=F, genomic survey sequence.//2.1e-93:462:97//AQ144362
 F-HM8B1000139//Homo sapiens Xp22 PAC RPC11-5G11 (from Roswell Park Cancer Center) complete sequence.//3.3e-14:322:65//AC002369
 F-HM8B1000143//Homo sapiens mRNA for KIAA0585 protein, complete cds.//6.9e-25:148:97//AB014585
 F-HM8B1000155//Homo sapiens homeobox transcription factor barx2 (BARX2) mRNA, complete cds.//1.0e-29:219:87//AF031924
 F-HM8B1000163
 F-HM8B1000171//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence.//6.3e-14:92:88//AC005393
 F-HM8B1000173//Mus musculus SH3-containing protein SH3P7 mRNA, complete cds, similar to Human Drebrin.//2.2e-114:698:87//U58884
 F-HM8B1000175//HS_3050_B1_B03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=5 Row=D, genomic survey sequence.//6.2e-73:357:99//AQ102678
 F-HM8B1000183//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//4.6e-94:904:73//AL023808
 F-HM8B1000198//Z. diploperennis repetitive DNA (clone ZEAR 266).//0.18:152:70//X53610
 F-HM8B1000221//Human Chromosome 15q11-q13 PAC clone pDJ778a2, complete sequence.//0.017:99:75//AC004583
 F-HM8B1000227//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 467K16, WORKING DRAFT SEQUENCE.//0.36:312:62//AL031283
 F-HM8B1000241//HS_3217_B1_B02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3217 Col=3 Row=D, genomic survey sequence.//1.9e-94:456:98//AQ193401
 F-HM8B1000251//Homo sapiens NF2 gene.//0.00092:270:64//Y18000
 F-HM8B1000254//Plasmodium falciparum 307 chromosome 12 PFYACB8-42 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.0034:777:57//AC005140
 F-HM8B1000257//Homo sapiens DNA sequence from PAC 201D7 on chromosome 6p22.1-22.3. Contains EST and STS.//0.00036:230:65//AL022717
 F-HM8B1000264//Homo sapiens (subclone 9_15 from P1 H17) DNA sequence, complete sequence.//1.5e-30:499:68//L81612
 F-HM8B1000266//Bacillus lyncis strain pMEL12 Bag320 satellite DNA.//0.28:218:64//AF034430
 F-HM8B1000270//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//1.4e-157:788:96//AF001549
 F-HM8B1000277//Mycobacterium tuberculosis H37Rv complete genome, segment 48/162.//0.70:320:61//AL021897
 F-HM8B1000278//Sequence 23 from patent US 5708157.//9.3e-103:540:95//180055
 F-HM8B1000279//Human DNA sequence from clone 769D20 on chromosome Xp21.1-21.3 Contains EST, STS, GSS, complete sequence.//2.4e-49:262:77//AL031643
 F-HM8B1000284//cSRL-165E12-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-165E12, genomic survey sequence.//1.1e-30:324:75//B03004
 F-HM8B1000287//Homo sapiens, clone hRPK.15_A_1, complete sequence.//2.7e-54:401:83//AC006213
 F-HM8B1000302//Drosophila melanogaster complete mitochondrial genome.//0.0051:307:61//U37541
 F-HM8B1000307//Homo sapiens chromosome 12p13.3 clone RPC15-1154L15, WORKING DRAFT SEQUENCE, 67 unordered pieces.//0.15:449:59//AC006205
 F-HM8B1000309//cDNA coding human apolipoprotein E3.//0.00010:691:58//E00359
 F-HM8B1000312//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 798A17, WORKING DRAFT SEQUENCE.//0.27:301:60//AL031274
 F-HM8B1000313
 F-HM8B1000331//Human Chromosome 16 BAC clone CIT987SK-A-735G6, complete sequence.//9.8e-06:151:71//AC002400
 F-HM8B1000339
 F-HM8B1000340//HS_2181_B2_F07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2181 Col=14 Row=L, genomic survey sequence.//4.3e-05:181:68//AQ024288
 F-HM8B1000348//Homo sapiens chromosome 17, clone HRP843B9, complete sequence.//5.3e-30:575:66//AC004139
 F-HM8B1000356//Homo sapiens clone RC038K21, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-52:264:76//AC005052
 F-HM8B1000360//Homo sapiens PAC clone DJ0755G17 from Tpl1-p22, complete sequence.//6.5e-91:569:88//AC004879
 F-HM8B1000361//Human DNA sequence from PAC 507115 on chromosome Xq26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//1.4e-42:315:83//Z98950
 F-HM8B1000372//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//2.9e-114:516:89//AL022345
 F-HM8B1000385//CITB1-E1-251E13.TF CITB1-E1 Homo sapiens genomic clone 251E13, genomic survey sequence.//6.9e-26:377:71//AQ279944
 F-HM8B1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds.//3.7e-148:710:98//AB015132
 F-HM8B1000395
 F-HM8B1000402//Homo sapiens clone DJ0718N17, complete sequence.//4.0e-115:845:85//AC005999
 F-HM8B1000410//HS_3245_A1_C02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3245 Col=3 Row=E, genomic survey sequence.//9.6e-42:350:80//AQ205768
 F-HM8B1000413//HS_3223_B2_F01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=2 Row=L, genomic

【0720】

【表421】

mic survey sequence.//1.6e-48:318:89//AQ188456
 F-MAHMA1000414//HS_2027_B2_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=8 Row=F, genomic survey sequence.//1.4e-46:286:92//AQ231369
 F-MAHMA1000416//Drosophila melanogaster DNA sequence (Pls DS07528 (D169) and DS06665 (D220)), complete sequence.//9.4e-33:310:72//AC004540
 F-MAHMA1000421//Homo sapiens clone DJ1129005, complete sequence.//3.3e-29:223:84//AC005630
 F-MAHMA1000422
 F-MAHMA1000423//Drosophila yakuba mitochondrial DNA molecule.//2.2e-10:639:57//X03240
 F-MAHMA1000424//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.6e-47:556:68//AC003973
 F-MAHMA1000429//Mus musculus SDBP mRNA, complete cds.//8.0e-99:54:5:92//AF062484
 F-MAHMA1000431//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.8e-41:289:79//AC005283
 F-MAHMA1000444//Human DNA sequence from clone 71487 on chromosome 22q12.2-13.2 Contains CYTOCHROME C OXIDASE VIIB precursor like pseudogene and ESTs, complete sequence.//2.3e-34:291:80//Z99755
 F-MAHMA1000446
 F-MAHMA1000458//Mus musculus clone OST9003, genomic survey sequence.//5.0e-53:231:84//AF046620
 F-MAHMA1000468//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 291J10, WORKING DRAFT SEQUENCE.//0.75:303:60//Z93017
 F-MAHMA1000472//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 41407, WORKING DRAFT SEQUENCE.//4.0e-41:403:77//AL033543
 F-MAHMA1000478//Homo sapiens clone RG270013, WORKING DRAFT SEQUENCE, 18 unordered pieces.//9.5e-54:359:77//AC005081
 F-MAHMA1000483//Homo sapiens Chromosome 16 BAC clone CIT987SK-44N2, complete sequence.//3.6e-34:332:77//AC004381
 F-MAHMA1000490//Homo sapiens 12q13.1 PAC RPC11-90J4 (Roswell Park Cancer Institute Human PAC library) complete sequence.//8.9e-128:8:22:87//AC003686
 F-MAHMA1000500//CIT-HSP-231905, TF CIT-HSP Homo sapiens genomic clone 231905, genomic survey sequence.//4.8e-29:175:94//AQ044812
 F-MAHMA1000501//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxytalar-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//5.7e-45:334:82//AL022336
 F-MAHMA1000516//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//2.9e-43:529:69//Z92545
 F-MAHMA1000522//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence.//2.0e-14:380:63//AL022576
 F-MAHMA1000524//Homo sapiens chromosome 10 clone CIT-HSP-1338F24 map 10p11.2-10p12.1, complete sequence.//1.4e-22:420:66//AC006101
 F-MAHMA1000559//Human HepG2 3' region cDNA, clone hmd3108.//5.4e-2:9:168:97//D16922
 F-MAHMA1000565//RPC111-61K6, TJ RPC111 Homo sapiens genomic clone R-61K6, genomic survey sequence.//1.7e-120:561:100//AQ194238
 F-MAHMA1000567//Human DNA sequence from PAC 17903, between markers DXS6791 and DXS8038 on chromosome X contains S10 GTP-binding protein, ESTs and CpG island.//3.1e-43:387:80//Z81370
 F-MAHMA1000576//Homo sapiens BAC clone RC442F18 from 2, complete sequence.//1.2e-30:237:75//AC005104
 F-MAHMA1000583//RPC111-60M22, TJ RPC111 Homo sapiens genomic clone R-60M22, genomic survey sequence.//9.6e-102:487:99//AQ198091
 F-MAHMA1000585//Homo sapiens clone UGCC:djs14 from 7p14-15, complete sequence.//5.2e-39:370:78//AC006195
 F-MAHMA1000594//Homo sapiens chromosome 19, cosmid R31646, complete sequence.//3.9e-43:328:83//AC005338
 F-MAHMA1000597//Homo sapiens chromosome 17, clone hRPK.481_C_4, complete sequence.//1.5e-32:259:82//AC005839
 F-MAHMA1000605//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE.//2.4e-59:318:83//AL031297
 F-MAHMA1000612//HS_2188_A2_D02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=4 Row=G, genomic survey sequence.//4.8e-30:171:96//AQ116793
 F-MAHMA1000616//HS_3176_A1_E06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3176 Col=11 Row=I, genomic survey sequence.//4.7e-28:287:79//AQ300310
 F-MAHMA1000621//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 273F20, WORKING DRAFT SEQUENCE.//0.015:478:58//AL034371
 F-MAHMA1000623
 F-MAHMA1000625//DNA encoding Hepatitis C virus antigen.//0.93:196:61//E06898
 F-MAHMA1000643//Homo sapiens nephrocytin (NPHPI) mRNA, partial cds.//0.95:365:59//AF023674
 F-MAHMA1000664//HS_3096_B1_C02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3096 Col=3 Row=F, genomic survey sequence.//2.7e-51:257:99//AQ145137
 F-MAHMA1000669//Homo sapiens chromosome 19, cosmid R26908, complete sequence.//2.0e-66:586:67//AC004785
 F-MAHMA1000670//HS_2243_B2_A08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2243 Col=16 Row=8, genomic survey sequence.//8.7e-05:94:80//AQ153650
 F-MAHMA1000672//Mus musculus clone OST8270, genomic survey sequence.//3.9e-64:471:81//AF046705
 F-MAHMA1000684//Suid herpesvirus 1 Rsp40 mRNA, partial cds.//1.2e-07:185:67//U27489
 F-MAHMA1000696//Human oligodendrocyte myelin glycoprotein (OMG) exons 1-2: neurofibromatosis 1 (NF1) exons 28-49: ecotropic viral integration site 2B (EVI2B) exons 1-2: ecotropic viral integration site 2A (EVI2A) exons 1-2: adenylate kinase (AK3) exons 1-2.//3.0e-53:653:70//L05367
 F-MAHMA1000707//CIT-HSP-2302019, TR CIT-HSP Homo sapiens genomic clone 2302019, genomic survey sequence.//1.8e-08:131:77//AQ017947
 F-MAHMA1000713//Rattus norvegicus clonal polymeric immunoglobulin receptor mRNA 3' untranslated region, CA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats.//0.062:134:67//U00762
 F-MAHMA1000714//Chicken hsp90 gene for 90 kDa-heat shock protein 5'-end.//1.0:266:61//X15028
 F-MAHMA1000718//CIT-HSP-2171810, TF CIT-HSP Homo sapiens genomic clone 2171810, genomic survey sequence.//3.6e-05:289:60//B95401
 F-MAHMA1000720//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//4.4e-184:842:98//AC005781
 F-MAHMA1000723//Homo sapiens clone DJ0892G19, complete sequence.//8.8e-05:430:60//AC004917
 F-MAHMA1000731//Drosophila melanogaster DNA sequence (P1 DS07049 (D133)), complete sequence.//3.8e-55:796:66//AC004274
 F-MAHMA1000732//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a.//6.6e-77:555:74//AF064859
 F-MAHMA1000733//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P6, WORKING DRAFT SEQUENCE.//0.98:479:58//AL031749
 F-MAHMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds.//7.3e-168:802:98//AF100141
 F-MAHMA1000738//S. cerevisiae chromosome XIV reading frame ORF YNL132w.//8.6e-31:626:63//Z71408
 F-MAHMA1000744//Coriaria Alu-repetitive sequence in beta-globin gene cluster.//2.7e-54:410:82//X06123
 F-MAHMA1000746//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-10 F4, complete sequence.//3.7e-109:779:83//AC004158
 F-MAHMA1000752//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.2e-20:444:63//AC005075
 F-MAHMA1000760//Homo sapiens clone RG015P03, complete sequence.//1.5e-44:403:79//AC005048
 F-MAHMA1000761//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.3e-22:159:81//AC004166
 F-MAHMA1000775//Homo sapiens chromosome 17, clone hRPK.849_N_15, complete sequence.//1.3e-51:789:68//AC005703
 F-MAHMA1000776//Human DNA sequence from BAC 57C9 on chromosome 22q12.1 Contains ESTs, CA repeat, GSS.//5.7e-40:238:78//Z95116
 F-MAHMA1000778//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 153G14, WORKING DRAFT SEQUENCE.//7.6e-29:222:84//AL031118
 F-MAHMA1000782//Human 2.4-dienoyl-CoA reductase gene, exon 9.//0.9:0:137:62//U94987
 F-MAHMA1000798//*** SEQUENCING IN PROGRESS *** EPM1/APECD region of chromosome 21, clones A68E8, B127P21, B173L3, B23M8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE, 50 unordered pieces.//0.00058:163:71//AC003656
 F-MAHMA1000802//Homo sapiens chromosome 19, cosmid R33729, complete sequence.//6.3e-151:714:99//AC005339
 F-MAHMA1000824//Homo sapiens 12p13.3 BAC RPC111-543P15 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//4.2e-10:4:503:99//AC005912
 F-MAHMA1000831//Homo sapiens clone UGCC:g121a139, complete sequence.//0.76:302:58//AC005502
 F-MAHMA1000839//Human BAC clone RG013L03 from 7q21, complete sequence.

【0721】

【表422】

nce.//1.9e-54:322:68//AC002456	ontains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//1.4e-18:396:65//AL022394
F-MAMMA1000841//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968022, WORKING DRAFT SEQUENCE.//6.7e-140:647:92//AL023755	F-MAMMA1000975//Human DNA sequence from clone 34417 on chromosome Xp11.21-11.3. Contains a Keratin, Type II Cytoskeletal 8 (Cytokeratin 8, CYK8, KRT8) pseudogene, ESTs and a GSS, complete sequence.//1.4e-79:690:77//AL024458
F-MAMMA1000842//, complete sequence.//0.0068:499:59//AC005817	F-MAMMA1000979//Homo sapiens PAC clone DJ1186C01 from 7q21.2-q31.1, complete sequence.//0.089:214:66//AC004991
F-MAMMA1000843//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE. 2 unordered pieces.//0.13:439:59//AC004710	F-MAMMA1000987//Human PAC clone DJ527C21 from Xq23, complete sequence.//1.1e-58:458:82//AC000114
F-MAMMA1000845//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//2.2e-05:208:64//AL034557	F-MAMMA1000998//Human DNA sequence from PAC 997K18 on chromosome 20p12. Contains ESTs and CA repeat.//1.1e-05:439:62//AL021406
F-MAMMA1000851//Gallus domesticus filamin gene 5' region, partial cds.//0.86:193:63//U00146	F-MAMMA1001003//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CHM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A 1, Choroideremia protein, Tapetochochoidal Dystrophy (TCD) protein). Contains ESTs and an STS, complete sequence.//0.24:166:68//AL022401
F-MAMMA1000855//Human minisatellite region detected by myoglobin 3 repeat probe, clone lambda 33.10.//0.081:229:62//M30549	F-MAMMA1001008//Homo sapiens *** SEQUENCING IN PROGRESS *** WORKING DRAFT SEQUENCE.//1.6e-103:139:99//AJ011929
F-MAMMA1000856//B. taurus microsatellite marker ETH8 (D6S3) DNA.//0.0024:253:60//Z22747	F-MAMMA1001021//Homo sapiens clone 24544 beta-dystrobrevin mRNA, partial cds.//6.5e-48:465:76//AF070567
F-MAMMA1000859//Sequence 6 from Patent WO9722695.//2.3e-79:533:82//A63553	F-MAMMA1001024//CITB1-E1-2501L21.TF.1 CITB1-E1 Homo sapiens genomic clone 2501L21, genomic survey sequence.//1.0:175:62//AQ241701
F-MAMMA1000863//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//1.0e-28:439:64//AP000050	F-MAMMA1001030//Homo sapiens G protein-coupled receptor LGR5 (LGR5) mRNA, complete cds.//1.1e-30:753:61//AF061444
F-MAMMA1000865	F-MAMMA1001035//Human Chromosome 16 BAC clone CIT987SK-A-1000D7, complete sequence.//7.9e-24:256:76//AC002990
F-MAMMA1000867//CIT-HSP-2385J8.TR.1 CIT-HSP Homo sapiens genomic clone 2385J8, genomic survey sequence.//0.00017:158:70//AQ240906	F-MAMMA1001038//CIT-HSP-2284N21.TF CIT-HSP Homo sapiens genomic clone 2284N21, genomic survey sequence.//0.96:78:75//AQ000903
F-MAMMA1000875//Homo sapiens DNA sequence from PAC 232C24 on chromosome Xq27.1-q27.3. Contains two exons similar to MACE gene family, EST, CA repeat, STS, complete sequence.//1.0:121:68//AL022152	F-MAMMA1001041//Chicken mRNA for alpha-actinin, complete cds.//2.8e-09:355:63//D26597
F-MAMMA1000876//Homo sapiens clone HS19.6 Alu-Ya5 sequence.//8.4e-41:185:90//AF015152	F-MAMMA1001050//Homo sapiens BAC clone RG060P12 from 7q21, complete sequence.//2.6e-40:378:76//AC002457
F-MAMMA1000877//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//8.3e-57:522:75//AL022336	F-MAMMA1001059//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//4.8e-97:661:83//L25125
F-MAMMA1000880//Homo sapiens full length insert cDNA clone ZD54A1.0.//5.2e-26:143:100//AF086327	F-MAMMA1001067//Homo sapiens genomic intron breakpoint sequence of MLL rearrangement, 285 bp.//2.8e-18:110:100//AJ000169
F-MAMMA1000883//Human DNA sequence from clone 786D3 on chromosome 22q13.31-33 Contains GSS, complete sequence.//0.99:225:63//AL023801	F-MAMMA1001073//HS_3046_A2_G08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3046 Col=16 Row=M, genomic survey sequence.//1.0:142:68//AQ098420
F-MAMMA1000897//R. norvegicus mRNA for plasma protein.//4.8e-07:47:9:58//Y11283	F-MAMMA1001074//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 455J7, WORKING DRAFT SEQUENCE.//1.2e-23:386:70//AL031733
F-MAMMA1000905//F26L5TRB ICF Arabidopsis thaliana genomic clone F26L5, genomic survey sequence.//0.94:115:66//B61433	F-MAMMA1001075//Homo sapiens (clone F4) transmembrane protein mRNA sequence.//1.1e-27:559:65//L09749
F-MAMMA1000906//HS_3110_B2_A11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3110 Col=22 Row=B, genomic survey sequence.//2.5e-63:548:78//AQ182819	F-MAMMA1001078//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//2.0e-22:334:69//AC006120
F-MAMMA1000908//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27K12, WORKING DRAFT SEQUENCE.//5.2e-80:480:90//AL033397	F-MAMMA1001080//Human immunoglobulin heavy chain variable region (VH III family) from IgM rheumatoid factor.//6.4e-58:327:92//L29155
F-MAMMA1000914//Plasmodium falciparum MAL3P8, complete sequence.//7.6e-09:596:58//AL034560	F-MAMMA1001082//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//3.8e-87:695:77//AC004087
F-MAMMA1000921//CIT-HSP-2171D8.TR CIT-HSP Homo sapiens genomic clone 2171D8, genomic survey sequence.//6.6e-07:249:66//B89575	F-MAMMA1001091//Homo sapiens chromosome 19, cosmid F21967, complete sequence.//7.0e-05:594:60//AC005256
F-MAMMA1000931//Homo sapiens clone DJ089C19, complete sequence.//2.9e-43:415:66//AC004917	F-MAMMA1001092//Human DNA sequence from PAC 49C23 on chromosome X contains malate dehydrogenase pseudogene and STS.//1.6e-91:174:87//Z93019
F-MAMMA1000940//HS-1056-A2-E02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 778 Col=4 Row=I, genomic survey sequence.//6.1e-44:235:78//B47296	F-MAMMA1001105//Homo sapiens OVO-like 1 binding protein (OVOL1) mRNA, complete cds.//6.4e-23:507:66//AF016045
F-MAMMA1000941//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 - complete genomic sequence, complete sequence.//9.4e-48:443:75//AC002299	F-MAMMA1001110//Homo sapiens chromosome 19, cosmid F16815, complete sequence.//0.77:316:60//AC004637
F-MAMMA1000942//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, DCX (doublecortin) ESTs, CA repeat, GSS, complete sequence.//1.8e-14:175:76//AL031117	F-MAMMA1001126//Homo sapiens PAC 50H2 in the CUTL1 locus, complete sequence.//3.3e-21:237:73//AF047825
F-MAMMA1000943//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE. 5 unordered pieces.//0.0082:684:56//AC005308	F-MAMMA1001133//Human DNA sequence from BAC 57C9 on chromosome 22q12.1 Contains ESTs, CA repeat, GSS.//0.97:202:63//Z95116
F-MAMMA1000956//Homo sapiens chromosome 16, cosmid clone 363E3 (LA NL), complete sequence.//3.3e-30:530:67//AC004643	F-MAMMA1001139//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt].//1.6e-84:406:82//S70011
F-MAMMA1000957//HS_3039_A2_C08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3039 Col=16 Row=E, genomic survey sequence.//1.3e-72:390:94//AQ155121	F-MAMMA1001143//Homo sapiens DNA sequence from cosmid N75B3 on chromosome 22 Contains EST, exon trap, complete sequence.//1.3e-14:182:76//AL022339
F-MAMMA1000962//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE. 5 unordered pieces.//1.8e-58:318:86//AC006001	F-MAMMA1001145//Human DNA sequence from cosmid cu115G11, between markers DXS6791 and DXS8038 on chromosome X contains ESTs and STS.//5.2e-87:714:78//Z71187
F-MAMMA1000968//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOPI gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-1), the KIAA0395 gene for a probable Zinc Finger F domain protein and a 60S Ribosomal Protein L23 LIKE pseudogene. C	F-MAMMA1001154//CIT-HSP-2341D13.TF CIT-HSP Homo sapiens genomic clone 2341D13, genomic survey sequence.//0.00051:249:61//AQ055735
	F-MAMMA1001161//Homo sapiens chromosome 14, BAC CITB-135H17 containing the RAD51L1 gene, complete sequence.//2.2e-30:410:70//AC004518
	F-MAMMA1001162//Homo sapiens full length insert cDNA clone ZAT9C0

【0722】

【表423】

1.//2.4e-13:87:100//AF086123	F-MAMMA1001419//HS_2053_B1_F12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2053 Col=23 Row=L, genomic survey sequence.//1.9e-75:424:93//AQ244585
F-MAMMA1001181//Mus musculus C2C12 unknown mRNA, partial cds.//9.3e-15:432:60//U31629	F-MAMMA1001420//Homo sapiens chromosome 4 clone B203C23 map 4q25, complete sequence.//2.4e-09:199:70//AC004049
F-MAMMA1001186//Homo sapiens chromosome 17, clone hRPK.74_E_22, complete sequence.//6.8e-57:670:72//AC005696	F-MAMMA1001435//Homo sapiens chromosome 16p11.2 BAC clone CIT9875 K-201104, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.1e-42:558:69//AC004529
F-MAMMA1001191	F-MAMMA1001442//Plasmodium falciparum chromosome 2, section 37 of 73 of the complete sequence.//0.0019:516:56//AE001400
F-MAMMA1001198//Mus musculus eps15R mRNA, complete cds.//1.5e-117:759:84//U29156	F-MAMMA1001446//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//3.6e-42:486:70//AC003684
F-MAMMA1001202	F-MAMMA1001452//RPC111-48022.TJ RPC111 Homo sapiens genomic clone R-48022, genomic survey sequence.//5.3e-87:423:98//AQ199294
F-MAMMA1001203//Homo sapiens chromosome 17, clone hRPK.192_M_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.5e-161:764:98//AC005412	F-MAMMA1001465//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 41407, WORKING DRAFT SEQUENCE.//0.00038:114:75//AL033543
F-MAMMA1001206//Homo sapiens chromosome 17, clone HC1T421K24, complete sequence.//5.1e-30:535:65//AC004099	F-MAMMA1001476//Mus musculus uridine kinase mRNA, partial cds.//4.1e-99:604:87//L31783
F-MAMMA1001215//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence.//8.4e-182:860:98//AC005393	F-MAMMA1001487//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.0e-13:158:77//AC005486
F-MAMMA1001220//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//7.7e-58:690:70//AC004875	F-MAMMA1001501//Human mRNA for calcium activated neutral protease large subunit (nuCaMP, calpain, EC 3.4.22.17).//9.6e-52:438:81//X04366
F-MAMMA1001222//Mouse loricrin mRNA, complete cds.//2.7e-07:624:58//U34398	F-MAMMA1001502//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 356B7, WORKING DRAFT SEQUENCE.//3.7e-152:720:99//AL031714
F-MAMMA1001243//Homo sapiens chromosome 17, clone hRPK.192_M_23, complete sequence.//0.91:177:66//AC005726	F-MAMMA1001510//Human PAC clone DJ43804 from 22q12.1-qter, complete sequence.//1.1e-05:371:61//AC002378
F-MAMMA1001244	F-MAMMA1001522
F-MAMMA1001249//Human 28S ribosomal RNA pseudogenes and silu repeat region sequence.//6.7e-09:502:58//U67616	F-MAMMA1001547
F-MAMMA1001256//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//5.0e-37:342:80//Z99495	F-MAMMA1001551//Homo sapiens mRNA for KIAA0462 protein, partial cds.//2.3e-128:614:98//AB007931
F-MAMMA1001259	F-MAMMA1001575//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//0.97:154:68//AF001548
F-MAMMA1001260//Homo sapiens mRNA for KIAA0651 protein, complete cds.//8.7e-40:659:64//AB014561	F-MAMMA1001576//Human gamma-tubulin mRNA, complete cds.//1.8e-95:529:91//U61764
F-MAMMA1001268//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//4.9e-43:265:81//AC004453	F-MAMMA1001590//Human DNA sequence from clone 125H2 on chromosome 22q11-12 Contains part of myosin heavy chain gene, EST, CA repeat, STS, GSS, complete sequence.//1.8e-07:104:84//Z98949
F-MAMMA1001271//Salmo salar DNA for a cryptic repeat.//2.6e-06:311:63//AJ012206	F-MAMMA1001600//HS_3022_A2_H01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022 Col=2 Row=0, genomic survey sequence.//1.6e-66:405:90//AQ163791
F-MAMMA1001274//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//6.6e-70:327:83//AC004840	F-MAMMA1001604//Human DNA sequence from clone 1114G22 on chromosome 1q24-25 Contains EST, CA repeat, Ninenin like sequence, complete sequence.//0.00043:715:58//AL008626
F-MAMMA1001280//Homo sapiens Xp22 bins 87-93 PAC RPC11-122K4 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0e-05:276:66//AC003035	F-MAMMA1001606//jd114 Trypanosoma Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 2C6, genomic survey sequence.//0.19:266:22//B13685
F-MAMMA1001292//Human DNA sequence from clone 1170K4 on chromosome 22q12.2-13.1. Contains three novel genes, one of which codes for a Trypsin family protein with class A LDL receptor domains, and the IL2RB gene for Interleukin 2 Receptor, Beta (IL-2 Receptor, CD122 antigen). Contains a putative CpG island, ESTs, and GSSs, complete sequence.//3.6e-98:199:98//AL022314	F-MAMMA1001620//Homo sapiens monocyte/neutrophil elastase inhibitor gene, complete cds.//9.7e-54:442:69//AF053630
F-MAMMA1001296//RPC111-3884, TV RPC111 Homo sapiens genomic clone RPC11-3884, genomic survey sequence.//4.7e-33:292:71//AQ030084	F-MAMMA1001627//X.borealis ribosomal spacer DNA, with a DNaseI-hypersensitive site.//0.14:221:62//U29833
F-MAMMA1001298//Homo sapiens chromosome 17, clone hRPK.849_M_15, complete sequence.//1.6e-182:860:98//AC005703	F-MAMMA1001630//Homo sapiens chromosome 17, clone hRPK.22_M_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//2.0e-47:611:71//AC005412
F-MAMMA1001305//Human DNA sequence from clone 116F5 on chromosome 22q13. Contains part of an unknown gene and part of a RhoGAP (CDC42 GTPase Activating Protein) LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D22S1168 and a CA repeat polymorphism, complete sequence.//1.9e-70:163:97//Z93244	F-MAMMA1001633//Human zinc finger protein (LD5-1) mRNA, complete cds.//1.1e-42:611:67//U57796
F-MAMMA1001322//Human DNA sequence from clone 774124 on chromosome 1q24.1-24.3 Contains protein similar to pregnancy-associated plasma protein A precursor neuronal migration protein astrotactin, ESTs, STS and GSS, complete sequence.//2.6e-19:379:68//AL031290	F-MAMMA1001635//Human BAC clone RC072E11 from 7q21-7q22, complete sequence.//4.0e-35:407:70//AC000118
F-MAMMA1001324//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 197L1, WORKING DRAFT SEQUENCE.//4.5e-131:751:90//AL031390	F-MAMMA1001649//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SMF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.44:245:63//AL022577
F-MAMMA1001330	F-MAMMA1001654//Mouse transcriptional control element.//0.0025:189:63//M17284
F-MAMMA1001341//Sus scrofa.//1.6e-36:420:73//Z46906	F-MAMMA1001663//CIT-HSP-2165E16, TR CIT-HSP Homo sapiens genomic clone 2165E16, genomic survey sequence.//9.7e-05:146:66//B95491
F-MAMMA1001343//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MALIP1, WORKING DRAFT SEQUENCE.//1.1e-05:818:58//AL031744	F-MAMMA1001670//HS_3136_A1_C06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3136 Col=11 Row=M, genomic survey sequence.//3.1e-28:237:85//AQ148779
F-MAMMA1001346	F-MAMMA1001671//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//3.3e-181:863:98//AC005614
F-MAMMA1001383//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//2.0e-44:505:74//AC004086	F-MAMMA1001679//HS_3054_A1_H11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=21 Row=0, genomic survey sequence.//1.0:89:70//AQ106118
F-MAMMA1001388//Human IGF binding protein complex acid-labile subunit mRNA, complete cds.//1.5e-07:415:58//U86826	F-MAMMA1001683//Spermatozopsis similis mRNA for 90 kD basal apparatus-protein.//8.3e-07:480:62//AJ224970
F-MAMMA1001397//Human DNA sequence from clone 46208 on chromosome 22q11.21-12.1 Contains EST, STS and GSS, complete sequence.//1.6e-23:209:75//AL022332	F-MAMMA1001686//HS_3219_B1_A03_MR CIT Approved Human Genomic Sperm

【表424】

Library D Homo sapiens genomic clone Plate=3219 Col=5 Row=8, genomic survey sequence.//0.00072:180:65//AQ180345
 F-MAMMA1001692//HS_3047_B1_B10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=19 Row=D, genomic survey sequence.//2.5e-94:459:98//AQ134228
 F-MAMMA1001711//Homo sapiens clone DJ0635005, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-42:316:82//AC004845
 F-MAMMA1001715//CIT-HSP-2347A14.TF CIT-HSP Homo sapiens genomic clone 2347A14, genomic survey sequence.//1.1e-60:413:87//AQ059125
 F-MAMMA1001730//Homo sapiens brain and nasopharyngeal carcinoma susceptibility protein NSG-x mRNA, partial cds.//1.8e-133:646:97//AF095687
 F-MAMMA1001735//chicken brain tubulin beta chain mRNA.//3.5e-110:740:84//J00913
 F-MAMMA1001740//Human DNA sequence from PAC 136017 on chromosome X contains ESTs and STS.//0.98:416:57//Z72001
 F-MAMMA1001743//Homo sapiens clone DJ0981007, complete sequence.//3.2e-16:194:75//AC006017
 F-MAMMA1001744//Homo sapiens DNA sequence from clone 46618 on chromosome Xq11.1-13.2. Contains an unknown gene similar to Coagulation Factor V (Activated Protein C Cofactor), Coagulation Factor VIII (Procoagulant Component) and Ceruloplasmin (EC 1.16.3.1, Ferroxidase). Contains ESTs and an STS, complete sequence.//0.0036:181:66//AL030998
 F-MAMMA1001745//Homo sapiens BAC clone 529F11 from 8q21, complete sequence.//1.2e-60:822:68//AF070718
 F-MAMMA1001751//Human potassium channel KCNO1 mRNA, complete cds.//1.2e-35:583:65//U90065
 F-MAMMA1001754//Bos taurus vacuolar proton pump subunit SFD alpha isoform (SFD) mRNA, complete cds.//8.4e-102:627:87//AF041338
 F-MAMMA1001757//HS_2058_B2_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=8 Row=F, genomic survey sequence.//1.7e-24:173:88//AQ243865
 F-MAMMA1001760//Human DNA sequence from clone 354N19 on chromosome 6q22. Contains the 3' part of the gene for Mannosyl-Oligosaccharide Alpha-1,2-Mannosidase (Man(9)-alpha-mannosidase, EC 3.2.1.113), a Cytochrome C Oxidase Polypeptide I (EC 1.9.3.1) pseudogene and a pseudogene similar to 60S Ribosomal Protein L13A. Contains genomic markers D6S287 and D6S1696, ESTs, STSs, GSSs and two CA repeat polymorphisms, complete sequence.//6.6e-76:349:87//AL022722
 F-MAMMA1001764//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COX1) gene, complete cds.//0.23:633:57//M97514
 F-MAMMA1001768//Bovine herpesvirus 1 complete genome.//2.3e-11:547:60//AJ004801
 F-MAMMA1001769//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.1e-76:509:78//AC004801
 F-MAMMA1001771//M.musculus mRNA for semaphorin B.//2.7e-106:744:82//X85991
 F-MAMMA1001783//Human PAC clone 127H14 from 12q, complete sequence.//6.0e-20:228:75//AC002563
 F-MAMMA1001785
 F-MAMMA1001788//Human DNA sequence from clone 425C14 on chromosome 6q22. Contains the HSF2 gene for Heat Shock Factor 2 (Heat Shock Transcription Factor 2, HSF2) and an unknown gene similar to the placental protein DIFF33 gene. Contains ESTs, STSs and GSSs, complete sequence.//5.0e-05:152:74//Z99129
 F-MAMMA1001790//Homo sapiens chromosome 12p13.3 clone RPC13-45482.3, WORKING DRAFT SEQUENCE, 48 unordered pieces.//4.5e-53:318:80//AC005845
 F-MAMMA1001806//Homo sapiens chromosome 19, cosmid R29368, complete sequence.//1.0:131:67//AC004262
 F-MAMMA1001812//Human Chromosome X clone BXND187, complete sequence.//3.0e-34:257:83//AC004383
 F-MAMMA1001815//Homo sapiens PAC clone DJ0850G01 from 7q21.2-q22, complete sequence.//5.2e-61:516:79//AC004128
 F-MAMMA1001817//Homo sapiens 12q24 PAC RPC11-261P5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//3.1e-32:295:78//AC004031
 F-MAMMA1001818//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 787, complete sequence bases 1..333303.//0.71:179:67//AJ011930
 F-MAMMA1001820//Rattus norvegicus mRNA for PAG608 gene.//3.0e-91:726:79//Y13148
 F-MAMMA1001824//HS_3108_A1_G12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=23 Row=M, genomic survey sequence.//3.4e-05:119:74//AQ107508
 F-MAMMA1001836//Homo sapiens chromosome 18, clone hRPK.537_E_1, complete sequence.//3.4e-45:312:85//AC006211
 F-MAMMA1001837//Rattus norvegicus zinc finger protein Y1 (RLZF-Y) mRNA, complete cds.//4.5e-51:480:75//AF052042
 F-MAMMA1001848//CITB1-E1-2516P17.TF CITB1-E1 Homo sapiens genomic clone 2516P17, genomic survey sequence.//1.0e-100:486:98//AQ279620
 F-MAMMA1001851//Human DNA from overlapping chromosome 19-specific cosmid R30072 and R28588, genomic sequence, complete sequence.//5.1e-07:197:67//AC002390
 F-MAMMA1001854
 F-MAMMA1001858//RPC11-11L22.TP RPC11-11 Homo sapiens genomic clone RPC11-11L22, genomic survey sequence.//0.091:161:65//B75631
 F-MAMMA1001864//Human PAC clone DJ0205E24 from Xq23, complete sequence.//2.6e-09:397:61//AC003013
 F-MAMMA1001868//HS_2196_B2_A12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2196 Col=24 Row=B, genomic survey sequence.//5.8e-13:86:100//AQ032455
 F-MAMMA1001874//H.sapiens CpG island DNA genomic MseI fragment, clone 63h5, reverse read cpg63h5.rta.//1.0:127:63//Z62129
 F-MAMMA1001878//Human DNA sequence from BAC 999D10 on chromosome 2 2q13.3. Contains two BAC end-sequences (GSSs).//1.7e-19:372:67//Z94802
 F-MAMMA1001880//RPC11-90K3.TJ RPC11 Homo sapiens genomic clone R-90K3, genomic survey sequence.//6.6e-11:362:62//AQ283465
 F-MAMMA1001890//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 508115, WORKING DRAFT SEQUENCE.//1.8e-45:317:86//AL02107
 F-MAMMA1001907//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//2.7e-23:255:77//Z82207
 F-MAMMA1001908//HS_2225_A1_A03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2225 Col=5 Row=A, genomic survey sequence.//5.4e-08:264:82//AQ301597
 F-MAMMA1001931//HS_3049_B2_D09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3049 Col=18 Row=H, genomic survey sequence.//1.7e-47:295:90//AQ100157
 F-MAMMA1001956//H.sapiens DNA sequence.//0.056:233:66//Z22493
 F-MAMMA1001963//Homo sapiens adenylosuccinate lyase gene, complete cds.//0.99:173:68//AF106656
 F-MAMMA1001969//Human DNA sequence from cosmid 232L22, between markers DXS366 and DXS87 on chromosome X contains ESTs glycerol kinase pseudogene.//5.3e-63:479:78//Z73986
 F-MAMMA1001970//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.4e-126:699:93//AC003071
 F-MAMMA1001992//HS_3078_A1_A09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=17 Row=A, genomic survey sequence.//3.3e-08:257:65//AQ143646
 F-MAMMA1002009//Homo sapiens chromosome 17, clone hRPK.214_0_1, complete sequence.//1.5e-07:244:62//AC005224
 F-MAMMA1002011//HS_3252_B1_B05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=9 Row=D, genomic survey sequence.//1.3e-07:170:69//AQ304711
 F-MAMMA1002032//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 37 unordered pieces.//2.1e-34:315:79//AC004803
 F-MAMMA1002033//HS_3023_A2_C04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=8 Row=M, genomic survey sequence.//4.3e-69:366:94//AQ105493
 F-MAMMA1002041//Genomic sequence from Human 9q34, complete sequence.//5.3e-85:439:82//AC001227
 F-MAMMA1002042//Homo sapiens chromosome 3, clone hRPK.165_1_16, complete sequence.//1.4e-20:314:70//AC005659
 F-MAMMA1002047//Homo sapiens 12p13.3 BAC RPC11-429A20 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//6.8e-14:526:62//AC005906
 F-MAMMA1002056//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, Cl-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//1.1e-47:648:71//AL030996
 F-MAMMA1002058//Homo sapiens PAC clone DJ0732C22 from 7p11.2-p13, complete sequence.//2.4e-19:256:74//AC004869
 F-MAMMA1002068//Homo sapiens, clone hRPK.2_A_1, complete sequence.//5.4e-41:407:78//AC006197
 F-MAMMA1002078//Human DNA sequence from PAC 106120 on chromosome 2 2q12. Contains ESTs and STS, complete sequence.//0.021:333:64//Z81313
 F-MAMMA1002082
 F-MAMMA1002084//Caenorhabditis elegans cosmid F28C12, complete sequence.//0.032:469:58//Z93380
 F-MAMMA1002093//HS_3050_B1_F06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=11 Row=L, genomic survey sequence.//1.0:77:71//AQ105997

【0724】

【表425】

F-MAMMA1002108//Homo sapiens anion exchanger 3 gene, exons 1 and 2 and complete 5' UTR.//8.3e-10:464:60//AF017308
 F-MAMMA1002118
 F-MAMMA1002125//Homo sapiens chromosome 17, clone HC17217L10, complete sequence.//1.0e-35:619:68//AC003962
 F-MAMMA1002132//RPC111-78F11.TJ RPC111 Homo sapiens genomic clone R-78F11, genomic survey sequence.//1.0e-90:357:97//AQ286460
 F-MAMMA1002140//Homo sapiens 12q24 PAC RPC11-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-45:583:64//AC004216
 F-MAMMA1002143//Human serum constituent protein (MSE55) mRNA, complete cds.//6.0e-11:192:70//M88338
 F-MAMMA1002145//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 102024, WORKING DRAFT SEQUENCE.//0.0028:570:59//AL021391
 F-MAMMA1002153//HS_3005_A1_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3005 Col=7 Row=G, genomic survey sequence.//4.9e-41:213:99//AQ132213
 F-MAMMA1002155//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 462023, WORKING DRAFT SEQUENCE.//1.2e-45:303:78//AL031431
 F-MAMMA1002156
 F-MAMMA1002158//CITB1-E1-250BP18.TR CITB1-E1 Homo sapiens genomic clone 250BP18, genomic survey sequence.//7.1e-42:255:92//AQ266165
 F-MAMMA1002170//Homo sapiens chromosome 17, clone HC17187N2, complete sequence.//2.0e-81:604:81//AC004448
 F-MAMMA1002174//Homo sapiens clone UWGC:y67c126 from 6p21, complete sequence.//3.2e-43:333:83//AC004212
 F-MAMMA1002198//H. sapiens thiol-specific antioxidant protein mRNA.//1.0e-34:121:98//Z22548
 F-MAMMA1002209//HS_2197_E1_E07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-2197 Col=13 Row=J, genomic survey sequence.//9.6e-18:163:84//AQ210058
 F-MAMMA1002215//Homo sapiens anion exchanger 3 gene, exons 1 and 2 and complete 5' UTR.//6.3e-08:435:60//AF017308
 F-MAMMA1002219//Rattus norvegicus rex070 mRNA, complete cds.//1.8e-124:752:87//AF032667
 F-MAMMA1002230//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.67:356:59//AC004710
 F-MAMMA1002236//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//9.3e-140:836:87//U38253
 F-MAMMA1002243//Homo sapiens chromosome 17, clone hRPC.112_H_10, complete sequence.//1.4e-145:691:98//AC005666
 F-MAMMA1002250//Homo sapiens chromosome 16, PI clone 109-9G (LANL), complete sequence.//6.0e-138:660:98//AC005600
 F-MAMMA1002267//Homo sapiens chromosome 2, PI clone 777H5 (LBNL H27), complete sequence.//0.066:333:60//AC003676
 F-MAMMA1002268//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds.//1.1e-39:404:74//AF068748
 F-MAMMA1002269//HS_3163_B1_D03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3163 Col=5 Row=H, genomic survey sequence.//1.0:150:63//AQ171576
 F-MAMMA1002282//Human chromosome 16 BAC clone CIT987SK-327024, complete sequence.//1.5e-22:315:67//AC003108
 F-MAMMA1002292//B. garinii (strain Tis1) p83/100 gene (partial).//0.73:200:64//X81533
 F-MAMMA1002293//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//1.6e-56:408:75//AC006023
 F-MAMMA1002294//Sequence 2 from Patent W09516779.//1.8e-06:401:62//A45258
 F-MAMMA1002297
 F-MAMMA1002298//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//0.0056:525:61//AC004221
 F-MAMMA1002299//CIT-HSP-2345B2.TR CIT-HSP Homo sapiens genomic clone 2345B2, genomic survey sequence.//1.2e-90:446:98//AQ053994
 F-MAMMA1002308//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 850H21, WORKING DRAFT SEQUENCE.//1.3e-35:329:78//AL031680
 F-MAMMA1002310//Human gastric (H+ + K+)-ATPase gene, complete cds.//0.0060:301:60//J05451
 F-MAMMA1002311//Human chromosome 15q11-q13 clone pDJ276c12 from the Prader-Willi/Angelman syndrome region, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.6e-50:327:69//AC004737
 F-MAMMA1002312//Homo sapiens DNA sequence from PAC 43501 on chromosome Xq25. Contains ESTs and STS.//1.3e-09:741:58//Z86064
 F-MAMMA1002317
 F-MAMMA1002319//Homo sapiens chromosome 19, fosmid 39347, complete sequence.//1.9e-158:746:99//AC005756
 F-MAMMA1002322//Homo sapiens chromosome 11p14.3 PAC clone pDJ1034g 4, complete sequence.//5.3e-52:617:70//AC004796
 F-MAMMA1002329//Homo sapiens Rap2 interacting protein 8 (RPI8) mRNA, complete cds.//0.22:143:67//U93871
 F-MAMMA1002332//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30G7, WORKING DRAFT SEQUENCE.//1.6e-31:287:74//AL034402
 F-MAMMA1002333//Mycobacterium tuberculosis H37Rv complete genome: segment 148/162.//2.5e-09:674:59//AL022022
 F-MAMMA1002339//Homo sapiens chromosome 21q22.3, cosmid clone Q4H9 complete sequence bases 1..41604.//2.1e-57:522:77//AJ011932
 F-MAMMA1002347//Homo sapiens BAC clone RG136N17 from 7p15-p21, complete sequence.//2.0e-14:258:69//AC004129
 F-MAMMA1002351//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1059H15, WORKING DRAFT SEQUENCE.//7.8e-132:723:91//AL02100
 F-MAMMA1002352//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 12803, WORKING DRAFT SEQUENCE.//5.8e-17:326:70//Z98742
 F-MAMMA1002353//Homo sapiens clone DJ0292L20, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.1e-14:399:63//AC004825
 F-MAMMA1002355//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 109CG, WORKING DRAFT SEQUENCE.//3.7e-43:420:75//AL023879
 F-MAMMA1002356//Plasmodium falciparum 3D7 chromosome 12 PFYAC182 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0022:534:59//AC004153
 F-MAMMA1002359//Homo sapiens 12p13.3 PAC RPC15-1180012 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.3e-18:156:75//AC005831
 F-MAMMA1002360//Human DNA sequence from cosmid L21F12B, Huntington's Disease Region, chromosome 4p16.3, contains EST.//4.9e-43:353:69//Z68885
 F-MAMMA1002361//Human DNA sequence from clone 342B11 on chromosome 22q12.1-12.3. Contains ESTs and a GSS, complete sequence.//1.8e-22:282:74//AL008719
 F-MAMMA1002362//Platymys spixii CRI-like LINE, partial sequence.//0.00058:83:79//D82938
 F-MAMMA1002380//CIT-HSP-2383K24.TR CIT-HSP Homo sapiens genomic clone 2383K24, genomic survey sequence.//4.4e-10:85:92//AQ196889
 F-MAMMA1002384//RPC111-80J20.TV RPC111 Homo sapiens genomic clone R-80J20, genomic survey sequence.//2.7e-56:286:98//AQ284134
 F-MAMMA1002385//CIT-HSP-2328G13.TR CIT-HSP Homo sapiens genomic clone 2328G13, genomic survey sequence.//5.5e-46:335:84//AQ043985
 F-MAMMA1002392//Homo sapiens PAC clone DJ0797C05 from 7q31, complete sequence.//8.5e-29:273:78//AC004888
 F-MAMMA1002411//Human DNA sequence from clone 1044017 on chromosome Xp11.3-11.4 Contains GSS and STS, complete sequence.//8.2e-09:287:63//AL023875
 F-MAMMA1002413//Plasmodium falciparum (strain Dd2) variant-specific surface protein (var-1) gene, complete cds.//9.6e-08:730:57//L40608
 F-MAMMA1002417//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30G7, WORKING DRAFT SEQUENCE.//4.1e-06:181:72//AL034402
 F-MAMMA1002427//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C036HD7, HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//1.3e-51:593:72//AC004604
 F-MAMMA1002428
 F-MAMMA1002434//Homo sapiens DNA sequence from PAC 95883 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//7.3e-56:388:81//Z93023
 F-MAMMA1002446//CIT-HSP-2324022.TR CIT-HSP Homo sapiens genomic clone 2324022, genomic survey sequence.//2.3e-56:302:95//AQ027479
 F-MAMMA1002454//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.1e-54:190:94//AC005229
 F-MAMMA1002461//Rattus norvegicus calcium channel alpha-1 subunit gene, partial cds.//0.00045:457:60//U14005
 F-MAMMA1002470//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//9.7e-33:709:60//U10556
 F-MAMMA1002475//Homo sapiens 12p13.3 PAC RPC13-34013 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.092:506:58//AC004671
 F-MAMMA1002480//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.025:100:76//AC005077
 F-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.//2.9e-118:560:98//AF055460
 F-MAMMA1002494//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome Systems Human BAC Library) complete sequence.//1.5e-22:297:73//AC005913
 F-MAMMA1002498//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//7.2e-10:330:64//AC002477
 F-MAMMA1002524//Homo sapiens huntingtin gene, partial exon.//0.0080:124:72//L49359

【0725】

【表426】

F-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds.//1.4e-160:775:97//AF065214

F-MAMMA1002545//Homo sapiens chromosome 17, clone hRPK.74_E22, complete sequence.//1.9e-41:345:80//AC005696

F-MAMMA1002554

F-MAMMA1002556

F-MAMMA1002566

F-MAMMA1002571//CIT-HSP-2296N17, TR CIT-HSP Homo sapiens genomic clone 2296N17, genomic survey sequence.//1.7e-07:76:90//AQ006579

F-MAMMA1002573//Homo sapiens DNA, trinucleotide repeats region, clone GAA C27.//2.7e-08:195:70//AB018507

F-MAMMA1002585

F-MAMMA1002590//Homo sapiens BAC clone GS250A16 from 7p21-p22, complete sequence.//2.1e-26:361:69//AC005019

F-MAMMA1002597//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1103G7, WORKING DRAFT SEQUENCE.//1.3e-34:550:69//AL034548

F-MAMMA1002598//H. sapiens mRNA for ribosomal protein L7.//1.1e-21:123:100//X57958

F-MAMMA1002603//Homo sapiens chromosome 20, BAC clone 99 (LBNL H8D), complete sequence.//0.0018:358:61//AC005220

F-MAMMA1002612//Homo sapiens PAC clone DJ0696N01 from 7p21-p22, complete sequence.//2.1e-13:336:63//AC004861

F-MAMMA1002617//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.14:229:64//AC005486

F-MAMMA1002618

F-MAMMA1002619//Homo sapiens chromosome 21 PAC RPC1P704E14135Q2.//9.5e-71:319:85//AJ010598

F-MAMMA1002622//Homo sapiens advillin mRNA, complete cds.//1.5e-2:0:157:90//AF041449

F-MAMMA1002623//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.//8.3e-06:137:72//AE000660

F-MAMMA1002625//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1056L3, WORKING DRAFT SEQUENCE.//1.9e-171:819:98//AL031727

F-MAMMA1002629//Human BAC clone RG385F02 from 7p15, complete sequence.//4.8e-85:478:78//AC003093

F-MAMMA1002636//Human POU domain factor (Brn-3a) gene, exon 2, complete cds.//5.6e-09:499:62//U10063

F-MAMMA1002637//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//3.6e-115:785:82//AF055666

F-MAMMA1002646//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//1.5e-45:291:90//AC002038

F-MAMMA1002650//Homo sapiens candidate tumor suppressor HIC-1 (HIC-1) gene, complete cds.//6.6e-06:661:59//L41919

F-MAMMA1002655//HS_2003_A2_A11, MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2003 Col=22 Row=A, genomic survey sequence.//9.0e-15:198:74//AQ224233

F-MAMMA1002662

F-MAMMA1002665//Homo sapiens BAC clone GS58B818 from 7p12-p14, complete sequence.//1.4e-37:235:84//AC005029

F-MAMMA1002671//Human Cdk-inhibitor p57KIP2 (KIP2) mRNA, complete cds.//0.00027:272:64//U22398

F-MAMMA1002673

F-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds.//3.7e-161:752:99//D86987

F-MAMMA1002685//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 39417, WORKING DRAFT SEQUENCE.//6.2e-45:510:70//AL023585

F-MAMMA1002698//HS_3024_B1_C06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3024 Col=11 Row=F, genomic survey sequence.//1.7e-10:155:75//AQ072214

F-MAMMA1002699//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds.//5.9e-75:509:83//AF018261

F-MAMMA1002701//Homo sapiens gene for AF-5, complete cds.//1.2e-15:9:749:99//AB011399

F-MAMMA1002708//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//3.0e-57:347:79//AL031053

F-MAMMA1002711//Homo sapiens BAC clone GS589P19 from 7p13-p14, complete sequence.//3.4e-31:484:69//AC005030

F-MAMMA1002721//CIT-HSP-2350M5, TR CIT-HSP Homo sapiens genomic clone 2350M5, genomic survey sequence.//1.4e-06:265:63//AQ061245

F-MAMMA1002727//Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs and an AAT repeat polymorphism, complete sequence.//0.18:386:58//AL023584

F-MAMMA1002728//Human DNA sequence from PAC 296K21 on chromosome X

contains cytochrome exon, delta-aminolevulinic acid synthase (erythroid): 5-aminolevulinic acid synthase. (EC 2.3.1.37). 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46), ESTs and STS.//3.2e-05:362:63//Z83821

F-MAMMA1002744//Plasmodium falciparum chromosome 2, section 5 of 7 of the complete sequence.//0.00010:535:58//AE001368

F-MAMMA1002746//Homo sapiens chromosome 17, clone hRPK.136_H_19, complete sequence.//1.2e-182:880:97//AC005856

F-MAMMA1002748//Homo sapiens 3p22 Contig 7 PAC RPC14-672N11 (Roewe 11 Park Cancer Institute Human PAC Library) complete sequence.//2.7e-175:829:98//AC006055

F-MAMMA1002754//Homo Sapiens Chromosome X clone bWID171, WORKING CRAFT SEQUENCE, 1 ordered pieces.//3.1e-31:372:75//AC004676

F-MAMMA1002758//Homo sapiens KIAA0442 mRNA, partial cds.//3.3e-26:151:98//AB007902

F-MAMMA1002764//Human Chromosome 11 Cosmid cSRL166a1, complete sequence.//5.2e-49:355:81//U73636

F-MAMMA1002765//RPC111-20A22, TPB RPC11-11 Homo sapiens genomic clone RPC11-11-20A22, genomic survey sequence.//6.7e-13:155:76//B92153

F-MAMMA1002769//CIT-HSP-2323G1, TF CIT-HSP Homo sapiens genomic clone 2323G1, genomic survey sequence.//9.7e-21:151:90//AQ028244

F-MAMMA1002775//Human ABL gene, exon 1b and intron 1b, and putative M8504 Met protein (M8504 Met) gene, complete cds.//5.6e-105:17:9:99//U07561

F-MAMMA1002780//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-08, complete sequence.//0.071:277:58//Z98546

F-MAMMA1002782//HS_3213_B2_808, MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=16 Row=D, genomic survey sequence.//0.00018:219:63//AQ175845

F-MAMMA1002796

F-MAMMA1002807//Human Chromosome X PAC RPC11-290C9 from the Pieter de Jong Human PAC library: complete sequence.//6.9e-22:332:69//AC002404

F-MAMMA1002820//Homo sapiens Xp22 bins 87-93 PAC RPC11-122K4 (Roewe 11 Park Cancer Institute Human PAC Library) complete sequence.//5.9e-11:483:62//AC003035

F-MAMMA1002830//Homo sapiens chromosome 17, clone hCIT529110, complete sequence.//1.0e-64:320:83//AC002553

F-MAMMA1002833//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//2.8e-47:413:80//AC004875

F-MAMMA1002835

F-MAMMA1002838//A-916H10, TP CIT978SK Homo sapiens genomic clone A-916H10, genomic survey sequence.//1.1e-39:164:83//B14462

F-MAMMA1002842//Mus musculus c-Cbl associated protein CAP mRNA, complete cds.//1.9e-62:373:81//U58883

F-MAMMA1002843//Homo sapiens mRNA for KIAA0810 protein, partial cds.//1.7e-135:635:99//AB018353

F-MAMMA1002844//F1707-T7 IGF Arabidopsis thaliana genomic clone F1707, genomic survey sequence.//6.7e-17:383:66//B11616

F-MAMMA1002858

F-MAMMA1002858//RPC111-54F9, TJ RPC111 Homo sapiens genomic clone R-54F9, genomic survey sequence.//8.3e-81:392:99//AQ081566

F-MAMMA1002869//Sequence 1 from patent US 5552529.//2.2e-86:696:78//125863

F-MAMMA1002871//Lupinus angustifolius nodulin-45 gene, complete cds.//0.029:370:59//L12388

F-MAMMA1002880//RPC111-23M23, TV RPC11-11 Homo sapiens genomic clone RPC11-11-23M23, genomic survey sequence.//1.8e-20:271:74//B86518

F-MAMMA1002881//Homo sapiens mRNA for 25 kDa trypsin inhibitor, complete cds.//1.2e-28:680:61//D45027

F-MAMMA1002886//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 380A1, WORKING DRAFT SEQUENCE.//0.00040:505:57//Z97653

F-MAMMA1002887//HS_3238_B2_808, MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=16 Row=N, genomic survey sequence.//5.5e-79:401:97//AQ219814

F-MAMMA1002890//Mus musculus MHC class III region RD gene, partial cds: 8f, C2, G9A, NC22, G9, HSP70, HSP70, HSC70t, and snRNP genes, complete cds: G7A gene, partial cds: and unknown genes.//4.6e-3:5:136:73//AF109906

F-MAMMA1002892//Mouse Cosmid ma66a100 from 14D1-D2, complete sequence.//5.7e-14:450:60//AC004096

F-MAMMA1002895//H. sapiens CpG island DNA genomic MseI fragment, clone 46b6, forward read cpq46b6, f11a.//3.7e-36:190:100//Z58616

F-MAMMA1002908//Penaeus monodon microsatellite locus Pmo27.//1.1e-05:195:62//AF068828

F-MAMMA1002909//Human Chromosome 11 pac pDJ205d23, complete sequence.//1.0e-13:457:61//AC002402

F-MAMMA1002930//Homo sapiens Xp22 BAC GSHB-512P14 (Genome Systems Human BAC library) complete sequence.//0.25:260:62//AC004467

F-MAMMA1002937//H. sapiens ZNF74-1 mRNA.//6.3e-13:577:59//X71623

【0726】

【表427】

F-MAMMA1002938//Human sapiens mRNA for KIAA0698 protein, complete cds.//5.1e-193.910:98//AB014598

F-MAMMA1002941//Homo sapiens Chromosome 22q11.2 BAC Clone b437g10 In BCRL2-CGT Region, complete sequence.//2.7e-23:174:77//AC004032

F-MAMMA1002941//Rhodobacter capsulatus strain SB1003, partial gene me.//1.3e-09:475:61//AF010496

F-MAMMA1002964//Human thiopurine methyltransferase (TPMT) gene, ex on 5.//0.0029:314:60//AF019366

F-MAMMA1002970//Human DNA sequence from PAC 436M11 on chromosome X p22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RSI gene for retinosis is (X-linked, juvenile) 1 (XLR51). Contains ESTs, an STS and GSSs, complete sequence.//4.0e-10:194:71//Z94056

F-MAMMA1002972//H. sapiens CpG island DNA genomic HseI fragment, cl one 2g10, forward read cpg2g10.ftaa.//0.38:156:66//Z55272

F-MAMMA1002973//Homo sapiens chromosome 17, clone hRPK.142_M.19, c omplete sequence.//2.9e-41:234:79//AC005919

F-MAMMA1002982//Homo sapiens DNA sequence from PAC 510L9 on chromo some 6p24.1-p25.3.//1.7e-05:322:63//AL022098

F-MAMMA1002987//CITBI-EI-2514J12.TR CITBI-EI Homo sapiens genomic clone 2514J12, genomic survey sequence.//0.0064:135:66//AQ275871

F-MAMMA1003003//cSRL-145D12-u cSRL flow sorted Chromosome 11 specifi c cosmid Homo sapiens genomic clone cSRL-145D12, genomic survey sequence.//2.8e-31:201:89//BD1998

F-MAMMA1003004//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 7237C10, WORKING DRAFT SEQUENCE.//1.6e-10:180:73//AL031 601

F-MAMMA1003007//Homo sapiens (clone cosmid c11q-8D1) tetranucleoti de repeat polymorphism at the D11S488 locus.//3.5e-12:435:61//L047 32

F-MAMMA1003011//Rattus norvegicus histone macroH2A1.2 mRNA, comple te cds.//2.3e-50:734:67//U79139

F-MAMMA1003013//Mus musculus chromosome 19, clone CIT282B21, compl ete sequence.//1.2e-86:341:79//AC003694

F-MAMMA1003015//Homo sapiens Chromosome 16 BAC clone CIT987SK-591M 7, complete sequence.//2.6e-13:443:61//AC003661

F-MAMMA1003019//HS_3221_A1_A01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=1 Row=A, geno mic survey sequence.//2.8e-51:299:92//AQ184271

F-MAMMA1003026

F-MAMMA1003031//Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.//0.0037:134:73//AC005214

F-MAMMA1003035//RPC111-11P4.TP RPC1-11 Homo sapiens genomic clone RPC1-11-11P4, genomic survey sequence.//1.1e-07:66:100//B74936

F-MAMMA1003039//Homo sapiens 12p13.3 PAC RPC13-34013 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.1e-19:2 20:76//AC004671

F-MAMMA1003040//Human DNA sequence from PAC 340N1 on chromosome 1p 35-36.2. Contains ESTs, polymorphic CA repeat, trna and endogenous retrovirus.//9.5e-91:469:78//Z98257

F-MAMMA1003044//Human DNA sequence from clone 496N17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//0.21:289:61//A L031321

F-MAMMA1003047//Homo sapiens protein inhibitor of activated STAT p rotein PIASy mRNA, complete cds.//1.7e-139:663:98//AF077952

F-MAMMA1003049

F-MAMMA1003055//HS_3014_B2_F10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3014 Col=20 Row=L, gen omic survey sequence.//4.2e-05:215:64//AQ164940

F-MAMMA1003056//HS_3221_B2_D12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=24 Row=N, gen omic survey sequence.//1.4e-16:206:74//AQ302772

F-MAMMA1003057//M. domesticus MD6 mRNA.//8.5e-128:654:94//X54352

F-MAMMA1003066//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 273F20, WORKING DRAFT SEQUENCE.//1.0:142:71//AL034371

F-MAMMA1003089//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g- 4, complete sequence.//1.7e-42:373:78//AC004796

F-MAMMA1003099//Homo sapiens beta-filamin mRNA, complete cds.//2.6 e-42:288:88//AF042166

F-MAMMA1003104//Mus musculus rostral cerebellar malformation prote in (rcm) mRNA, complete cds.//1.6e-12:477:64//U72634

F-MAMMA1003113//Mus musculus COP9 complex subunit 7a (COPS7a) mRN A, complete cds.//3.4e-121:789:85//AF071316

F-MAMMA1003127//R. norvegicus MYR1 mRNA for myosin I heavy chain.// 9.4e-58:423:83//X68199

F-MAMMA1003135//Mus musculus dentin sialophosphoprotein precursor (DSPP) mRNA, complete cds.//0.62:676:58//U67916

F-MAMMA1003140

F-MAMMA1003146//Homo sapiens mRNA for GalT3 protein.//2.2e-80:397: 97//Y15062

F-MAMMA1003150//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 598F2, WORKING DRAFT SEQUENCE.//7.3e-123:266:88//AL0215 79

F-MAMMA1003166//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 250D10, WORKING DRAFT SEQUENCE.//1.6e-33:143:82//Z99716

F-NT2RM1000001//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs, complete sequence.//0.50:216:61//Z95 400

F-NT2RM1000018//Human mRNA for KIAA0066 gene, partial cds.//4.8e-6 5:385:92//D31886

F-NT2RM1000032

F-NT2RM1000035//Cricetulus griseus SREBP cleavage activating prote in (SCAP) mRNA, complete cds.//6.3e-135:565:84//U67060

F-NT2RM1000037//Homo sapiens mRNA for KIAA0690 protein, partial cd s.//1.1e-106:542:95//AB014590

F-NT2RM1000039//Mouse genetic suppressor element mRNA.//0.080:239: 60//L27155

F-NT2RM1000055//Rattus norvegicus mRNA for TIP120, complete cds.// 8.4e-96:535:91//D87671

F-NT2RM1000059//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 390E6, WORKING DRAFT SEQUENCE.//1.0:257:59//AL031600

F-NT2RM1000062//Nephila clavipes dragline silk protein spidroin 1 gene, partial cds.//0.54:306:63//U37520

F-NT2RM1000080//Sequence 2 from patent US 5763589.//1.5e-115:566:9 7//AR012692

F-NT2RM1000085//Homo sapiens mRNA for KIAA0661 protein, complete c ds.//1.8e-114:550:97//AB014561

F-NT2RM1000092//Homo sapiens chromosome 19, cosmid R26894, complet e sequence.//0.63:180:65//AC005594

F-NT2RM1000118//Homo sapiens clone 23763 unknown mRNA, partial cd s.//0.027:126:70//AF007155

F-NT2RM1000119//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 466N1, WORKING DRAFT SEQUENCE.//0.022:644:58//Z97630

F-NT2RM1000127//RPC111-44E5.TJ RPC111 Homo sapiens genomic clone R-44E5, genomic survey sequence.//1.6e-45:254:94//AQ195884

F-NT2RM1000131//Homo sapiens mRNA for KIAA0792 protein, complete c ds.//5.5e-153:778:95//AB018335

F-NT2RM1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUF56 subunit mRNA, nuclear gene encoding mitochondrial protein, comple te cds.//1.1e-90:448:97//AF044959

F-NT2RM1000153//Human NotI linking clone 924A081D, genomic survey sequence.//5.9e-07:66:96//U49890

F-NT2RM1000186//Homo sapiens clone 23763 unknown mRNA, partial cd s.//0.025:126:70//AF007155

F-NT2RM1000187//CITBI-EI-2510J4.TR CITBI-EI Homo sapiens genomic c lone 2510J4, genomic survey sequence.//1.1e-05:56:98//AQ261184

F-NT2RM1000199//Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds.//1.6e-38:711:65//D64009

F-NT2RM1000242

F-NT2RM1000244//HS_2229_A1_C04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2229 Col=7 Row=E, geno mic survey sequence.//2.0e-13:95:95//AQ298474

F-NT2RM1000252//Homo sapiens chromosome 17, clone hRPK.206_C_20, c omplete sequence.//0.023:225:61//AC006070

F-NT2RM1000256//Caenorhabditis elegans cosmid F22B3, complete sequ ence.//8.5e-24:473:64//Z68336

F-NT2RM1000257//Homo sapiens MAGOH mRNA, complete cds.//6.4e-69:45 5:85//AF035940

F-NT2RM1000260//Human mRNA for KIAA0130 gene, complete cds.//6.5e- 57:460:80//D50920

F-NT2RM1000271

F-NT2RM1000272

F-NT2RM1000280//Bos gaurus vacuolar H-ATPase subunit D (VATD) mRN A, complete cds.//6.7e-97:430:92//U11927

F-NT2RM1000300//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 92N15, WORKING DRAFT SEQUENCE.//2.1e-96:170:100//Z93097

F-NT2RM1000314//Human mRNA for KIAA0159 gene, complete cds.//8.1e- 127:708:92//D63880

F-NT2RM1000318//Homo sapiens mRNA for ribosomal protein L39, compl ete cds.//5.7e-34:182:99//D79205

F-NT2RM1000341//Homo sapiens full length insert cDNA clone YP11F0 6.//1.3e-100:504:97//AF085879

F-NT2RM1000354//HS_2001_B1_E06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2001 Col=11 Row=J, gen omic survey sequence.//1.6e-11:201:73//AQ218494

F-NT2RM1000355//Mus musculus E258 protein mRNA, complete cds.//1.8 e-77:578:82//U76253

F-NT2RM1000365//Homo sapiens clone DJ0098022, WORKING DRAFT SEQUEN CE, 5 unordered pieces.//9.4e-113:367:97//AC004821

F-NT2RM1000377//H. sapiens mRNA for MAP kinase phosphatase 4.//6.1

【0727】

【表428】

e-14:362:62//Y08302	F-NT2RM1000388//Azospirillum lateral flagellin (laf1) gene, complete cds.//1.0:482:58//U26679	F-NT2RM1000867//H.sapiens DNA sequence surrounding NotI site, clone MRLA143D.//1.2e-31:172:98//X95834
F-NT2RM1000394//M.musculus mRNA for histone H3.3A.//1.7e-94:549:89//Z85979	F-NT2RM1000399	F-NT2RM1000874//Homo sapiens KEO5 protein mRNA, complete cds.//2.8e-131:632:97//AF064605
F-NT2RM1000421//HS_2213_B1_E01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=1 Row=J, genomic survey sequence.//3.6e-08:195:72//AQ032737	F-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//3.7e-84:418:97//AF084928	F-NT2RM1000882//Homo sapiens Chromosome 11q12.2 PAC clone pDJ519ol3 containing human gene for ferritin heavy chain (FTH), complete sequence.//1.2e-98:214:99//ACD04228
F-NT2RM1000499//Human mRNA for KIAA0167 gene, complete cds.//1.3e-35:525:69//D79989	F-NT2RM1000539//Homo sapiens PAC clone DJ1194E14 from Tp21, complete sequence.//4.6e-73:533:83//ACD04993	F-NT2RM1000883//Homo sapiens l-1 receptor candidate protein mRNA, complete cds.//2.7e-156:762:97//AF082516
F-NT2RM1000553	F-NT2RM1000555//Homo sapiens clone 24514 unknown mRNA.//2.3e-110:55:97//AF070542	F-NT2RM1000885//Homo sapiens mRNA for KIAA0661 protein, complete cds.//2.0e-17:310:67//AB014561
F-NT2RM1000563//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.3e-123:477:100//ACD04873	F-NT2RM1000623//HS_2213_B1_E01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=1 Row=J, genomic survey sequence.//8.2e-06:75:89//AQ032737	F-NT2RM1000894//Mus musculus second largest subunit of RNA polymerase I (RPA2) mRNA, complete cds.//3.2e-95:469:83//U58280
F-NT2RM1000648//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//3.7e-84:418:97//AF084928	F-NT2RM1000648//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//3.7e-84:418:97//AF084928	F-NT2RM1000898
F-NT2RM1000661//Homo sapiens cap-binding protein 4EHP mRNA, complete cds.//9.3e-54:275:97//AF047695	F-NT2RM1000666//HS_2016_B2_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=16 Row=P, genomic survey sequence.//5.7e-13:199:73//AQ227865	F-NT2RM1000905//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 466N1, WORKING DRAFT SEQUENCE.//1.8e-74:188:98//Z97630
F-NT2RM1000669//Human DNA sequence from clone 281HB on chromosome 6q25.1-25.3. Contains up to four novel genes, one with similarity to KIAA0323 and worm C30F12.1 and another with Ubiquitin-Like protein gene SMT3 (the latter in an intron of a novel gene). Contains ESTs, STSs, GSSs, a putative CpG island and genomic marker D6S1553, complete sequence.//2.7e-94:499:94//AL031133	F-NT2RM1000672	F-NT2RM1000924//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.7e-148:601:98//ACD04873
F-NT2RM1000691//Homo sapiens HRHFB2060 mRNA, partial cds.//2.2e-19:582:98//AB015348	F-NT2RM1000699//Caenorhabditis elegans cosmid Y41C4A, complete sequence.//0.95:284:61//AL032627	F-NT2RM1000927//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//0.071:392:60//ACD04846
F-NT2RM1000702//HS_3005_A1_A02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3005 Col=3 Row=A, genomic survey sequence.//0.073:290:58//AQ089514	F-NT2RM1000725//Homo sapiens mRNA for neuropathy target esterase.//4.8e-65:435:85//AJ004832	F-NT2RM1000962//H.sapiens CpG island DNA genomic MseI fragment, clone 140d1, forward read cpg140d1.ftla.//4.1e-35:187:99//Z56803
F-NT2RM1000741//Homo sapiens mRNA for KIAA0567 protein, partial cds.//8.0e-126:690:92//AB011139	F-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds.//2.5e-66:524:83//AF027208	F-NT2RM1000978//Homo sapiens Chromosome 15q22.3-23 PAC 88m3, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.1e-23:266:77//ACD05959
F-NT2RM1000746//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.//0.92:395:58//AJ011930	F-NT2RM1000770//Homo sapiens inosine monophosphate dehydrogenase type I gene, complete cds.//2.1e-70:407:92//L39210	F-NT2RM1001003//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//4.0e-160:760:98//U97067
F-NT2RM1000772//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.6e-36:98:93//ACD00380	F-NT2RM1000780//Human DNA for 5' terminal region of LINE-1 transposable element clone CGL1-4.//9.3e-22:126:99//X52233	F-NT2RM1001008//Kaposi's sarcoma-associated herpes-like virus ORF7 3 homolog gene, complete cds.//1.7e-11:602:61//U52064
F-NT2RM1000781//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.1e-09:540:59//ACD04153	F-NT2RM1000800//Mus musculus mRNA for B-IND1 protein.//4.0e-81:497:88//Z97207	F-NT2RM1001043//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-Xp11.4. Contains monooxygenase B (MAOB), ESTs and polymorphic CA repeats.//3.9e-93:645:86//Z95125
F-NT2RM1000802	F-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds.//3.7e-63:490:84//AF027208	F-NT2RM1001044//S.pombe chromosome III cosmid c320.//0.90:128:66//AL022245
F-NT2RM1000826//Homo sapiens clone 24514 unknown mRNA.//7.2e-153:749:96//AF070542	F-NT2RM1000829//HS_3047_A1_A05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=9 Row=A, genomic survey sequence.//0.74:215:67//AQ099134	F-NT2RM1001059//Homo sapiens chromosome 5, BAC clone 58g14 (LBML H76), complete sequence.//3.8e-53:261:80//ACD05915
F-NT2RM1000850//F.rubripes GSS sequence, clone 163A22aF11, genomic survey sequence.//1.1e-26:279:74//AL018762	F-NT2RM1000852//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//9.3e-148:726:97//AJ010840	F-NT2RM1001066//CIT-HSP-2172N17, TF CIT-HSP Homo sapiens genomic clone 2172N17, genomic survey sequence.//0.64:285:59//B94391
F-NT2RM1000857//Rattus norvegicus gene for cytochrome P450/6 beta B, exon 2.//0.97:124:65//AB008378		F-NT2RM1001072//HS_3115_B1_D07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3115 Col=13 Row=H, genomic survey sequence.//7.3e-23:140:95//AQ147905
		F-NT2RM1001074//Homo sapiens chromosome 19, cosmid F20489, complete sequence.//5.0e-50:186:98//ACD05263
		F-NT2RM1001082//Sequence 1 from Patent W09718303.//2.1e-144:736:95//A62731
		F-NT2RM1001085//CIT-HSP-2310F21, TR CIT-HSP Homo sapiens genomic clone 2310F21, genomic survey sequence.//8.8e-45:235:97//AQ020757
		F-NT2RM1001092//HS_3055_B1_G05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=9 Row=N, genomic survey sequence.//1.1e-89:471:95//AQ155489
		F-NT2RM1001102//Human HEM45 mRNA, complete cds.//1.2e-28:482:63//U88964
		F-NT2RM1001105//Homo sapiens hRED1 gene, exon 1 (5' UTR).//0.0014:349:61//Z95973
		F-NT2RM1001112//Homo sapiens chromosome 19, cosmid R34094, complete sequence.//0.060:429:58//ACD04678
		F-NT2RM1001115//Plasmodium falciparum merozoite surface protein 3 (MSP-3) gene, partial cds.//0.93:156:62//AF024624
		F-NT2RM1001139//Homo sapiens chromosome 19, fosmid 37502, complete sequence.//1.2e-10:466:59//ACD04755
		F-NT2RM2000006//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796F18, WORKING DRAFT SEQUENCE.//5.3e-150:724:98//AL031291
		F-NT2RM2000013//D.melanogaster DmRP128 gene for RNA polymerase III second-largest subunit.//1.5e-58:749:69//X58826
		F-NT2RM2000030//Homo sapiens clone DJ0768P22, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.1e-97:270:77//ACD04863
		F-NT2RM2000032//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//1.9e-25:172:76//AL034379
		F-NT2RM2000042//Human DNA sequence from cosmid USSE4, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//5.0e-05:325:65//Z73418
		F-NT2RM2000092//Homo sapiens (D8S321 locus) DNA sequence, tetranucleotide repeat polymorphism.//0.63:117:68//L12269
		F-NT2RM2000093//Mus musculus major histocompatibility locus class III regions Hsc70T gene, partial cds: smRNP, C7A, NC23, MutS homolog, CLCP, NC24, NC25, and NC26 genes, complete cds: and unknown genes.//0.38:312:62//AF109905
		F-NT2RM2000101
		F-NT2RM2000124//Mouse cAMP-dependent protein kinase catalytic subu

【0728】

【表429】

nit mRNA, complete cds.//3.8e-58:297:97//M12303
 F-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A2 (PDE9A) mRNA, complete cds.//3.8e-138:653:98//AF067224
 F-NT2RM2000192//CIT-HSP-2172B3.TF CIT-HSP Homo sapiens genomic clone 2172B3, genomic survey sequence.//2.2e-33:191:95//B93289
 F-NT2RM2000239//F. rubripes GSS sequence, clone 156P04G12, genomic survey sequence.//8.9e-44:445:69//AL018549
 F-ntnnnnnnnnnn//Homo sapiens fibroblast growth factor 18 (FGF18) mRNA, complete cds.//0.00020:380:61//AF075292
 F-NT2RM2000250//Homo sapiens mRNA for KIAA0590 protein, complete cds.//3.1e-128:615:98//AB011162
 F-NT2RM2000259//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 310013, WORKING DRAFT SEQUENCE.//0.0013:305:63//AL031658
 F-NT2RM2000260//Mus musculus WW domain binding protein 15 mRNA, partial sequence.//3.0e-14:645:61//AF073934
 F-NT2RM2000287//*** SEQUENCING IN PROGRESS *** EPM1/APECD region of chromosome 21, clones A6B8, B127P21, B173L3, B23N8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center, WORKING DRAFT SEQUENCE. 50 unordered pieces.//1.3e-11:96:86//AC003656
 F-NT2RM2000322//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYN1). ESTs, STS, GSS, CpG Island, complete sequence.//8.5e-115:233:97//AL031864
 F-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds.//8.8e-175:805:99//AB011132
 F-NT2RM2000363//RPC111-90B10.TJ RPC111 Homo sapiens genomic clone R-90B10, genomic survey sequence.//6.7e-15:96:98//AQ285300
 F-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK7 mRNA, partial cds.//1.2e-94:599:86//U48251
 F-NT2RM2000371//RPC111-5714.TJ RPC111 Homo sapiens genomic clone R-5714, genomic survey sequence.//1.1e-52:312:91//AQ083343
 F-NT2RM2000374//M. musculus nodal gene, a TGF-beta-like gene.//6.7e-31:196:91//X70514
 F-NT2RM2000395//Leishmania major chromosome 1, complete sequence.//0.99:345:58//AE001274
 F-NT2RM2000402//Arabidopsis thaliana BAC T19D16 genomic sequence.//2.1e-23:414:63//U95973
 F-NT2RM2000407//Mus musculus semaphorin 11a mRNA, complete cds.//1.4e-131:439:88//AF030430
 F-NT2RM2000420//HS_3063_B2_F11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3063 Col=22 Row=L, genomic survey sequence.//3.2e-25:154:95//AQ103204
 F-NT2RM2000422//Rat orphan transporter v7-3 (NTT73) mRNA, complete cds.//1.7e-128:782:86//L22022
 F-NT2RM2000452//HS_3009_B2_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=10 Row=H, genomic survey sequence.//1.2e-16:122:90//AQ130794
 F-NT2RM2000469//HS_2019_A1_G02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2019 Col=3 Row=M, genomic survey sequence.//9.6e-22:176:85//AQ229041
 F-NT2RM2000490//Homo sapiens mRNA for KIAA0747 protein, partial cds.//7.5e-15:386:63//AB018290
 F-NT2RM2000502
 F-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//5.1e-171:824:97//AF061243
 F-NT2RM2000522
 F-NT2RM2000540
 F-NT2RM2000556//Homo sapiens 12q13.1 PAC RPC15-1057120 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.9e-42:344:82//AC004466
 F-NT2RM2000566//Homo sapiens integrin alpha-7 mRNA, complete cds.//2.8e-154:751:97//AF072132
 F-NT2RM2000567//Pseudomonas aeruginosa enoyl-CoA hydratase gene, partial cds: pilin biosynthetic protein (fimL) gene, complete cds: and unknown gene.//3.0e-06:664:58//AF083252
 F-NT2RM2000569//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE.//1.3e-15:348:67//AL031658
 F-NT2RM2000577//RPC111-43G22.TJ RPC111 Homo sapiens genomic clone R-43G22, genomic survey sequence.//1.6e-14:155:80//AQ199391
 F-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds.//5.4e-174:820:98//D86987
 F-NT2RM2000588//Homo sapiens 12q13.1 PAC RPC15-1057120 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.1e-60:344:82//AC004466
 F-NT2RM2000594//Mus musculus DNA cytosine-5 methyltransferase 3B1 (Dnmt3b) mRNA, alternatively spliced, complete cds.//4.9e-118:761:85//AF068626
 F-NT2RM2000599//O. sativa osr40g3 gene.//0.30:585:56//Y08988
 F-NT2RM2000609
 F-NT2RM2000612//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//7.8e-102:709:83//U35776
 F-NT2RM2000623//Homo sapiens chromosome 19, cosmid F19847, complete sequence.//3.4e-17:450:65//AC005952
 F-NT2RM2000624
 2.9e-06:231:64//Z82061
 F-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds.//6.3e-142:664:98//AB018272
 F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds.//7.4e-138:664:98//AB014558
 F-NT2RM2000639//RPC111-69E5.TJ RPC111 Homo sapiens genomic clone R-69E5, genomic survey sequence.//3.7e-14:97:97//AQ267491
 F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds.//1.1e-167:518:99//AB014576
 F-NT2RM2000669
 F-NT2RM2000691//Homo sapiens chromosome 2 clone 101B6 map 2p11, complete sequence.//1.1e-106:748:82//AC002038
 F-NT2RM2000714//Human mRNA for KIAA0231 gene, partial cds.//6.8e-49:748:64//D86984
 F-NT2RM2000718//Homo sapiens HRIHFB2436 mRNA, partial cds.//2.4e-124:594:98//AB015342
 F-NT2RM2000735//Human ZNF43 mRNA.//8.4e-111:756:82//X59244
 F-NT2RM2000740//Mus musculus lymphocyte specific helicase mRNA, complete cds.//1.3e-141:815:89//U25691
 F-NT2RM2000795//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 439F8, WORKING DRAFT SEQUENCE.//1.0e-78:723:76//AL021392
 F-NT2RM2000821//Rat mRNA for beta COP.//2.0e-150:879:88//X57228
 F-NT2RM2000837//Homo sapiens BAC clone GS214M13 from 7p14-p15, complete sequence.//1.1e-05:361:62//AC005017
 F-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//8.7e-184:847:99//AB015046
 F-NT2RM2000952
 F-NT2RM2000984//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds: sMRNP, G7A, NC23, MutS homolog, CLCP, NC24, NC25, and NC26 genes, complete cds: and unknown genes.//7.6e-41:239:76//AF109905
 F-NT2RM2001004//CIT-HSP-2333N18.TR CIT-HSP Homo sapiens genomic clone 2333N18, genomic survey sequence.//1.1e-11:298:66//AQ035862
 F-NT2RM2001035//Mus musculus mCAF1 protein mRNA, complete cds.//1.4e-120:627:91//U21855
 F-NT2RM2001065//Mus musculus COP9 complex subunit 4 (COPS4) mRNA, complete cds.//6.8e-118:690:88//AF071314
 F-NT2RM2001100//Homo sapiens clone DJ0742P04, WORKING DRAFT SEQUENCE. 6 unordered pieces.//2.3e-145:614:99//AC004873
 F-NT2RM2001105//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.//2.7e-95:461:99//AL034380
 F-NT2RM2001131//Kaposi's sarcoma-associated herpes-like virus ORF73 homolog gene, complete cds.//7.2e-24:726:62//U52064
 F-NT2RM2001141
 F-NT2RM2001152//Homo sapiens DNA sequence from PAC 93L7 on chromosome Xq21. Contains part of the CMM (TCD, REP1) gene coding for RAB Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase component A1, Choroideraemia protein, Tapetochochoidal Dystrophy (TCD) protein). Contains ESTs and an STS, complete sequence.//0.98:300:62//AL022401
 F-NT2RM2001177//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUENCE. 15 unordered pieces.//1.2e-147:741:96//AC005488
 F-NT2RM2001194//Suid herpesvirus 1 UL5 gene, partial cds. UL6 and UL7 genes, complete cds. UL8 gene, partial cds.//0.026:408:59//U66829
 F-NT2RM2001196//Homo sapiens clone DJ1173120, WORKING DRAFT SEQUENCE. 5 unordered pieces.//2.2e-135:627:98//AC004987
 F-NT2RM2001201//Mus musculus clone OST431, genomic survey sequence.//6.1e-80:503:86//AF046700
 F-NT2RM2001221//Chimpanzee (P. paniscus) involucrin, complete cds.//0.53:670:55//M26514
 F-NT2RM2001238//Rat glutaminase mRNA, complete cds.//3.4e-128:719:90//M65150
 F-NT2RM2001243
 F-NT2RM2001247//CITBI-E1-2521M18.TR CITBI-E1 Homo sapiens genomic clone 2521M18, genomic survey sequence.//0.0011:274:59//AQ276184
 F-NT2RM2001256//M. musculus mRNA for 200 kD protein.//2.3e-129:742:90//X80169
 F-NT2RM2001291//CIT-HSP-2010115.TR CIT-HSP Homo sapiens genomic clone

【0729】

【表430】

one 2010115, genomic survey sequence.//4.6e-09:156:72//B57734
 F-NT2RM2001306//RPC111-2815, TP RPC1-11 Homo sapiens genomic clone
 RPC1-11-2815, genomic survey sequence.//0.069:234:64//B84850
 F-NT2RM2001312//Homo sapiens chromosome 17, clone hRPK.142_H_19, c
 omplete sequence.//1.1e-22:111:81//ACD05919
 F-NT2RM2001319//Borrelia burgdorferi (section 4 of 70) of the comp
 lete genome.//0.99:340:58//AE001118
 F-NT2RM2001324//Human DNA sequence *** SEQUENCING IN PROGRESS ***
 from clone 209H1, WORKING DRAFT SEQUENCE.//3.7e-44:340:85//Z84465
 F-NT2RM2001345//HS_3005_A1_A02_MR CIT Approved Human Genomic Sperm
 Library D Homo sapiens genomic clone Plate=3005 Col=3 Row=A, geno
 mic survey sequence.//0.042:290:58//AQ089514
 F-NT2RM2001360//Human HeLa mRNA isolated as a false positive in a
 two-hybrid-screen.//5.0e-60:365:87//U56429
 F-NT2RM2001370//Homo sapiens PAC clone DJ0815020 from Tpl1-pl3, co
 mplete sequence.//0.98:415:58//AC004899
 F-NT2RM2001393//Homo sapiens Chromosome 22q11.2 PAC Clone p_m11 in
 BCRL2-CGT Region, complete sequence.//4.0e-54:394:75//AC004033
 F-NT2RM2001420//Human DNA sequence *** SEQUENCING IN PROGRESS ***
 from clone 349A12, WORKING DRAFT SEQUENCE.//2.8e-169:789:99//AL033
 520
 F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protei
 n.//7.1e-96:453:99//AJ007509
 F-NT2RM2001499//Rattus norvegicus mRNA for cationic amino acid tra
 nsporter 3, complete cds.//7.1e-91:601:83//AB000113
 F-NT2RM2001504//Homo sapiens chromosome 19, cosmid R30017, complet
 e sequence.//0.81:200:69//AC005624
 F-NT2RM2001524//Arabidopsis thaliana DNA chromosome 4, ESSA I AP2
 contig fragment No. 2.//3.8e-16:316:65//Z99708
 F-NT2RM2001544
 F-NT2RM2001547//Caenorhabditis elegans cosmid Y47H9C, complete seq
 uence.//3.3e-24:318:67//AL032657
 F-NT2RM2001575//Human 52-kD ribonucleoprotein Ro/SSA mRNA, complet
 e cds.//2.1e-26:582:64//M34551
 F-NT2RM2001582//M. musculus red-1 gene.//1.4e-102:581:90//X92750
 F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds.//7.0e-10:
 282:65//AB007902
 F-NT2RM2001592//Rattus norvegicus rexo70 mRNA, complete cds.//9.6
 e-131:736:90//AF032667
 F-NT2RM2001605//RBP2=retinoblastoma binding protein 2 [human, Nal
 m-6 pre-B cell leukemia, mRNA, 6455 nt].//2.3e-85:749:75//S66431
 F-NT2RM2001613//Rattus rattus sec61 homologue mRNA, complete cds.//
 8.6e-118:779:85//M96630
 F-NT2RM2001632//Homo sapiens PAC clone DJ0740002 from Tpl4-pl5, co
 mplete sequence.//1.5e-50:561:71//AC004691
 F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete c
 ds.//9.2e-153:740:98//AB014518
 F-NT2RM2001637//F. rubripes GSS sequence, clone 155D22bD8, genomic
 survey sequence.//2.5e-13:224:64//Z91020
 F-NT2RM2001641//CIT-HSP-2347F23, TF CIT-HSP Homo sapiens genomic cl
 one 2347F23, genomic survey sequence.//1.3e-67:340:98//AQ060913
 F-NT2RM2001648//Canis familiaris sec61 homologue mRNA, complete cd
 s.//1.4e-110:459:89//M96629
 F-NT2RM2001652//Bos taurus guanine nucleotide-exchange protein (AR
 F-GEPI) mRNA, complete cds.//1.2e-153:807:93//AF023451
 F-NT2RM2001659//nxb0002cE07f CUGI Rice BAC Library Oryza sativa g
 enomic clone nxb0002J13f, genomic survey sequence.//1.0:485:56//A
 Q051653
 F-NT2RM2001664//Homo sapiens IkappaB kinase complex associated pro
 tein (IKAP) mRNA, complete cds.//3.7e-172:802:99//AF044195
 F-NT2RM2001668
 F-NT2RM2001670//Homo sapiens complete genomic sequence between D16
 S3070 and D16S3275, containing Familial Mediterranean Fever gene d
 isease.//3.2e-18:279:70//AJ003147
 F-NT2RM2001671//Oryctolagus cuniculus sarcolemmal associated prote
 in-3 mRNA, complete cds.//1.6e-137:683:94//U21157
 F-NT2RM2001675//RPC111-51J16.TJ RPC111 Homo sapiens genomic clone
 R-51J16, genomic survey sequence.//1.0:394:58//AQ053677
 F-NT2RM2001681//Arabidopsis thaliana DNA chromosome 4, BAC clone T
 805 (ESSA11 project).//0.87:220:61//AL021890
 F-NT2RM2001688//B. paraperussis bvg locus (transcription regulator
 s of virulence factors) with bvgA and bvgS genes.//1.0:286:62//X52
 948
 F-NT2RM2001695//CIT-HSP-345H13.TVB CIT-HSP Homo sapiens genomic cl
 one 345H13, genomic survey sequence.//3.2e-53:241:82//B59854
 F-NT2RM2001696//Mouse DNA with homology to EBV IR3 repeat, segment
 2, clone Mu2.//1.2e-05:306:58//M10668
 F-NT2RM2001698//Homo sapiens DNA sequence from PAC 163M9 on chromo
 some 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1
 F1551A pseudogene, ESTs, STS, GSS, complete sequence.//6.0e-05:
 8:59//AL021920
 F-NT2RM2001699//HS_3195_B2_D01_T7 CIT Approved Human Genomic Sperm
 Library D Homo sapiens genomic clone Plate=3195 Col=2 Row=H, geno
 mic survey sequence.//2.7e-07:322:61//AQ189056
 F-NT2RM2001700//Mycobacterium tuberculosis H37Rv complete genome:
 segment 109/162.//7.8e-05:354:58//Z95556
 F-NT2RM2001706//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT
 SEQUENCE, 99 unordered pieces.//7.5e-42:335:81//AC004469
 F-NT2RM2001716
 F-NT2RM2001718//Drosophila melanogaster DNA sequence (P1 DS04106
 (D172)), complete sequence.//4.2e-08:536:58//AC004290
 F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence.//1.4e-26:1
 63:95//AF052123
 F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cd
 s.//6.2e-111:530:98//AB007931
 F-NT2RM2001730//Homo sapiens chromosome 21 PAC RPC1P704E14135Q2.//
 3.1e-102:248:95//AJ010598
 F-NT2RM2001743
 F-NT2RM2001753//Caenorhabditis elegans cosmid F45E6, complete sequ
 ence.//0.11:138:66//Z68117
 F-NT2RM2001760//Canis familiaris sec61 homologue mRNA, complete cd
 s.//9.4e-100:418:88//M96629
 F-NT2RM2001768//HS_3064_B2_A04_MF CIT Approved Human Genomic Sperm
 Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, geno
 mic survey sequence.//3.1e-28:153:100//AQ136993
 F-NT2RM2001771//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC30
 1323), complete sequence.//1.3e-66:680:72//AC006116
 F-NT2RM2001782
 F-NT2RM2001784//Bovine herpesvirus type 1 (Cooper) DNA (30 kb).//
 0.027:384:60//Z48053
 F-NT2RM2001785//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC2
 69730) containing the hFEN1 gene, complete sequence.//1.6e-18:229:
 65//AC004770
 F-NT2RM2001797//HS_3045_A1_D01_MF CIT Approved Human Genomic Sperm
 Library D Homo sapiens genomic clone Plate=3045 Col=1 Row=G, geno
 mic survey sequence.//1.4e-74:381:97//AQ129456
 F-NT2RM2001800
 F-NT2RM2001803//Homo sapiens IkappaB kinase complex associated pro
 tein (IKAP) mRNA, complete cds.//8.3e-178:827:99//AF044195
 F-NT2RM2001805//Malus domestica leucine-rich receptor-like protein
 kinase (LRPKml) gene, 5' flanking region and 5' UTR.//1.0:290:58/
 AF053126
 F-NT2RM2001813//CIT-HSP-2169F21, TR CIT-HSP Homo sapiens genomic c
 l one 2169F21, genomic survey sequence.//3.3e-16:109:95//B89870
 F-NT2RM2001823//Drosophila melanogaster DNA sequence (P1 DS07049
 (D133)), complete sequence.//5.8e-62:819:68//AC004274
 F-NT2RM2001839//Homo sapiens caluemin (Calu) mRNA, complete cds.//
 3.6e-131:738:90//AF013759
 F-NT2RM2001840//Homo sapiens chromosome 17, clone 297N7, complete
 sequence.//1.1e-57:422:79//AC002347
 F-NT2RM2001855//HS_3224_A1_H07_MR CIT Approved Human Genomic Sperm
 Library D Homo sapiens genomic clone Plate=3224 Col=13 Row=0, gen
 omic survey sequence.//0.00012:68:91//AQ205285
 F-NT2RM2001867//Human DNA sequence from clone 889N15 on chromosome
 Xq22.1-22.3. Contains part of the gene for a novel protein simila
 r to X. laevis Cortical Thymocyte Marker CTX, the possibly alterna
 tively spliced gene for 26S Proteasome subunit p28 (Ankyrin repeat
 protein), a novel gene and exons 36 through 45 of the COL4A6 for
 Collagen Alpha 6(IV). Contains ESTs, STSs, GSSs and a putative CpG
 island, complete sequence.//0.068:102:70//AL031177
 F-NT2RM2001879//Human DNA sequence from cosmid cU72E5, between mar
 kers DXS366 and DXS87 on chromosome X.//0.0029:500:59//Z68328
 F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete c
 ds.//1.9e-187:866:97//AB014610
 F-NT2RM2001896//S. cerevisiae chromosome III complete DNA sequence.
 //8.6e-30:613:63//X59720
 F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cd
 s.//2.9e-176:859:97//AB007931
 F-NT2RM2001930//M. musculus mRNA for semaphorin G.//4.7e-117:730:85
 //X97818
 F-NT2RM2001935//Sequence 11 from Patent W09610637.//1.0:356:60//A5
 0028
 F-NT2RM2001936//Homo sapiens clone 614 unknown mRNA, complete sequ
 ence.//6.9e-138:653:98//AF091080
 F-NT2RM2001950//RPC111-24L12, TP RPC1-11 Homo sapiens genomic clone
 RPC1-11-24L12, genomic survey sequence.//2.7e-19:188:81//B86700
 F-NT2RM2001982//Arabidopsis thaliana chromosome II BAC T24121 geno
 mic sequence, complete sequence.//0.42:179:65//AC005825
 F-NT2RM2001983//Homo sapiens RGS-GAIP interacting protein GIPC mRN
 A, complete cds.//3.8e-20:123:98//AF089816

【表431】

F-NT2RM2001989//Sequence 3 from patent US 5747317.//1.9e-167:786:98//AR004981	F-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA. complete cds.//7.9e-153:609:93//M99438
F-NT2RM2001997//Human HepG2 partial cDNA, clone had1b08m5.//9.6e-25:160:95//D16955	F-NT2RM4000324
F-NT2RM2001998//Homo sapiens DNA, chromosome 21q22.2, PAC clone 25 P16 complete sequence, encoding carbonyl reductase and carbonyl reductase 3 (complete cds).//0.88:380:60//AB003151	F-NT2RM4000327//Rattus norvegicus guanine nucleotide binding protein in beta 4 subunit mRNA, partial cds.//3.9e-44:727:68//AF022085
F-NT2RM2002004//Human Chromosome X, complete sequence.//5.0e-88:831:77//AC002407	F-NT2RM4000344//Mus musculus ATP-dependent metalloprotease FtsH1 mRNA, complete cds.//1.0e-143:801:90//AF090430
F-NT2RM2002014	F-NT2RM4000349//Mus musculus clone OST431, genomic survey sequence.//6.1e-80:503:86//AF046700
F-NT2RM2002030//Mus musculus glutamine:fructose-6-phosphate amidotransferase mRNA, complete cds.//1.5e-89:822:74//U00932	F-NT2RM4000354//HS_2221_A2_C07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2221 Col=14 Row=E, genomic survey sequence.//1.0e-20:180:83//AQ253449
F-NT2RM2002049//Bovine elastin mRNA, partial cds.//8.8e-11:125:81//M26132	F-NT2RM4000356
F-NT2RM2002055	F-NT2RM4000366//Homo sapiens mRNA for KIAA0542 protein, partial cds.//1.6e-133:628:99//AB014542
F-NT2RM2002088//Mus musculus WW domain binding protein 17 mRNA, partial sequence.//1.4e-15:421:63//AF073936	F-NT2RM4000368//RPC111-91B5.TJ RPC111 Homo sapiens genomic clone R-91B5, genomic survey sequence.//5.0e-12:431:61//AQ283217
F-NT2RM2002091//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.//4.6e-160:771:98//AL034380	F-NT2RM4000386//Mus musculus Doc4 (Doc4) mRNA, complete cds.//7.4e-86:845:72//AF059485
F-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//7.7e-164:776:98//AJ010840	F-NT2RM4000395//Saccharomyces cerevisiae chromosome VI cosmid 996 S.//2.5e-34:767:61//D44597
F-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//2.4e-143:684:98//AF030435	F-NT2RM4000414//Homo sapiens XYLB mRNA for xylulokinase, complete cds.//1.5e-15:114:94//AB015046
F-NT2RM2002128//Mesocricetus auratus guanine nucleotide-binding protein beta 5 (Gnb5) mRNA, complete cds.//7.0e-27:330:73//U13152	F-NT2RM4000421
F-NT2RM2002142//Danio rerio gastrulation specific (G12) mRNA, complete cds.//6.3e-10:135:80//U27121	F-NT2RM4000425//Homo sapiens chromosome 17, clone hRPK.294.J.22, complete sequence.//1.5e-37:295:82//AC005921
F-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//4.2e-143:800:92//AF084928	F-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Str a6) mRNA, complete cds.//3.9e-94:740:78//AF062476
F-NT2RM2002178//Homo sapiens mRNA for KIAA0467 protein, partial cds.//5.2e-164:787:97//AB007936	F-NT2RM4000457//CIT-HSP-2346B17, TR CIT-HSP Homo sapiens genomic clone 2346B17, genomic survey sequence.//1.5e-22:149:92//AQ062111
F-NT2RM2002580//Drosophila melanogaster DNA sequence (P1 DS02110 (D147)), complete sequence.//7.4e-13:337:62//AC004423	F-NT2RM4000471//Homo sapiens mRNA for putative tRNA splicing protein, partial.//1.3e-76:386:97//AJ010952
F-NT2RM4000024//D.melanogaster DmP128 gene for RNA polymerase III second-largest subunit.//1.2e-62:801:70//X58826	F-NT2RM4000486//Homo sapiens mRNA, complete cds, clone:RES4-22A.//1.1e-22:356:67//AB000459
F-NT2RM4000027//Caenorhabditis elegans cosmid F09E5.//0.36:336:60//U37429	F-NT2RM4000496//Homo sapiens 12p13.3 BAC RPC111-476M19 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.53:198:70//AC005908
F-NT2RM4000030//H.sapiens CpG island DNA genomic MseI fragment, clone 56h10, forward read cpg56h10.ftla.//9.3e-22:127:100//Z55685	F-NT2RM4000511
F-NT2RM4000046//Curcubita maxima 25S - 18S rDNA intergenic spacer.//4.1e-05:386:60//X13059	F-NT2RM4000514
F-NT2RM4000061	F-NT2RM4000515//CIT-HSP-2285L3, TR CIT-HSP Homo sapiens genomic clone 2285L3, genomic survey sequence.//0.0012:200:66//AQ000113
F-NT2RM4000085//B.taurus mRNA for nuclear DNA helicase II.//1.9e-10:485:59//X82829	F-NT2RM4000520
F-NT2RM4000086	F-NT2RM4000531//Human zinc finger protein 42 (ZNF-1) mRNA, complete cds.//2.9e-31:732:64//M58297
F-NT2RM4000104//Homo sapiens chromosome 16 zinc finger protein ZNF210 (ZNF210) mRNA, complete cds.//4.2e-23:345:69//AF060865	F-NT2RM4000532//HS_3231_B1_C05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3231 Col=9 Row=F, genomic survey sequence.//1.3e-59:362:90//AQ192093
F-NT2RM4000139//R.norvegicus trp mRNA.//1.4e-56:708:69//X68101	F-NT2RM4000534
F-NT2RM4000155//CIT-HSP-2282N15, TR CIT-HSP Homo sapiens genomic clone 2282N15, genomic survey sequence.//3.0e-09:88:90//AQ000070	F-NT2RM4000585//CITB1-E1-2508118, TR CITB1-E1 Homo sapiens genomic clone 2508118, genomic survey sequence.//1.1e-34:208:93//AQ260706
F-NT2RM4000156//H.sapiens HPBRI1-7 gene.//2.0e-21:586:60//X67336	F-NT2RM4000590//CIT-HSP-2291M14, TF CIT-HSP Homo sapiens genomic clone 2291M14, genomic survey sequence.//8.3e-34:180:99//AQ004125
F-NT2RM4000167//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//2.7e-143:810:90//D12646	F-NT2RM4000595//Homo sapiens chromosome 17, clone hCIT.131_K.11, complete sequence.//1.2e-09:203:66//AC005288
F-NT2RM4000169//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0054:746:57//AC004157	F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds.//5.3e-14:305:68//AB002390
F-NT2RM4000191//Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.//0.00018:468:60//AF051726	F-NT2RM4000611//CIT-HSP-2169F21, TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence.//8.4e-16:109:94//B89870
F-NT2RM4000197	F-NT2RM4000616//D.melanogaster mRNA for acetyl-CoA synthetase.//2.3e-59:721:68//Z46786
F-NT2RM4000199//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 620E11, WORKING DRAFT SEQUENCE.//0.67:461:60//AL031667	F-NT2RM4000674
F-NT2RM4000200	F-NT2RM4000689//CIT-HSP-2381O13, TF CIT-HSP Homo sapiens genomic clone 2381O13, genomic survey sequence.//2.6e-31:174:97//AQ110303
F-NT2RM4000202//H.sapiens CpG island DNA genomic MseI fragment, clone 34c2, forward read cpg34c2.ftla.//1.7e-27:190:90//Z65361	F-NT2RM4000698
F-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//1.4e-182:856:98//AB018255	F-NT2RM4000700
F-NT2RM4000215//S.cerevisiae MAK16 protein gene, complete cds, and LTE1 protein gene, 3' end.//3.1e-31:731:62//J03852	F-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme 1 (UBH1) mRNA, partial cds.//1.1e-89:744:77//AF022789
F-NT2RM4000229//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//4.6e-102:233:94//AC005383	F-NT2RM4000717
F-NT2RM4000233//Mus musculus semaphorin 15a mRNA, complete cds.//1.6e-135:835:86//AF030430	F-NT2RM4000733//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//2.1e-140:299:99//AL034379
F-NT2RM4000244//RPC111-24P15, TV RPC111 Homo sapiens genomic clone RPC111-24P15, genomic survey sequence.//5.5e-08:422:62//B86757	F-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds.//3.8e-158:743:98//AB018303
F-NT2RM4000251//Mus musculus clone UNGC:mbac92 from 14D1-D2 (T-Cell Receptor Alpha Locus), complete sequence.//0.98:207:60//AC005855	F-NT2RM4000741
F-NT2RM4000265//Homo sapiens Chromosome 11q12.2 PAC clone p0J1081b4 containing human mRNA for T-cell glycoprotein CD6, complete sequence.//5.2e-41:707:65//AC003689	F-NT2RM4000751//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//7.1e-95:754:77//M99593
	F-NT2RM4000764
	F-NT2RM4000778//Caenorhabditis elegans cosmid F36H12.//0.30:523:60//AF078790
	F-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete c

【0731】

【表432】

ds. //5.5e-172:810:98//AB007920	/2.5e-77:474:89//Z46973
F-NT2RM4000787//Human DNA sequence from PAC 370M22 on chromosome 2. 2q12-pter. contains GRB2 ADAPTOR LIKE PROTEIN, UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR SUBUNIT PRECURSOR (UQCRCF1) exon, ESTs, STS, CA repeat and CpG island. //0.0057:163:69//Z82206	F-NT2RM4001316//Caenorhabditis elegans cosmid K09H11. //1.2e-16.23 0:73//U97092
F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216, complete sequence. //6.9e-39:237:94//AC005306	F-NT2RM4001320//Homo sapiens mRNA for Neuroblastoma, complete cds. //1.1e-41:642:66//D89016
F-NT2RM4000795//Rattus norvegicus neurologilin 3 mRNA, complete cds. //5.9e-97:857:74//U41663	F-NT2RM4001340//EP(3)0614 Drosophila melanogaster EP line Drosophila melanogaster genomic Sequence recovered from 5' end of P element t. genomic survey sequence. //0.0040:141:68//AQ025127
F-NT2RM4000796//HS_3214_B1_F11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3214 Col=21 Row=L, genomic survey sequence. //1.1e-14:254:68//AQ175988	F-NT2RM4001344//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone YIE3, WORKING DRAFT SEQUENCE. //5.5e-06:469:60//AL021388
F-NT2RM4000798//Bos taurus guanine nucleotide-exchange protein (ARF-GAP1) mRNA, complete cds. //6.2e-78:816:72//AF023451	F-NT2RM4001347
F-NT2RM4000813//Leishmania major glycoprotein 96-92 (GP 96-92) gene, partial cds. //0.33:276:63//M63109	F-NT2RM4001371//Arabidopsis thaliana chromosome 11 BAC T20K9 genomic sequence, complete sequence. //0.10:400:61//AC004786
F-NT2RM4000820//, complete sequence. //2.6e-142:450:97//AC005406	F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds. //2.2e-167:790:98//AF098799
F-NT2RM4000833//Drosophila melanogaster DNA sequence (P1 DS05273 (DS0)), complete sequence. //1.9e-52:501:71//AC004373	F-NT2RM4001384//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence. //0.99:255:59//AL021393
F-NT2RM4000848//Homo sapiens chromosome 17, clone hRPK.167_N_20, complete sequence. //1.0:477:56//AC005940	F-NT2RM4001410//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5. WORKING DRAFT SEQUENCE. //0.027:336:58//AP000023
F-NT2RM4000852	F-NT2RM4001411//Mus musculus Pro-rich, PH, SH2 domain-containing signaling mediator (PSM) mRNA, complete cds. //5.9e-124:783:85//AF020526
F-NT2RM4000855//Homo sapiens chromosome 17, clone hCIT.457_L_16, complete sequence. //3.4e-29:229:83//AC003957	F-NT2RM4001412//Rattus norvegicus GTPase activating protein SynGAP mRNA, complete cds. //2.2e-34:418:71//AF050183
F-NT2RM4000887	F-NT2RM4001414//Homo sapiens full length insert cDNA clone ZE16C1. //9.1e-76:363:100//AF085563
F-NT2RM4000895//Homo sapiens HuLAP1 mRNA for UDP-N-acetylglucosamine pyrophosphorylase, complete cds. //2.1e-20:407:64//AB011004	F-NT2RM4001437//Homo sapiens chromosome 5, BAC clone 313n8 (LBML H146), complete sequence. //2.0e-47:623:69//AC004226
F-NT2RM4000950//Homo sapiens clone DJ0917G04, WORKING DRAFT SEQUENCE, 35 unordered pieces. //0.41:311:64//AC004929	F-NT2RM4001444//Streptococcus pneumoniae penicillin-binding protein 2b (pbp2b), RecM (recM), D-Ala-D-Ala ligase (ddl), D-Ala-D-Ala adding enzyme (murF), MutT (mutT), cell division protein FtsA (ftsA), cell division protein FtsZ (ftsZ), YlmE (ylmE), YlmF (ylmF), YlmG (ylmG), YlmH (ylmH), cell division protein DivIVA (divIVA), and isoleucine-tRNA synthetase (ileS) genes, complete cds: and unknown gene. //3.6e-09:566:58//AF068901
F-NT2RM4000971//RPC111-53H3.TJ RPC111 Homo sapiens genomic clone R-53H3, genomic survey sequence. //1.0:208:64//AQ053735	F-NT2RM4001454
F-NT2RM4000979//Homo sapiens chromosome 17, clone hRPK.642_C_21, complete sequence. //1.3e-19:207:78//AC005245	F-NT2RM4001455
F-NT2RM4000996//CITB1-EI-2506B10.TF CITB1-EI Homo sapiens genomic clone 2506B10, genomic survey sequence. //1.4e-73:361:98//AQ263651	F-NT2RM4001483//Human zinc finger protein ZNF135. //3.2e-36:329 78//U09367
F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds. //5.1e-170:803:98//AB018272	F-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds. //1.2e-155:724:99//AB014585
F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds. //3.3e-125:584:99//AB014539	F-NT2RM4001519//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces. //0.00019:418:59//AC004688
F-NT2RM4001032//Callus gallus chicken brain factor-2 (CBF-2) mRNA, complete cds. //0.00034:777:58//U47276	F-NT2RM4001522//Human HepG2 3' region Nbo1 cDNA, clone hmd6a08a3. //1.4e-16:130:88//D17274
F-NT2RM4001047//MO25 gene [wice, embryos, mRNA, 2322 nt]. //2.5e-9 2:776:74//S51858	F-NT2RM4001557
F-NT2RM4001054//Canis familiaris sec61 homologue mRNA, complete cds. //3.1e-102:859:76//M96629	F-NT2RM4001565
F-NT2RM4001084//CIT-HSP-2330F9.TR CIT-HSP Homo sapiens genomic clone 2330F9, genomic survey sequence. //4.6e-78:379:99//AQ044479	F-NT2RM4001566
F-NT2RM4001092//cSRL-71b1-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-71b1, genomic survey sequence. //1.1e-12:152:75//B05776	F-NT2RM4001569//HS_2050_B1_C08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2050 Col=15 Row=F, genomic survey sequence. //2.7e-09:109:84//AQ234720
F-NT2RM4001116	F-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds. //1.2e-127:740:89//AF071317
F-NT2RM4001140//Homo sapiens PAC clone DJ0964C11 from 7p14-p15, complete sequence. //1.9e-136:717:93//AC004593	F-NT2RM4001592//Mus musculus mRNA of enhancer-trap-locus 1. //7.3e-11 7:710:88//X69942
F-NT2RM4001151//Streptomyces antibioticus ATP-binding protein and membrane protein (oleC-ORF1, oleC-ORF2, oleC-ORF3, oleC-ORF4, and oleC-ORF5) genes, complete cds: 3427 base-pairs. //0.0083:368:60//L06249	F-NT2RM4001594//Homo sapiens chromosome 9q34, clone 107G20, WORKING DRAFT SEQUENCE, 2 ordered pieces. //0.34:388:59//AC002355
F-NT2RM4001155//Bos taurus 50 kDa protein (adp50) mRNA, complete cds. //3.9e-120:764:85//U04706	F-NT2RM4001597//Mus musculus red-1 gene. //6.2e-139:788:90//X92750
F-NT2RM4001160	F-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds. //3.3e-162:750:99//AB018334
F-NT2RM4001187	F-NT2RM4001611//Synechocystis sp. PCC6803 complete genome, 12/27. 1430419-1576592. //2.5e-05:490:58//D90910
F-NT2RM4001191//CIT-HSP-2010E7.TF CIT-HSP Homo sapiens genomic clone 2010E7, genomic survey sequence. //6.2e-12:181:72//B53378	F-NT2RM4001629//Mus musculus palmytoylated protein p55 mRNA, complete cds. //0.65:186:64//U38196
F-NT2RM4001200//H. sapiens HZF10 mRNA for zinc finger protein. //1.3e-66:799:69//X78933	F-NT2RM4001650//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0435P12: HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces. //0.99:422:59//AC004689
F-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds. //4.2e-152:707:99//AF004828	F-NT2RM4001662//Human mRNA for KIAA0322 gene, partial cds. //2.6e-8 1:449:93//AB002320
F-NT2RM4001204	F-NT2RM4001666
F-NT2RM4001217//Homo sapiens ectoderm-neural cortex-1 protein (EN-C-1) mRNA, complete cds. //1.6e-62:715:70//AF005381	F-NT2RM4001682//Mus musculus clone OST9187, genomic survey sequence. //3.2e-35:240:87//AF046599
F-NT2RM4001256//Human Nott linking clone 924A058R, genomic survey sequence. //7.6e-14:109:90//U49884	F-NT2RM4001710//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE. //1.9e-151:564:97//AL031447
F-NT2RM4001258//HS_3171_B2_C09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3171 Col=18 Row=M, genomic survey sequence. //2.5e-18:215:77//AQ149676	F-NT2RM4001714//Human mRNA for KIAA0202 gene, partial cds. //7.0e-8 5:748:74//D86957
F-NT2RM4001309//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VTA protein pseudogene, EST, GSS, complete sequence. //4.9e-28:5 26:66//AL022163	
F-NT2RM4001313//H. sapiens mRNA for phosphatidylinositol 3-kinase. /	

【0732】

【表433】

F-NT2RM4001715//Human DNA sequence from clone 931K24 on chromosome 20p12. Contains ESTs and GSSs, complete sequence.//1.2e-91:488:94//AL034430

F-NT2RM4001731//Orang-utan involucrin gene, complete cds.//0.40:530:59//M25312

F-NT2RM4001741//Mouse mRNA for talin.//1.1e-129:737:90//X56123

F-NT2RM4001746//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 316G12. WORKING DRAFT SEQUENCE.//2.3e-49:320:89//AL031709

F-NT2RM4001754//Homo sapiens 12p13.3 PAC RPC15-1180D12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//6.3e-64:379:76//AC005831

F-NT2RM4001758//R. norvegicus mRNA for serine/threonine kinase MARK1.//3.7e-146:871:87//Z83868

F-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds.//2.3e-173:803:99//AB018270

F-NT2RM4001783//Homo sapiens clone DJ0981007, complete sequence.//2.0e-165:593:99//AC006017

F-NT2RM4001810

F-NT2RM4001813//Homo sapiens BAC clone NHD364H22 from 2, complete sequence.//7.1e-31:176:84//AC005036

F-NT2RM4001819//Human p58/GTA (galactosyltransferase associated protein kinase) mRNA, complete cds.//4.4e-34:195:95//M37712

F-NT2RM4001823//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//3.3e-51:490:75//U49046

F-NT2RM4001828//Human zinc finger containing protein ZNF157 (ZNF157) mRNA, complete cds.//5.6e-74:688:72//U28687

F-NT2RM4001836//Homo sapiens Chromosome 22q11.2 Cosmid Clone 2h in DCCR Region, complete sequence.//1.0:406:60//AC000076

F-NT2RM4001841//Mus musculus A kinase anchor protein (AKAP-KL) mRNA, alternatively spliced isoform 2, complete cds.//1.6e-131:831:86//AF033275

F-NT2RM4001842//HS_3163_A2_G10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=20 Row=M, genomic survey sequence.//1.5e-05:355:60//AQ168513

F-NT2RM4001856//Caenorhabditis elegans cosmid K08F11.//4.0e-23:823:60//U70855

F-NT2RM4001858//Motophthalmus viridescens NvTbox1 mRNA, partial cds.//6.4e-11:266:66//U64433

F-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CA LC.//6.9e-149:704:98//Y17711

F-NT2RM4001876//F. rubripes GSS sequence, clone 06D022bA4, genomic survey sequence.//5.7e-48:600:68//Z88651

F-NT2RM4001880//CIT-HSP-2348J1, TF CIT-HSP Homo sapiens genomic clone 2348J1, genomic survey sequence.//0.0025:61:88//AQ060809

F-NT2RM4001905//R. norvegicus CYP3A1 gene, 5' flanking region.//2.5e-29:535:67//X98335

F-NT2RM4001922//HS_2237_A1_C10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=19 Row=E, genomic survey sequence.//2.2e-73:364:98//AQ033732

F-NT2RM4001930//Arabidopsis thaliana genomic DNA, chromosome 5, PI clone: MX110, complete sequence.//4.9e-10:269:63//AB005248

F-NT2RM4001938//Homo sapiens chromosome 17, clone hRPC.1081_P_3, complete sequence.//7.6e-152:311:100//AC005207

F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//1.1e-170:808:98//AF098162

F-NT2RM4001953//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B13E4: HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.7e-45:310:85//AC004046

F-NT2RM4001965//Homo sapiens genomic DNA of Bp21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11.//1.6e-107:622:90//AB020868

F-NT2RM4001969//R. norvegicus mRNA for IP63 protein.//3.9e-24:221:76//X99330

F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds.//1.0e-61:527:76//AB018341

F-NT2RM4001984//Human DNA sequence from cosmid U151E3, between markers on chromosome X.//5.8e-07:502:60//Z82253

F-NT2RM4001987//RPC111-49L11.TJ RPC111 Homo sapiens genomic clone R-49L11, genomic survey sequence.//2.6e-33:177:99//AQ051701

F-NT2RM4002013//Homo sapiens chromosome 17, clone hRPC.294_J_22, complete sequence.//0.019:65:90//AC005921

F-NT2RM4002018//Human high molecular weight B cell growth factor mRNA sequence.//1.0:527:57//L15344

F-NT2RM4002034//Human DNA sequence from PAC 84F12 on chromosome Xq25-Xq26.3. Contains glypican-3 precursor (intestinal protein OC15) (GTR2-2), ESTs and CA repeat.//0.11:322:60//AL008712

F-NT2RM4002044//Homo sapiens SS-A/Ro autoantigen 52 kda component gene, complete cds.//0.015:513:61//U01882

F-NT2RM4002054//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.0e-44:473:76//AC005283

F-NT2RM4002055//Homo sapiens mRNA for KIAA0640 protein, partial cds.//1.0e-171:803:98//AB014540

F-NT2RM4002062//Drosophila melanogaster: Chromosome 2L: Region 36B 1-36B3: PI clone D502528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0031:298:59//AC005122

F-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//1.1e-147:705:98//U82267

F-NT2RM4002066//Human mRNA for KIAA0192 gene, partial cds.//3.4e-73:889:69//D83783

F-NT2RM4002067//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H 192), complete sequence.//1.1e-53:295:76//AC005216

F-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//7.8e-25:277:75//AF072758

F-NT2RM4002075//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//9.0e-23:588:61//AF059569

F-NT2RM4002093//Rat PYBP1 mRNA for pyrimidine binding protein 1.//3.1e-68:544:69//X60789

F-NT2RM4002109//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//2.0e-121:762:86//D12646

F-NT2RM4002128//HS_3084_A1_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=7 Row=C, genomic survey sequence.//7.7e-18:117:95//AQ186312

F-NT2RM4002140

F-NT2RM4002145//Homo sapiens chromosome 19, fosmid 37308, complete sequence.//1.8e-49:736:65//AC004152

F-NT2RM4002146//Homo sapiens MACOH mRNA, complete cds.//6.5e-70:454:85//AF035940

F-NT2RM4002161//Homo sapiens mRNA for LAFPTase, isoform 1, partial cds.//4.2e-151:763:95//AJ130763

F-NT2RM4002174//Helicobacter pylori 26695 section 18 of 134 of the complete genome.//2.1e-16:580:60//AE000540

F-NT2RM4002189//Homo sapiens DNA sequence from BAC 722E9 on chromosome 22q13.2-13.33. Contains ESTs.//1.0e-07:792:61//AL008636

F-NT2RM4002194//Mus musculus semaphorin 5A mRNA, complete cds.//3.2e-132:782:87//AF030430

F-NT2RM4002205//Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds.//1.5e-40:292:84//L14684

F-NT2RM4002213

F-NT2RM4002226//Mus musculus p190-B gene, complete cds.//0.099:350:59//U67160

F-NT2RM4002251//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//1.0:428:58//AC004448

F-NT2RM4002256//Mouse genomic DNA, chromosome 17, clone cosmid 49.1, genomic survey sequence.//9.4e-60:294:81//AB005959

F-NT2RM4002266//Fugu rubripes GSS sequence, clone 006118aG12, genomic survey sequence.//3.3e-12:217:67//AL024779

F-NT2RM4002278//HS_3089_A1_E05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3089 Col=9 Row=I, genomic survey sequence.//1.9e-64:381:92//AQ121653

F-NT2RM4002281

F-NT2RM4002287//CIT-HSP-2327E14, TF CIT-HSP Homo sapiens genomic clone 2327E14, genomic survey sequence.//9.0e-49:336:86//AQ042515

F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds.//2.1e-48:511:72//D87457

F-NT2RM4002301//Human NotI linking clone 924A053D, genomic survey sequence.//8.9e-05:62:91//U49881

F-NT2RM4002323//Human DNA sequence from clone 59B16 on chromosome 6p22.1-22.3. Contains a pseudogene similar to GPISG20 and other exonuclease. Contains ESTs, STSs, GSSs, genomic markers D6S1691 and D6S299 and a ca repeat polymorphism, complete sequence.//4.9e-115:729:87//AL032822

F-NT2RM4002339//Homo sapiens PAC clone DJ0728D04, complete sequence.//1.1e-97:457:93//AC004865

F-NT2RM4002344//Caenorhabditis elegans cosmid K04A8.//2.2e-06:190:69//U64849

F-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds.//2.8e-149:708:98//AB014549

F-NT2RM4002374//Homo sapiens 12q24 PAC P336P3 (Research Park Cancer Institute Human Genome PAC library) complete sequence.//0.00040:312:63//AC002978

F-NT2RM4002383//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 469D22. WORKING DRAFT SEQUENCE.//6.8e-29:378:66//AL031284

F-NT2RM4002390

F-NT2RM4002398//CIT-HSP-228B22, TR CIT-HSP Homo sapiens genomic clone 228B22, genomic survey sequence.//3.4e-35:184:100//AQ001110

F-NT2RM4002409//Archaeoglobus fulgidus section 15 of 172 of the complete genome.//2.0e-16:468:59//AE001092

F-NT2RM4002438//Human HLA class III region containing NOTCH4 gene,

【0733】

【表434】

partial sequence, homeobox PBX2 (HPBX) gene, receptor for advanced glycosylation end products (RAGE) gene, complete cds, and 6 unidentified cds, complete sequence.//1.6e-16:123:91//U89336
 F-NT2RM4002446//Human DNA sequence from cosmid 44309 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs, STS and CpG islands.//9.6e-64:467:84//Z92845
 F-NT2RM4002452
 F-NT2RM4002457//Human DNA sequence from PAC 151B14 on chromosome 2 2, complete sequence.//2.2e-24:201:86//Z85988
 F-NT2RM4002460//Homo sapiens PAC clone DJ0630C24 from 7q31-q32, complete sequence.//1.3e-45:487:70//AC004690
 F-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds.//2.7e-163:777:98//AF083255
 F-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds.//2.3e-93:464:97//AB014591
 F-NT2RM4002493
 F-NT2RM4002499//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-41:442:75//AC005484
 F-NT2RM4002504//Human DNA sequence from clone 391022 on chromosome 6p21.2-21.31 Contains pseudogenes similar to ribosomal protein, E STS, GSSs, complete sequence.//3.8e-31:233:87//AL031577
 F-NT2RM4002527//Fugu rubripes GSS sequence, clone 096G17aC8, genomic survey sequence.//7.7e-08:274:62//AL027162
 F-NT2RM4002532
 F-NT2RM4002534
 F-NT2RM4002558//Mus musculus fatty acid transport protein 4 mRNA, partial cds.//3.8e-53:394:81//AF072759
 F-NT2RM4002565//Mus musculus Sec8 mRNA, complete cds.//6.4e-160:90:2:89//AF022962
 F-NT2RM4002567//CITBI-E1-2503J7, TR CITBI-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//8.5e-31:220:88//AQ263402
 F-NT2RM4002571//Rattus norvegicus UDP-GalNAc:polypeptide N-acetylglucosaminyltransferase T5 mRNA, complete cds.//5.2e-05:199:65//AF049344
 F-NT2RM4002593//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//0.89:275:61//AC004875
 F-NT2RM4002594//Drosophila melanogaster, chromosome 2R, region 31C 1-31D6, P1 clone DS08879, complete sequence.//3.7e-44:768:64//AC005454
 F-NT2RM4002623//Drosophila melanogaster; Chromosome 2L; Region 36B 1-36B3; P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.8e-34:574:65//AC005122
 F-NT2RP1000018//Homo sapiens mRNA for NIK, partial cds.//3.9e-111:582:95//AB013385
 F-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP),//1.1e-153:747:96//AJ012449
 F-NT2RP1000040//Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SEQUENCE.//1.6e-125:243:88//AP000047
 F-NT2RP1000063//Caenorhabditis elegans cosmid F31C3, complete sequence.//9.6e-09:414:59//Z92784
 F-NT2RP1000086//H. sapiens mRNA for zinc finger protein, Hsa12.//2.8e-103:548:91//X98834
 F-NT2RP1000101//H. sapiens CpG island DNA genomic MseI fragment, clone 28b4, forward read cpg28b4.ftla.//5.0e-27:163:95//Z60555
 F-NT2RP1000111//CIT-HSP-2307014, TR CIT-HSP Homo sapiens genomic clone 2307014, genomic survey sequence.//1.2e-11:128:81//AQ016069
 F-NT2RP1000112//Human kinase (TTK) mRNA, complete cds.//1.0e-38:32:4:81//M86699
 F-NT2RP1000124//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//0.59:476:59//AL034557
 F-NT2RP1000130//DNA encoding human Hepatoma-derived Growth Factor.//2.7e-35:535:68//E08546
 F-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR2) mRNA, complete cds.//6.7e-05:77:90//AF011792
 F-NT2RP1000170//Homo sapiens clone NH0001PD9, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.9e-20:431:64//AC006030
 F-NT2RP1000174//Homo sapiens clone 24432 mRNA sequence.//2.5e-138:679:97//AF070535
 F-NT2RP1000191
 F-NT2RP1000202//Porcine mRNA for M130 of smooth muscle myosin phosphatase, partial cds.//5.3e-05:220:61//D89496
 F-NT2RP1000243//Drosophila melanogaster DNA sequence (P1 DS05273 (DBO)), complete sequence.//4.7e-51:508:69//AC004373
 F-NT2RP1000259
 F-NT2RP1000272//Mus musculus TLS-associated protein with SR repeat s mRNA, complete cds.//7.8e-142:866:88//AF042383
 F-NT2RP1000324//RPC111-81021.TJ RPC111 Homo sapiens genomic clone R-81021, genomic survey sequence.//2.8e-29:182:92//AQ285136
 F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene e

ncoding mitochondrial protein, complete cds.//4.2e-147:693:98//AF053551
 F-NT2RP1000333//Caenorhabditis elegans cosmid C03D6, complete sequence.//1.4e-08:281:61//Z75525
 F-NT2RP1000348//H. sapiens CpG island DNA genomic MseI fragment, clone 12f1, reverse read cpg12f1.rtlc.//1.7e-09:71:100//Z56610
 F-NT2RP1000357
 F-NT2RP1000358
 5.7e-16:403:61//AC005456
 F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds.//9.8e-125:497:86//AB014538
 F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA, complete cds.//1.8e-176:877:96//AF064594
 F-NT2RP1000409//Homo sapiens repetitive sequences, alphoid DNA, 2482bp.//4.6e-106:700:84//AJ001558
 F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds.//9.4e-178:710:98//AB011159
 F-NT2RP1000416
 F-NT2RP1000418//Oryctolagus cuniculus troponin T cardiac isoform mRNA, 3' end of cds.//1.0:198:60//L40178
 F-NT2RP1000439//HS_2182_A1_D06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=11 Row=G, genomic survey sequence.//2.1e-68:441:87//AQ024305
 F-NT2RP1000443//Homo sapiens genomic DNA, chromosome 21q11.1, segment 18/28, WORKING DRAFT SEQUENCE.//3.8e-57:185:88//AP000047
 F-NT2RP1000460//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//2.7e-132:204:99//AC004453
 F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R2709 0, genomic sequence, complete sequence.//4.9e-80:196:95//AC002985
 F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds.//1.9e-55:440:80//U47634
 F-NT2RP1000481//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronection, Myotendinous antigen)-LIKE gene and a mitochondrial/c chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker DIS2691 and STSs.//2.6e-92:562:88//Z99297
 F-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds.//2.0e-130:622:98//D87686
 F-NT2RP1000513//Xanthomonas campestris campestris xpsD, xpsM, and xpsN genes, complete cds's.//0.11:360:58//M81648
 F-NT2RP1000522//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//4.9e-34:209:93//AC004895
 F-NT2RP1000547//Cricetulus griseus COP-coated vesicle membrane protein Chp24 mRNA, partial cds.//1.2e-08:331:63//U26264
 F-NT2RP1000574//Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA, partial cds.//4.4e-81:295:92//AF017418
 F-NT2RP1000577//HS_2228_B2_C05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=10 Row=F, genomic survey sequence.//1.9e-31:179:75//AQ185128
 F-NT2RP1000581//Pan troglodytes von Willebrand factor (vWF) gene, partial cds.//4.7e-34:223:90//U31620
 F-NT2RP1000609//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC2 69730) containing the hFEN1 gene, complete sequence.//1.6e-18:229:65//AC004770
 F-NT2RP1000629//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//9.3e-89:584:84//M82419
 F-NT2RP1000630//Human DNA sequence from PAC 151B14 on chromosome 2 2 Contains EST, complete sequence.//1.0:203:63//Z85989
 F-NT2RP1000677//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//0.0034:350:61//AC005943
 F-NT2RP1000688//H. sapiens gene for mitochondrial ATP synthase c subunit (P1 form).//5.2e-10:120:80//X69907
 F-NT2RP1000695
 F-NT2RP1000701//Sequence 1 from patent US 5580968.//2.4e-99:624:86//130536
 F-NT2RP1000721//Homo sapiens clone DJ0943F02, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-19:188:81//AC004932
 F-NT2RP1000730
 F-NT2RP1000733//Human chromosome 16p13.1 BAC clone CIT987SK-55169 complete sequence.//1.3e-30:315:75//U95742
 F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2), complete cds.//8.0e-122:604:96//AF101434
 F-NT2RP1000746//HS_3084_A1_H03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=5 Row=0, genomic survey sequence.//1.5e-83:466:92//AQ186344
 F-NT2RP1000767//Homo sapiens full length insert cDNA clone ZD8180 4.//2.8e-21:144:91//AF086442
 F-NT2RP1000782//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//2.1e-121:591:97//AF054840

【0734】

【表435】

F-NT2RP1000796//T. thermophilus phosphofructokinase 1 (PFK1) gene, complete cds.//0.76:263:64//M71213	F-NT2RP1001286//Homo sapiens chromosome X region from filamin (FLN) gene to glucose-6-phosphate dehydrogenase (G6PD) gene, complete cds's.//0.54:292:63//L44140
F-NT2RP1000825//Human DNA sequence from clone 116F5 on chromosome 22q13. Contains part of an unknown gene and part of a RhoGAP (CDC42 GTPase Activating Protein) LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D2ZS1168 and a CA repeat polymorphism, complete sequence.//1.5e-77:163:96//Z93244	F-NT2RP1001294
F-NT2RP1000833//Homo sapiens cGMP-specific phosphodiesterase (PDE9A2) mRNA, complete cds.//1.3e-147:424:96//AF048837	F-NT2RP1001302
F-NT2RP1000834//Homo sapiens alpha-methylacyl-CoA racemase mRNA, complete cds.//1.9e-89:702:79//AF047020	F-NT2RP1001310//Rabbit skeletal muscle mRNA for ryanodine receptor.//1.5e-07:335:64//X15750
F-NT2RP1000836//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2B adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//8.7e-169:842:96//AL022398	F-NT2RP1001311//RPC111-67014.TK RPC111 Homo sapiens genomic clone R-67014, genomic survey sequence.//0.26:80:75//AQ239291
F-NT2RP1000846//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//3.3e-15:196:76//U96629	F-NT2RP1001313//Homo sapiens Chromosome 11q12.2 PAC clone pJ519013 containing human gene for ferritin heavy chain (FTH), complete sequence.//8.8e-75:304:98//AC004228
F-NT2RP1000851//Homo sapiens PAC clone 267011 from 12, complete sequence.//1.6e-144:724:96//AC004812	F-NT2RP1001361//B. taurus Cl-B14.5b mRNA for NADH dehydrogenase (ubiquinone).//2.7e-57:412:84//X68647
F-NT2RP1000856//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//2.1e-121:591:97//AF054840	F-NT2RP1001385
F-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds.//6.7e-106:551:95//AF064094	F-NT2RP1001395//Mus musculus COP9 complex subunit 7a (COPSTa) mRNA, complete cds.//1.4e-72:535:83//AF071316
F-NT2RP1000902//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 31605, WORKING DRAFT SEQUENCE.//0.0097:55:100//Z82199	F-NT2RP1001410//Homo sapiens DNA sequence from PAC 257120 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP207P, CYP208P, CYP206(D), TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS.//5.8e-105:570:94//AL021878
F-NT2RP1000915//H. sapiens genomic DNA fragment (clone J32A032R).//1.3e-30:174:97//Z94761	F-NT2RP1001424
F-NT2RP1000916	F-NT2RP1001432
F-NT2RP1000943//Hylobates lar huntingtin gene, partial exon.//0.19:103:72//L49362	F-NT2RP1001449//Homo sapiens clone 24733 mRNA sequence.//1.7e-84:422:97//AF052149
F-NT2RP1000944//HS_2179_B2_C12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=24 Row=F, genomic survey sequence.//0.032:140:63//AQ065269	F-NT2RP1001457//Xenopus laevis notchless (nle) mRNA, complete cds.//1.3e-47:471:73//AF069737
F-NT2RP1000947//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//3.7e-53:461:78//U62483	F-NT2RP1001466//HS_3006_A2_D08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=16 Row=G, genomic survey sequence.//0.56:289:60//AQ154336
F-NT2RP1000954//cSRL-143CA-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-143C4, genomic survey sequence.//0.030:89:78//B01950	F-NT2RP1001475//H. sapiens genomic DNA fragment (clone NLMA194R).//0.00011:91:79//Z95375
F-NT2RP1000958//Caenorhabditis elegans cosmid K01C8, complete sequence.//3.9e-11:445:61//Z49068	F-NT2RP1001482//Mouse oncogene (ect2) mRNA, complete cds.//4.0e-87:563:85//L11316
F-NT2RP1000959//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//3.3e-57:326:92//AC004263	F-NT2RP1001494
F-NT2RP1000966//Human nucleolin gene, complete cds.//3.4e-64:197:98//M08058	F-NT2RP1001543//Drosophila melanogaster DNA sequence (P1 DSD1142 (D148)), complete sequence.//1.9e-27:387:67//AC004280
F-NT2RP1000980//CIT-HSP-2314B10.TF CIT-HSP Homo sapiens genomic clone 2314B10, genomic survey sequence.//0.32:137:68//AQ017126	F-NT2RP1001546//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//8.0e-63:314:98//AF054840
F-NT2RP1000988//Human chromosome 3p21.1 gene sequence.//8.0e-72:665:80//L13435	F-NT2RP1001569//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.//1.2e-68:514:81//U17343
F-NT2RP1001011//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and THI gene, partial cds.//1.3e-31:497:65//U34925	F-NT2RP1001616//Human clone 23665 mRNA sequence.//7.6e-40:496:74//U0913
F-NT2RP1001013//HS_3068_B1_B09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3068 Col=17 Row=D, genomic survey sequence.//1.0e-24:414:66//AQ127667	F-NT2RP1001665//CIT-HSP-2059M5.TF CIT-HSP Homo sapiens genomic clone 2059M5, genomic survey sequence.//2.4e-45:305:88//B69912
F-NT2RP1001014//HS_3252_B1_B05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=9 Row=D, genomic survey sequence.//0.00052:83:81//AQ304711	F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequence.//1.5e-135:685:96//AF091081
F-NT2RP1001033//Homo sapiens chromosome 17, clone hRPC.1073_F_15, complete sequence.//1.3e-134:241:99//AC004686	F-NT2RP2000006//HS_3061_B2_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3061 Col=6 Row=F, genomic survey sequence.//1.9e-17:394:67//AQ178856
F-NT2RP1001073//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence.//2.5e-59:451:83//AC004993	F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds.//3.5e-14:241:68//AB002390
F-NT2RP1001079//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//4.5e-93:476:96//U82267	F-NT2RP2000008//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 257E24, WORKING DRAFT SEQUENCE.//1.7e-34:147:99//AL034424
F-NT2RP1001080//Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE, 18 unordered pieces.//6.6e-54:217:89//AC004938	F-NT2RP2000027//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence.//1.4e-32:345:75//AC005066
F-NT2RP1001113	F-NT2RP2000032//F. rubripes GSS sequence, clone 060E22aG10, genomic survey sequence.//5.0e-41:445:72//Z88655
F-NT2RP1001177	F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds.//1.9e-76:383:97//AB018290
F-NT2RP1001177//Rattus norvegicus histone macroH2A1.2 mRNA, complete cds.//8.1e-26:373:68//U79139	F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid55 homolog (TID1) mRNA, complete cds.//2.4e-95:467:97//AF061749
F-NT2RP1001185//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-32:388:73//AC006039	F-NT2RP2000054//CIT-HSP-2328J24.TF CIT-HSP Homo sapiens genomic clone 2328J24, genomic survey sequence.//3.3e-39:236:91//AQ043092
F-NT2RP1001199	F-NT2RP2000056//Rat mRNA for protein tyrosine phosphatase epsilon C, partial cds.//3.2e-50:311:90//D78610
F-NT2RP1001247//Homo sapiens signaling molecule LEFTY-A gene, exon 1.//2.0e-29:166:96//AF081508	F-NT2RP2000067//Mus musculus DOC4 (Doc4) mRNA, complete cds.//3.0e-55:766:66//AF058485
F-NT2RP1001248//Homo sapiens Chromosome 11q23 PAC clone pJ356d6, complete sequence.//7.3e-50:128:99//AC002036	F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//2.0e-118:597:95//AC005754
F-NT2RP1001253//Homo sapiens oscillin (hLn) mRNA, complete cds.//4.3e-91:344:93//AF029914	F-NT2RP2000076//Homo sapiens clone NH0263G22, complete sequence.//0.0017:423:60//AC006037
	F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds.//2.1e-77:278:97//AF050079
	F-NT2RP2000079//H. sapiens CpG island DNA genomic MseI fragment, clone 40c2, forward read cpg40c2.f1tk.//3.2e-33:197:95//Z55440
	F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//2.2e-158:752:98//AB018338
	F-NT2RP2000091//HS_2228_A2_B02_MR CIT Approved Human Genomic Sperm

【0735】

【表436】

Library D Homo sapiens genomic clone Plate=2228 Col=4 Row=C, genomic survey sequence.//0.26:55:90//AQ146363
 F-NT2RP2000097
 F-NT2RP2000098//Homo sapiens clone DJ1098J04, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.5e-05:482:60//AC004961
 F-NT2RP2000108//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.0e-22:274:69//AC003973
 F-NT2RP2000114//Homo sapiens mRNA for CM3 synthase, complete cds.//4.9e-114:551:97//AB018356
 F-NT2RP2000120//HS_3000_B1_E03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=5 Row=J, genomic survey sequence.//1.8e-21:129:97//AQ090365
 F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds.//4.2e-119:607:96//AF054177
 F-NT2RP2000133//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.3e-07:339:63//AC004827
 F-NT2RP2000147//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//9.0e-101:638:85//M62419
 F-NT2RP2000153//Human DNA sequence from clone 218J18 on chromosome Xp11.3-11.4. Contains the NDP (Morris Disease (Pseudoglioma)) gene and a CCL3 Splicing Factor pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.45:377:58//AL034370
 F-NT2RP2000157//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//4.0e-73:317:87//AC005924
 F-NT2RP2000161//CIT-HSP-2353L5.TF.1 CIT-HSP Homo sapiens genomic clone 2353L5, genomic survey sequence.//3.0e-14:123:90//AQ263431
 F-NT2RP2000173
 F-NT2RP2000175
 F-NT2RP2000183//F.rubripes GSS sequence, clone 168M02aC2, genomic survey sequence.//3.7e-05:152:66//AL007295
 F-NT2RP2000195//Human DNA sequence from clone 4514 on chromosome 6 q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence.//7.6e-62:170:99//AL023581
 F-NT2RP2000205
 F-NT2RP2000208//Homo sapiens chromosome 19, overlapping cosmid R2 9828 and F25496, complete sequence.//7.2e-80:170:90//AC003030
 F-NT2RP2000224//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-15 ZES, complete sequence.//5.5e-64:400:85//AC004382
 F-NT2RP2000232//Human DNA sequence from PAC 196E23 on chromosome X q26.1-27.2. Contains the TAT-SF1 (HIV-1 transcriptional elongation factor TAT cofactor TAT-SF1) gene, the BRS3 (Bombesin Receptor subtype-3 (Uterine Bombesin Receptor, BRS-3) gene, an unknown gene coding for two isoforms, a predicted CoG island, ESTs and STSs.//2.2e-07:280:66//Z97632
 F-NT2RP2000233//Mus musculus tumor metastasis associated gene product (MAC) mRNA, complete cds.//8.8e-30:508:67//U88401
 F-NT2RP2000239//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//4.0e-79:504:87//AC004056
 F-NT2RP2000248
 F-NT2RP2000257//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y1E3, WORKING DRAFT SEQUENCE.//0.0078:286:60//AL021388
 F-NT2RP2000258//CIT-HSP-2349P21.TF CIT-HSP Homo sapiens genomic clone 2349P21, genomic survey sequence.//5.7e-82:416:97//AQ059184
 F-NT2RP2000270//Homo sapiens chromosome 19, BAC CIT-B-393115 (BC30 1323), complete sequence.//4.5e-29:310:73//AC006116
 F-NT2RP2000274
 F-NT2RP2000283//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//6.3e-20:260:73//X74904
 F-NT2RP2000288
 F-NT2RP2000289
 F-NT2RP2000297//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//4.6e-69:744:70//M27877
 F-NT2RP2000298//Streptomyces coelicolor cosmid 2E9.//4.4e-05:502:59//AL021530
 F-NT2RP2000310//WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.1e-13:173:76//AC006082
 F-NT2RP2000327//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2B adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//8.3e-144:731:95//AL022398
 F-NT2RP2000328//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//1.9e-102:555:90//AL034430
 F-NT2RP2000329//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//6.4e-105:639:87//M25757
 F-NT2RP2000337//HS_2060_B1_E01_MR CIT Approved Human Genomic Sperm

Library D Homo sapiens genomic clone Plate=2060 Col=1 Row=J, genomic survey sequence.//0.78:218:60//AQ243333
 F-NT2RP2000346//Homo sapiens apoptosis associated protein (CADD34) mRNA, complete cds.//3.6e-129:627:97//U83981
 F-NT2RP2000369//HS_2182_B1_B11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=21 Row=D, genomic survey sequence.//2.5e-87:421:99//AQ024835
 F-NT2RP2000412//Human DNA sequence from PAC 12409 on chromosome 6q 21. Contains DNAJ2 (HDJ1) like pseudogene, ESTs, STSs and GSSs.//0.72:170:65//AL021327
 F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds.//5.0e-66:375:93//L28D10
 F-NT2RP2000420//Homo sapiens full length insert cDNA YQ86E07.//9.2e-77:423:93//AF075093
 F-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//2.1e-126:609:96//AF102265
 F-NT2RP2000438//CITB1-E1-2519019.TR CITB1-E1 Homo sapiens genomic clone 2519019, genomic survey sequence.//0.96:61:78//AQ276878
 F-NT2RP2000448//Homo sapiens PAC clone DJ0740002 from 7p14-p15, complete sequence.//7.1e-17:341:67//AC004691
 F-NT2RP2000459//H.sapiens mRNA for imogen 38.//5.7e-21:158:87//Z68747
 F-NT2RP2000498//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//3.2e-11:160:73//Z92844
 F-NT2RP2000503//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//0.0031:187:66//AC005229
 F-NT2RP2000510//Fugu rubripes GSS sequence, clone 066C04aC1, genomic survey sequence.//8.8e-07:179:64//AL026277
 F-NT2RP2000516//Mus musculus testis-specific protein (Tc: test2) gene, wild type, promoter sequence.//0.19:72:81//U21671
 F-NT2RP2000523//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 150C2, WORKING DRAFT SEQUENCE.//5.0e-115:570:96//AL022318
 F-NT2RP2000603//Homo sapiens mRNA for MCM3 import factor, complete cds.//8.4e-37:196:98//AB005543
 F-NT2RP2000617//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.81:354:60//AC005321
 F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//1.3e-149:732:97//AB014514
 F-NT2RP2000644//HS_3211_A1_F06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3211 Col=11 Row=K, genomic survey sequence.//3.6e-42:282:86//AQ175486
 F-NT2RP2000656
 F-NT2RP2000658//CITB1-E1-2518N15.TF CITB1-E1 Homo sapiens genomic clone 2518N15, genomic survey sequence.//0.57:141:66//AQ278386
 F-NT2RP2000668
 F-NT2RP2000678//Homo sapiens clone DJ0891L14, WORKING DRAFT SEQUENCE, 12 unordered pieces.//4.3e-22:433:62//AC004916
 F-NT2RP2000704//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome Systems Human BAC Library) complete sequence.//2.7e-22:270:75//AC005913
 F-NT2RP2000710//Drosophila melanogaster: Chromosome 2L: Region 36B 1-36B3: P1 clone DS02528, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.4e-32:574:64//AC005122
 F-NT2RP2000715//Homo sapiens PAC clone DJ1056K24 from 7p15, complete sequence.//4.8e-113:546:98//AC004540
 F-NT2RP2000731//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42 unordered pieces.//0.97:115:70//AC004965
 F-NT2RP2000758//Human LIM-kinase1 and alternatively spliced LIM-kinase1 (LIMK1) gene, complete cds.//9.7e-16:162:77//U62293
 F-NT2RP2000764//HS_2254_B2_D07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2254 Col=14 Row=H, genomic survey sequence.//0.071:45:95//AQ068887
 F-NT2RP2000809
 F-NT2RP2000812//Egernia stokesii clone EST3 microsatellite.//0.040:158:64//AF069698
 F-NT2RP2000814
 F-NT2RP2000816
 F-NT2RP2000819
 F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds.//1.1e-26:390:70//AB002292
 F-NT2RP2000842//H.sapiens mRNA for G protein-coupled receptor Edg-2.//1.2e-44:255:93//Y09479
 F-NT2RP2000845
 F-NT2RP2000863//Human partial cDNA sequence, clone x874.//5.9e-29:173:94//Z47045
 F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds.//2.4e-140:732:94//AB018284
 F-NT2RP2000892
 F-NT2RP2000931//Homo sapiens mRNA for KIAA0723 protein, complete c

【表437】

- ds. //3.4e-129:610:98//AB018266
 F-NT2RP2000932//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence. //1.8e-37:212:84//AC005014
 F-NT2RP2000938//Human DNA sequence from cosmid RJ14 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16 p13.3. Contains ESTs and CpG island. //1.6e-126:682:93//Z69890
 F-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds. //5.8e-112:533:98//AB018298
 F-NT2RP2000965
 F-NT2RP2000970//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D22S56, complete sequence. //9.2e-101:505:96//AL021393
 F-NT2RP2000985//Homo sapiens chromosome 17, clone hRPK.597_M_12, complete sequence. //1.6e-72:498:82//AC005277
 F-NT2RP2000987//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence. //7.4e-12:171:77//AC002394
 F-NT2RP2001036//Homo sapiens chromosome 17, clone hRPK1096F1, complete sequence. //1.2e-37:390:76//AC004167
 F-NT2RP2001044//HS_2253_B1_G01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=1 Row=N, genomic survey sequence. //0.21:276:61//AQ069224
 F-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488. //3.2e-144:696:97//AB007957
 F-NT2RP2001065
 F-NT2RP2001070//Rattus norvegicus pyridoxine 5'-phosphate oxidase mRNA, complete cds. //4.3e-104:775:81//U91561
 F-NT2RP2001081//Rattus norvegicus synaptotagmin XI mRNA, complete cds. //3.7e-69:488:82//AF000423
 F-NT2RP2001094//Human DNA sequence from PAC 410B11 on chromosome X contains STS. //7.4e-11:490:61//Z86063
 F-NT2RP2001119//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 745C22, WORKING DRAFT SEQUENCE. //5.1e-30:316:76//AL031596
 F-NT2RP2001127//Human mRNA for KIAA0234 gene, complete cds. //1.1e-31:519:63//D87072
 F-NT2RP2001137//HS_2193_B2_D12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2193 Col=24 Row=H, genomic survey sequence. //1.8e-11:136:78//AQ032187
 F-NT2RP2001149//Homo sapiens Chromosome 22q11.2 Cosmid Clone 2h in DGCR Region, complete sequence. //6.2e-29:247:78//AC000076
 F-NT2RP2001168//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog): translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STSS, GSSs, and a putative CpG island, complete sequence. //0.23:207:66//AL009178
 F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds. //2.3e-112:567:96//AB007949
 F-NT2RP2001174//RPC111-5BL2.TK RPC111 Homo sapiens genomic clone R-5BL2, genomic survey sequence. //7.6e-07:196:64//AQ237306
 F-NT2RP2001196
 F-NT2RP2001218
 F-NT2RP2001226//Homo sapiens LERK-6 (EPLG6) gene, exon 1. //1.1e-09:320:65//U92893
 F-NT2RP2001233//Human ZFP-36 mRNA for a zinc finger protein. //6.1e-71:681:72//X51760
 F-NT2RP2001245//HS_3062_B1_F07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3062 Col=13 Row=L, genomic survey sequence. //1.5e-05:268:63//AQ143177
 F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds. //2.5e-106:514:97//AB018353
 F-NT2RP2001271//Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence. //0.32:183:64//AE001430
 F-NT2RP2001290//M.musculus mRNA for 147 clone. //8.6e-102:641:86//X61455
 F-NT2RP2001295//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y105E8, WORKING DRAFT SEQUENCE. //0.20:171:63//AL022594
 F-NT2RP2001312//Bovine synaptophysin mRNA, complete cds. //0.98:253:58//M22967
 F-NT2RP2001327//Human B12 protein mRNA, complete cds. //5.8e-29:359:71//M80783
 F-NT2RP2001328//CIT-HSP-2335AS.TF CIT-HSP Homo sapiens genomic clone 2335AS, genomic survey sequence. //1.3e-65:366:94//AQ038539
 F-NT2RP2001347//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease. //3.8e-31:325:77//AJ003147
 F-NT2RP2001366//H.sapiens CpG island DNA genomic MseI fragment, clone 4e11, forward read cpG4e11 fla. //1.7e-12:98:92//Z61305
 F-NT2RP2001378//HS_3054_B2_A03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=6 Row=B, genomic survey sequence. //9.8e-17:131:89//AQ100721
 F-NT2RP2001381//Arabidopsis thaliana BAC T2LS. //0.080:434:59//AF096371
 F-NT2RP2001392//S.pristinaespiralis snbC gene & snbDE gene. //0.019:267:59//Y11548
 F-NT2RP2001394//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS. CpG islands and polymorphic CA repeat. //1.9e-16:133:78//Z93242
 F-NT2RP2001397//Bos taurus cyclin B2 (CYCB2) mRNA, complete cds. //1.3e-63:419:84//AF080219
 F-NT2RP2001420//Mus musculus nuclear protein NIP45 mRNA, complete cds. //3.1e-98:747:79//U76759
 F-NT2RP2001423//Xenopus laevis ER1 mRNA, complete cds. //3.7e-34:269:85//AF015454
 F-NT2RP2001427//Homo sapiens Chromosome 2p13 BAC Clone h173, complete sequence. //3.2e-13:164:78//AC003065
 F-NT2RP2001436//Mus musculus clone OST1784, genomic survey sequence. //3.0e-06:136:71//AF046702
 F-NT2RP2001440//cDNA sequence coding for gamma protein. //7.9e-83:553:86//E02350
 F-NT2RP2001445//P.falciparum complete gene map of plastid-like DNA (IR-A). //1.5e-09:829:57//X95275
 F-NT2RP2001449//B.taurus mRNA for cleavage and polyadenylation specificity factor. //1.3e-136:766:90//X75931
 F-NT2RP2001450
 F-NT2RP2001467
 F-NT2RP2001506//CIT-HSP-2374H21.TF CIT-HSP Homo sapiens genomic clone 2374H21, genomic survey sequence. //7.9e-14:151:80//AQ109561
 F-NT2RP2001511//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds. //2.6e-22:462:64//AF005355
 F-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALARI. //2.0e-136:657:97//Y14494
 F-NT2RP2001526//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence. //1.2e-37:357:64//AC004596
 F-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds. //1.6e-103:384:94//AF035586
 F-NT2RP2001560
 F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488. //4.4e-123:590:98//AB007957
 F-NT2RP2001576//Schistocerca americana Antennapedia homeotic protein (Antp) mRNA, complete cds. //0.038:580:58//U32943
 F-NT2RP2001581//Mus musculus semaphorin VIa mRNA, complete cds. //6.5e-09:222:66//AF030430
 F-NT2RP2001597//Homo sapiens alpha2-C4-adrenergic receptor gene, complete cds. //0.0057:361:60//U72648
 F-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds. //7.2e-137:647:98//AB018340
 F-NT2RP2001613
 F-NT2RP2001628//H.sapiens (xsl28) mRNA, 380bp. //1.7e-15:279:68//Z36784
 F-NT2RP2001634//Homo sapiens alpha-catenin-like protein (CTNNA1) mRNA, complete cds. //5.4e-123:606:96//AF030233
 F-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mRNA, complete cds. //4.2e-144:687:97//AF058718
 F-NT2RP2001663//H.sapiens mRNA for 2-phosphopyruvate-hydratase-alphha-enolase. //1.0e-36:372:74//X84907
 F-NT2RP2001675//S.pombe chromosome 1 cosmid c2G11. //0.070:507:59//Z54354
 F-NT2RP2001677//Mouse BAC CitbCJ7 219m7, genomic sequence, complete sequence. //2.0e-60:232:96//AC005259
 F-NT2RP2001678//HS_2007_A2_A04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2007 Col=8 Row=A, genomic survey sequence. //7.3e-62:370:91//AQ269699
 F-NT2RP2001699//RPC111-57B17.TK RPC111 Homo sapiens genomic clone R-57B17, genomic survey sequence. //0.99:141:63//AQ115592
 F-NT2RP2001720//Homo sapiens PAC clone DJ0167F23 from Tpl5, complete sequence. //9.4e-117:604:95//AC004079
 F-NT2RP2001721//Homo sapiens DNA sequence from clone 46618 on chromosome Xq11.1-13.2. Contains an unknown gene similar to Coagulation Factor V (Activated Protein C Cofactor), Coagulation Factor VIII (Procoagulant Component) and Ceruloplasmin (EC 1.16.3.1, Ferroxidase). Contains ESTs and an STS, complete sequence. //1.0:273:61//AL030998
 F-NT2RP2001740//Homo sapiens Chromosome 22q11.2 Cosmid Clone 8c in DGCR Region, complete sequence. //1.0:356:62//AC000090
 F-NT2RP2001748//Human mRNA for KIAA0003 gene, complete cds. //3.7e-

【0737】

【表438】

18:151:86//D14697	F-NT2RP2001762//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC26 2482), complete sequence.//6.0e-145:715:97//AC004783	F-NT2RP2002154//Mus musculus mRNA for myosin, complete cds.//1.0:2 58:63//D85923
F-NT2RP2001813//Plasmodium falciparum chromosome 2, section 15 of 73 of the complete sequence.//0.38:340:60//AE001378	F-NT2RP2002172//HS_3020_B1_H02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3020 Col=3 Row=P, genomic survey sequence.//1.2e-11:124:82//AQ093169	F-NT2RP2002185//RPC111-67B15.TJ RPC111 Homo sapiens genomic clone R-67B15, genomic survey sequence.//2.8e-18:109:100//AQ201833
F-NT2RP2001839//HS_3000_B1_C07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=13 Row=F, genomic survey sequence.//0.026:253:60//AQ090347	F-NT2RP2002192//Human PM-Scl-75 autoantigen (PM-scl), complete cds.//2.7e-36:353:78//U09215	F-NT2RP2002193//Rattus norvegicus potassium channel regulatory protein KChAP mRNA, complete cds.//9.5e-82:477:89//AF032872
F-NT2RP2001861//Homo sapiens mRNA for paraplegin.//0.89:146:71//Y1 6610	F-NT2RP2002208	F-NT2RP2002219//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//1.0:378:58//AL034557
F-NT2RP2001869//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//0.040:174:62//AF027219	F-NT2RP2002231//Plasmodium falciparum 307 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.6:560:56//AC005308	F-NT2RP2002235//P. falciparum glutamic acid-rich protein gnen, complete cds.//0.59:341:60//J03998
F-NT2RP2001876//Cyprinus carpio mRNA for allograft inflammatory factor-1, complete cds.//2.8e-44:483:71//AB012309	F-NT2RP2002252//Mus musculus mSin3A (sin3A) mRNA, complete cds.//3.5e-81:398:87//U22394	F-NT2RP2002259//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 118J21, WORKING DRAFT SEQUENCE.//9.7e-67:340:89//AL0335 27
F-NT2RP2001883//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein n, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG island, complete sequence.//1.8e-87:496:92//AL031864	F-NT2RP2002256//Homo sapiens retinoidic acid hydroxylase mRNA, complete cds.//6.6e-50:315:89//AF005418	F-NT2RP2002270//RPC111-77C23.TV RPC111 Homo sapiens genomic clone R-77C23, genomic survey sequence.//2.9e-18:79:93//AQ268098
F-NT2RP2001898//Human inositol polyphosphate 5-phosphatase (Sptase) mRNA, 3' end.//9.2e-112:633:90//N74161	F-NT2RP2002292//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 321D2, WORKING DRAFT SEQUENCE.//1.0:290:60//AL031033	F-NT2RP2002292//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 321D2, WORKING DRAFT SEQUENCE.//1.0:290:60//AL031033
F-NT2RP2001900//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone R08A5, WORKING DRAFT SEQUENCE.//0.0026:360:62//Z82281	F-NT2RP2002312//Homo sapiens CDP-diacetyl glycerol synthase 2 (CD52) mRNA, partial cds.//1.5e-93:467:96//AF069532	F-NT2RP2002316//HS_2171_B2_D11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2171 Col=22 Row=H, genomic survey sequence.//7.3e-94:463:97//AQ119673
F-NT2RP2001907//H. sapiens CpG island DNA genomic MseI fragment, clone 97111, forward read cpg97111.ftla.//4.2e-26:206:84//Z64125	F-NT2RP2002325//Homo sapiens mRNA for Pex1lp, complete cds.//3.9e-123:640:95//AB015594	F-NT2RP2002333
F-NT2RP2001926//Plasmodium falciparum 307 chromosome 12 PFYAC59 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.5e-06:621:59//AC004688	F-NT2RP2002373//F. rubripes GSS sequence, clone 026F10aB8, genomic survey sequence.//0.46:234:61//Z87330	F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//9.4e-138:673:97//AF038958
F-NT2RP2001936//cSRL-47D9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-47D9, genomic survey sequence.//3.1e-50:282:93//B04856	F-NT2RP2002408//F. rubripes GSS sequence, clone 080G11aB8, genomic survey sequence.//5.7e-15:220:71//AL015615	F-NT2RP2002394//P. falciparum complete gene map of plastid-like DNA (IR-A).//0.79:421:56//X95275
F-NT2RP2001943//Drosophila melanogaster cosmid 25EB.//0.00036:248:60//AL009196	F-NT2RP2002426//Sus scrofa SCAMPI gene, exon 9.//7.1e-71:582:80//AJ223742	F-NT2RP2002439//Caenorhabditis elegans cosmid T07D3.//0.0018:210:67//AF016682
F-NT2RP2001946//Homo sapiens clone NH0140K04, complete sequence.//3.8e-78:232:99//AC005033	F-NT2RP2002442//Caenorhabditis elegans cosmid T03F1.//2.8e-18:295:67//U88169	F-NT2RP2002457//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M 2, complete sequence.//1.9e-06:281:66//AC004381
F-NT2RP2001947//Homo sapiens full length insert cDNA clone ZDB180 4.//2.0e-28:172:94//AF086442	F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds.//0.03 9:207:63//D42045	F-NT2RP2002475
F-NT2RP2001969//H. sapiens CpG island DNA genomic MseI fragment, clone 152a8, reverse read cpg152a8.ftla.//1.0e-20:123:99//Z59378	F-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//2.4e-123:607:96//AB005289	F-NT2RP2002498//Arabidopsis thaliana BAC F3D13.//0.73:395:57//AF06 9300
F-NT2RP2001975	F-NT2RP2002503//Homo sapiens, clone hRPK.15_A.1, complete sequence.//7.2e-18:134:90//AC006213	F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds.//1.2e-157:761:97//AB018334
F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds.//0.0023:235:62//AB011117	F-NT2RP2002520	F-NT2RP2002520
F-NT2RP2001991//Rat orphan transporter v7-3 (NTT73) mRNA, complete cds.//3.1e-35:180:80//L22022	F-NT2RP2002537	F-NT2RP2002546//Homo sapiens Chromosome 11q12 pac pDJ741n15, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.83:252:60//AC004127
F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds.//9.8e-61:314:97//AB018299	F-NT2RP2002549//Human Chromosome 15q26.1 PAC clone pDJ457j11 containing DNA polymerase gamma (polg) gene, complete sequence.//5.9e-9 3:186:99//AC005317	F-NT2RP2002591//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE.//4.0e-38:175:78//Z98304
F-NT2RP2002032//Homo sapiens chromosome 5, BAC clone 5e9 (LBML H22 0), complete sequence.//0.76:189:65//AC005895	F-NT2RP2002606//Rattus norvegicus Rabin3 mRNA, complete cds.//1.9 e-43:282:87//U019181	F-NT2RP2002609//Mus musculus defender against death 1 (DAD1) gene, partial cds.//1.5e-11:99:90//AF051310
F-NT2RP2002033//Homo sapiens clone DJ029120, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.9e-12:160:79//AC004825		
F-NT2RP2002041//Human BAC clone RG035E18 from 7q31, complete sequence.//0.0014:123:73//AC004029		
F-NT2RP2002046//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems Human BAC library) complete sequence.//2.2e-85:722:77//AC004552		
F-NT2RP2002047//Human DNA sequence from clone 21F7 on chromosome 6 q16.1-21. Contains part of an exon of a putative new gene and STSs and GSSs, complete sequence.//0.13:350:61//AL033375		
F-NT2RP2002058//S. cerevisiae chromosome XII reading frame ORF YLR1 29w.//9.7e-11:480:60//Z73301		
F-NT2RP2002066//Rattus norvegicus transmembrane receptor Unc5H2 mRNA, complete cds.//6.5e-97:610:86//U87306		
F-NT2RP2002070//beta -ADD=adducin beta subunit 63 kda isoform/membrane skeleton protein, beta -ADD=adducin beta subunit 63 kda isoform/membrane skeleton protein (alternatively spliced, exon 10 to 13 region) [human, Genomic, 1851 nt, segment 3 of 3].//0.0059:107:73//S81083		
F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.//1.0e-127: 643:96//AF052183		
F-NT2RP2002078//F12016-T7.1 IQF Arabidopsis thaliana genomic clone F12016, genomic survey sequence.//0.14:191:64//AQ249805		
F-NT2RP2002079//Homo sapiens clone DJ0892G19, complete sequence.//0.0094:325:60//AC004917		
F-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein n.//9.8e-111:533:97//AJ007509		
F-NT2RP2002105//H. sapiens CpG island DNA genomic MseI fragment, clone 10h8, forward read cpg10h8.ftla.//2.4e-29:178:94//Z58857		
F-NT2RP2002124//CIT-HSP-2023E9.TF CIT-HSP.Homo sapiens genomic clone 2023E9, genomic survey sequence.//2.5e-32:202:92//B64468		
F-NT2RP2002137//Human plasma membrane calcium ATPase (hPMCA4) mRNA, complete cds.//0.095:319:59//M25874		

【0738】

【表439】

F-NT2RP2002618//H.sapiens mRNA for arginine methyltransferase, splice variant, 1316 bp.//5.6e-27:460:63//Y10806

F-NT2RP2002621

F-NT2RP2002643//Rat calmodulin III gene for calmodulin, promoter region and exon 1.//0.023:322:60//D90397

F-NT2RP2002672//Homo sapiens chromosome 10 clone CIT-HSP-1326H7 map 10q24.3-10q25.1, complete sequence.//3.9e-149:794:94//AC005384

F-NT2RP2002701//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.//9.2e-10:129:75//AL034380

F-NT2RP2002706//S.griseus secA gene.//1.3e-05:311:63//Y10980

F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete cds.//2.5e-40:631:65//AB014572

F-NT2RP2002727//Rattus norvegicus tulip 2 mRNA, complete cds.//4.8e-65:600:73//AF041107

F-NT2RP2002736//S.pombe chromosome II cosmid c887.//0.17:352:58//AL033388

F-NT2RP2002740//Absidia glauca ORF, 3' end: (+) mating type surface protein (PSSP15) gene, complete cds: ORF, 5' end.//0.0073:274:56//M94861

F-NT2RP2002741//Homo sapiens mRNA for Neuroblastoma, complete cds.//7.5e-29:628:62//D89016

F-NT2RP2002750//Homo sapiens Xp22 Bins 35-37 BAC GSHB-214D18 (Genome Systems Human BAC Library) complete sequence.//3.6e-31:568:67//AC005296

F-NT2RP2002752//Human BAC clone RG317M02 from Tp15-p21, complete sequence.//1.7e-08:206:63//AC002433

F-NT2RP2002753//Human DNA sequence from cosmid B1187 on chromosome 22 contains ESTs.//2.8e-71:195:89//Z82171

F-NT2RP2002769//Streptomyces fradiae ty lactone synthase, starter module and modules 1-7, (tylG) gene, complete cds.//0.0016:412:60//U78289

F-NT2RP2002778//CIT-HSP-2059C5.TF CIT-HSP Homo sapiens genomic clone 2059C5, genomic survey sequence.//6.8e-18:186:79//B69837

F-NT2RP2002800

F-NT2RP2002839//Homo sapiens Chromosome 11q12.2 PAC clone pJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.2e-41:134:94//AC006078

F-NT2RP2002857//Rat T-cell receptor active beta-chain V-region (V-beta5-J-beta2.5) mRNA, partial cds, clone TRB-4.//0.85:93:68//M18845

F-NT2RP2002862//HS_3084_A1_H03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=5 Row=0, genomic survey sequence.//5.0e-67:390:91//AQ186344

F-NT2RP2002880

F-NT2RP2002891//CIT-HSP-2310014.TF CIT-HSP Homo sapiens genomic clone 2310014, genomic survey sequence.//0.11:53:90//AQ019792

F-NT2RP2002925//Pig mRNA for carbonyl reductase, complete cds.//0.66:194:65//D16511

F-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//2.3e-135:628:99//AF038392

F-NT2RP2002929//F.rubripes GSS sequence, clone 123123a1, genomic survey sequence.//3.9e-06:66:83//AL017246

F-NT2RP2002939

F-NT2RP2002954

F-NT2RP2002959//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//1.3e-47:411:79//U62483

F-NT2RP2002979//CIT-HSP-2340012.TF CIT-HSP Homo sapiens genomic clone 2340012, genomic survey sequence.//4.6e-96:476:97//AQ057233

F-NT2RP2002980//Sequence 20 from Patent EP0705842.//4.0e-13:100:94//A52230

F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.4e-09:272:61//AF059569

F-NT2RP2002987//Homo sapiens (subclone 6_d9 from P1 H21) DNA sequence, complete sequence.//1.0e-22:293:67//AC000958

F-NT2RP2002993//Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA, complete cds.//4.0e-74:502:84//AF025424

F-NT2RP2003000//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces.//2.3e-46:474:76//AC004765

F-NT2RP2003034//Homo sapiens chromosome 17, clone hRPK.849_N_15, complete sequence.//4.2e-23:202:82//AC005703

F-NT2RP2003073//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//3.4e-59:330:82//Z83822

F-NT2RP2003099//HS_3008_B2_C09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3008 Col=18 Row=F, genomic survey sequence.//1.4e-71:362:96//AQ089786

F-NT2RP2003108//Sequence 59 from patent US 5773577.//0.95:123:69//AR014362

F-NT2RP2003117//HS_2034_B2_D12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2034 Col=24 Row=H, genomic survey sequence.//1.5e-88:461:96//AQ230797

F-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//4.3e-46:470:72//AF079765

F-NT2RP2003125//Homo sapiens chromosome 19, cosmid R34382, complete sequence.//5.7e-10:436:61//AC005329

F-NT2RP2003129//P.thunbergii cab gene.//0.00044:541:60//X61915

F-NT2RP2003137//CIT-HSP-2300J6.TR CIT-HSP Homo sapiens genomic clone 2300J6, genomic survey sequence.//5.0e-78:393:97//AQ012976

F-NT2RP2003157//Human DNA sequence from cDNA 16pHQC:16 from chromosome 16p13.3.//5.4e-07:137:71//Z84716

F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, complete cds.//1.8e-111:581:93//D67025

F-NT2RP2003161//CITB1-E1-2506E20.TR CITB1-E1 Homo sapiens genomic clone 2506E20, genomic survey sequence.//0.0025:156:67//AQ262657

F-NT2RP2003164

F-NT2RP2003165//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Ro Ret gene, and sodium phosphate transporter (NPT3) gene, complete cds.//1.4e-43:334:79//U91328

F-NT2RP2003177//Human signaling inositol polyphosphate 5 phosphatase SIP-110 mRNA, complete cds.//0.91:346:62//U50040

F-NT2RP2003194//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 996020, WORKING DRAFT SEQUENCE.//1.7e-108:511:90//AL031597

F-NT2RP2003206

F-NT2RP2003228//H.sapiens P1-Cdc21 mRNA.//2.9e-136:726:93//X74794

F-NT2RP2003230//Rattus norvegicus endo-alpha-D-mannosidase (Enman) mRNA, complete cds.//2.6e-51:348:86//AF023657

F-NT2RP2003237//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE.//2.6e-56:415:83//AL031447

F-NT2RP2003243//RPC111-36J1.TP RPC111 Homo sapiens genomic clone RPC111-36J1, genomic survey sequence.//2.1e-16:112:93//AQ047107

F-NT2RP2003265//Muridae sp. (mouse-rat, neuroblastoma-glioma hybrid cell line NGD5) mRNA, complete cds.//6.0e-114:696:87//L38481

F-NT2RP2003272//RPC111-67B15.TJ RPC111 Homo sapiens genomic clone R-67B15, genomic survey sequence.//3.8e-16:110:94//AQ201833

F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.5e-145:714:96//AB014525

F-NT2RP2003280//RPC111-1412.TVB RPC111 Homo sapiens genomic clone RPC111-1412, genomic survey sequence.//6.4e-77:400:95//B85286

F-NT2RP2003286//CIT-HSP-2336D3.TF CIT-HSP Homo sapiens genomic clone 2336D3, genomic survey sequence.//5.3e-29:287:73//AQ041024

F-NT2RP2003293//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.5e-54:508:74//AC003973

F-NT2RP2003295//Homo sapiens RNP mRNA for RPB5 meidating protein, complete cds.//6.1e-85:416:97//AB006572

F-NT2RP2003297//S.pombe pho2 gene for specific p-nitrophenylphosphate.//0.60:309:64//X62722

F-NT2RP2003307//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//1.0e-45:442:75//AF055666

F-NT2RP2003308//D.melanogaster crn mRNA.//1.1e-63:697:70//X58374

F-NT2RP2003329//Homo sapiens chromosome 17, clone hCIT.131_K_11, complete sequence.//0.040:145:64//AC005288

F-NT2RP2003339

F-NT2RP2003347//Plasmodium falciparum MAL3P7, complete sequence.//0.12:275:60//AL034559

F-NT2RP2003367//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//0.83:225:63//AC005510

F-NT2RP2003391

F-NT2RP2003393//HS_3218_A2_B09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=18 Row=C, genomic survey sequence.//0.021:93:79//AQ204356

F-NT2RP2003394

F-NT2RP2003401

F-NT2RP2003433//Rattus rattus sec61 homologue mRNA, complete cds.//4.2e-61:533:75//M96630

F-NT2RP2003445//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1/5, WORKING DRAFT SEQUENCE.//2.1e-49:301:72//AP000023

F-NT2RP2003446

F-NT2RP2003456//Rickettsia prowazekii strain Madrid E, complete genome: segment 3/4.//0.0018:366:60//AJ235272

F-NT2RP2003466//Homo sapiens chromosome 11, BAC CIT-HSP-311a8 (BC2 69730) containing the hFEM1 gene, complete sequence.//7.5e-16:189:68//AC004770

F-NT2RP2003480//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.9e-25:197:85//M21977

F-NT2RP2003499

2.1e-08:408:61//AB000826

F-NT2RP2003506//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE.

【0739】

【表440】

CE, 12 unordered pieces.//1.9e-33:192:96//AC005236	F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds.//2.1e-28:165:96//AB014458
F-NT2RP2003511//Ceratomyces richardii mRNA for CRHB11, partial cds.//1.0:328:60//AB013801	F-NT2RP2003976//Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP2 1/22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSRE, p58/GTA, Galactosyl transferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae) bacterial, worm and yeast hypothetical genes, and the GMB1 gene for Guanine Nucleotide Binding Protein (G protein), Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG island s, ESTs, STSs and GSSs, complete sequence.//2.6e-24:298:74//AL031282
F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds.//7.3e-76:403:93//D87460	F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds.//9.9e-160:783:96//AB018347
F-NT2RP2003517//Human osteosarcoma cell line U-2 OS mRNA fragment for PDGF-B chain (PDGF= platelet-derived growth factor).//1.5e-24:151:95//X03702	F-NT2RP2003984
F-NT2RP2003522//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end.//1.3e-101:564:91//M21977	F-NT2RP2003986//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.7e-26:260:77//AC000382
F-NT2RP2003533//Human DNA sequence from cosmid F1121 on chromosome 6.//2.0e-40:315:75//Z80899	F-NT2RP2003988//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE.//9.1e-61:701:70//AL031681
F-NT2RP2003543	F-NT2RP2004013//Human DNA sequence from clone 372K1 on chromosome 6q24 Contains EST, STS, GSS and CpG island, complete sequence.//3.0e-123:693:91//AL023580
F-NT2RP2003559//H. sapiens CpG island genomic MseI fragment, clone 90a5, reverse read cpg90a5.r11a.//1.1e-20:122:99//Z56144	F-NT2RP2004014
F-NT2RP2003564//Human 52-kD ribonucleoprotein Ro/SSA mRNA, complete cds.//8.8e-27:664:63//M34551	F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127, complete sequence.//5.8e-83:427:87//AC004780
F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cds.//4.1e-113:541:98//AB007931	F-NT2RP2004042
F-NT2RP2003581	F-NT2RP2004056//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 134019, WORKING DRAFT SEQUENCE.//5.6e-110:528:98//AL034555
F-NT2RP2003596//F. rubripes GSS sequence, clone 036L10aF12, genomic survey sequence.//1.9e-11:210:65//AL012756	F-NT2RP2004081
F-NT2RP2003604//Homo sapiens alpha-catenin-like protein (CTNNA1) mRNA, complete cds.//1.9e-123:587:98//AF030233	F-NT2RP2004098//HS_2216_A1_B12_MF CIT Approved Human Sperm Library D Homo sapiens genomic clone Plate=2216 Col=23 Row=C, genomic survey sequence.//1.0e-07:86:84//AQ145694
F-NT2RP2003629	F-NT2RP2004124//HS_3064_B2_A04_MF CIT Approved Human Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.0e-25:155:94//AQ136993
F-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase.//7.8e-88:582:84//AJ006215	F-NT2RP2004142//Arabidopsis thaliana genomic DNA, chromosome 5, TA clone: K8K14, complete sequence.//1.0:220:62//AB007645
F-NT2RP2003668//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//5.6e-47:335:83//AC005081	F-NT2RP2004152//Drosophila melanogaster DNA sequence (P1 DS02252 (DS7)), complete sequence.//0.93:480:56//AC002493
F-NT2RP2003687//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//1.2e-06:133:74//AC003684	F-NT2RP2004165//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-42 0 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.051:265:61//AC005140
F-NT2RP2003691//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 525L6, WORKING DRAFT SEQUENCE.//1.7e-47:337:81//AL023807	F-NT2RP2004170//Homo sapiens distal-less homeobox protein (DLX1) gene, complete cds.//1.0:162:66//AF028235
F-NT2RP2003702//Rattus norvegicus ovarian-specific protein mRNA, complete cds.//1.3e-65:458:82//U44803	F-NT2RP2004172//S. pombe chromosome 11 cosmid c24E9.//1.7e-06:466:59//AL021816
F-NT2RP2003704//H. sapiens CpG island genomic MseI fragment, clone 2a9, reverse read cpg2a9.r11a.//3.8e-17:170:84//Z60615	F-NT2RP2004187//Homo sapiens full length insert cDNA YQ86E07.//3.5e-17:354:64//AF075093
F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds.//2.6e-108:518:98//AB011097	F-NT2RP2004194//Rattus norvegicus Golgi SNARE GS15 mRNA, complete cds.//9.4e-53:397:82//AF003998
F-NT2RP2003713//HS_2016_B1_B05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=9 Row=D, genomic survey sequence.//1.3e-11:102:90//AQ226895	F-NT2RP2004196
F-NT2RP2003714//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.4e-27:249:78//AC003973	F-NT2RP2004207//Human von Willebrand factor pseudogene corresponding to exons 23 through 34.//0.0023:386:61//M60676
F-NT2RP2003727//RPC111-77119.TV RPC111 Homo sapiens genomic clone R-77119, genomic survey sequence.//3.4e-26:294:74//AQ268303	F-NT2RP2004226//HS_2186_A1_D03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2186 Col=5 Row=C, genomic survey sequence.//7.8e-58:370:87//AQ063813
F-NT2RP2003737//Homo sapiens clone DJ1022114, WORKING DRAFT SEQUENCE, 14 unordered pieces.//2.6e-74:194:91//AC004951	F-NT2RP2004232//H. sapiens mRNA for protein kinase C mu.//1.2e-34:448:67//X75756
F-NT2RP2003751//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-911E12, complete sequence.//1.7e-92:165:96//AC003964	F-NT2RP2004239//Homo sapiens lok mRNA for protein kinase, complete cds.//5.2e-108:510:99//AB015718
F-NT2RP2003760//B. primigenius mRNA for coat protein gamma-cop.//4.5e-76:696:73//X92987	F-NT2RP2004240//Pyrococcus horikoshii OT3 genomic DNA, 1166001-1485000 nt. position (6/7).//1.1e-12:489:61//AP000006
F-NT2RP2003764//Homo sapiens gene for MTG16, exon 1b, partial sequence.//1.0:109:69//AB013275	F-NT2RP2004242
F-NT2RP2003769	F-NT2RP2004245
F-NT2RP2003770//Homo sapiens chromosome 17, clone hRPC.1050_D_4, complete sequence.//3.0e-96:467:98//AC004771	F-NT2RP2004270//Streptomyces coelicolor cosmid 1A9.//7.5e-07:462:62//AL034446
F-NT2RP2003777	F-NT2RP2004300//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//3.5e-11:299:64//AC005781
F-NT2RP2003781//tricarboxylate carrier [rats, liver, mRNA Partial, 2986 nt].//7.2e-107:731:82//S70011	F-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds.//4.5e-150:735:97//AF000416
F-NT2RP2003793//CIT-HSP-2326L12.TF CIT-HSP Homo sapiens genomic clone 2326L12, genomic survey sequence.//7.0e-20:124:95//AQ038761	F-NT2RP2004321//Drosophila melanogaster DNA sequence (P1 DS02110 (D147)), complete sequence.//0.98:267:59//AC004423
F-NT2RP2003825//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//8.9e-06:151:74//AC004491	F-NT2RP2004339//Human Chromosome 16 BAC clone CIT987SK-A-355G7, complete sequence.//1.6e-40:419:75//AC002519
F-NT2RP2003840//Arabidopsis thaliana chromosome 11 BAC F12A24 genomic sequence, complete sequence.//0.018:145:69//AC005167	F-NT2RP2004347//Human DNA sequence *** SEQUENCING IN PROGRESS ***
F-NT2RP2003857//HS_3227_A2_C04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3227 Col=8 Row=W, genomic survey sequence.//0.96:257:61//AQ030467	
F-NT2RP2003859	
F-NT2RP2003871//Homo sapiens 12q24 PAC RPC11-74B13 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.0e-12:369:65//AC002375	
F-NT2RP2003885//CITB1-E1-2514D6.TF CITB1-E1 Homo sapiens genomic clone 2514D6, genomic survey sequence.//0.13:167:64//AQ265722	
F-NT2RP2003912//nekl-serine/threonine- and tyrosine-specific protein kinase [wice, erythroleukemia cells, mRNA, 4263 nt].//1.3e-136:838:86//S45828	
F-NT2RP2003952	

【0740】

【表441】

from clone 1018D12, WORKING DRAFT SEQUENCE.//1.2e-72:439:82//AL031650
 F-NT2RP2004364
 F-NT2RP2004365
 F-NT2RP2004366//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3. Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG island, complete sequence.//0.92:427:57//AL031864
 F-NT2RP2004373//Homo sapiens cosmid Qc15C1 and 94B6 from Xq28, complete sequence.//2.6e-26:493:65//AF035397
 F-NT2RP2004389//HS_2183_B2_H04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=8 Row=P, genomic survey sequence.//2.9e-11:83:96//AQ063969
 F-NT2RP2004392
 F-NT2RP2004396//Homo sapiens BAC clone RG135C18 from Tq21, complete sequence.//1.1e-171:875:95//AC005164
 F-NT2RP2004399//Homo sapiens SYBL1 gene.//1.4e-24:467:64//AJ004799
 F-NT2RP2004400//Arabidopsis thaliana BAC T19B17 from chromosome IV, near 19.3 cM, complete sequence.//0.00074:455:59//AF069441
 F-NT2RP2004412//H.sapiens CpG island DNA genomic MseI fragment, clone 34g4, reverse read cpg34g4.rta.//5.0e-27:154:98//Z65369
 F-NT2RP2004425
 F-NT2RP2004463//Streptomyces coelicolor cosmid ZER.//0.0053:196:65//AL021530
 F-NT2RP2004476//Drosophila melanogaster cosmid 67A9.//5.2e-15:377:63//AL034388
 F-NT2RP2004490//Homo sapiens chromosome 16, PI clone 94-10H (LANL), complete sequence.//4.3e-100:497:97//AC005591
 F-NT2RP2004512//Plasmodium falciparum MAL3P5, complete sequence.//2.3e-07:815:57//AL034556
 F-NT2RP2004523//Homo sapiens clone DJ0800G07, complete sequence.//8.5e-138:718:95//AC004890
 F-NT2RP2004538//Homo sapiens mRNA for KIAA0591 protein, partial cds.//1.4e-137:687:96//AB011163
 F-NT2RP2004551//CIT-HSP-2387G7.TF.1 CIT-HSP Homo sapiens genomic clone 2387G7, genomic survey sequence.//2.1e-85:484:91//AQ239555
 F-NT2RP2004568//H.vulgaris GAA-satellite DNA.//2.0e-07:292:62//Z50100
 F-NT2RP2004580//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//4.5e-44:512:72//AL023755
 F-NT2RP2004587//Candida albicans cytoskeleton assembly control protein (SLA2) gene, partial cds.//1.0:344:56//AF092908
 F-NT2RP2004594//nbsb0019H13r CUGI Rice BAC Library Oryza sativa genomic clone nbsb0019H13r, genomic survey sequence.//0.053:324:60//AQ258020
 F-NT2RP2004600
 F-NT2RP2004602//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//0.12:109:73//AC005176
 F-NT2RP2004614
 F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//2.6e-102:496:98//AJ006291
 F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds.//1.6e-153:728:98//AB007929
 F-NT2RP2004675//Homo sapiens chromosome 12q24.1, WORKING DRAFT SEQUENCE, 33 unordered pieces.//0.092:239:61//AC005805
 F-NT2RP2004681//Human DNA sequence from clone 51J23 on chromosome Xq26.3-27.3. Contains an EST and GSSs, complete sequence.//1.0:23:61//AL031312
 F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.3e-59:327:94//AB014525
 F-NT2RP2004709//HS_2033_B2_E04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=8 Row=J, genomic survey sequence.//1.9e-15:187:74//AQ230714
 F-NT2RP2004710//HS_3185_B2_D07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=14 Row=H, genomic survey sequence.//9.9e-10:110:84//AQ172885
 F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds.//6.4e-117:582:96//AB007947
 F-NT2RP2004743//Human DNA sequence from PAC 37M17 chromosome X.//0.14:138:71//Z78022
 F-NT2RP2004767//H.sapiens CpG island DNA genomic MseI fragment, clone 65c11, reverse read cpg65c11.rta.//1.3e-24:217:81//Z62210
 F-NT2RP2004768//Homo sapiens STE20-like kinase 3 (mt-3) mRNA, complete cds.//1.6e-45:541:71//AF024636
 F-NT2RP2004775//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//5.8e-13:697:59//AE001398
 F-NT2RP2004791//Human HeLa mRNA isolated as a false positive in a two-hybrid-screen.//5.0e-53:353:84//U56252
 F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//1.5e-116:594:95//AF058953
 F-NT2RP2004802
 F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds.//2.1e-101:495:97//AF054179
 F-NT2RP2004841//Human DNA sequence from cosmid J138017, between markers DXS6791 and DXS8038 on chromosome X contains EST CA repeat and an endogenous retroviral like element.//7.6e-82:531:84//Z72519
 F-NT2RP2004861//Fugu rubripes GSS sequence, clone 040017bA3, genomic survey sequence.//0.96:183:64//AL025645
 F-NT2RP2004897//Human Chromosome X clone BXID187, complete sequence.//4.8e-142:710:96//AC004383
 F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds.//2.0e-82:418:95//AB007144
 F-NT2RP2004936
 F-NT2RP2004959//HS_3197_A2_G11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=22 Row=M, genomic survey sequence.//3.5e-25:218:83//AQ150183
 F-NT2RP2004961//Rattus norvegicus KRAB/zinc finger suppressor protein 1 (KS1) mRNA, complete cds.//2.5e-59:339:79//U56732
 F-NT2RP2004962//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Ro Ret gene, and sodium phosphate transporter (NPT3) gene, complete cds.//3.6e-19:187:72//U91328
 F-NT2RP2004967//Plasmodium falciparum MAL3P6, complete sequence.//0.0020:297:61//Z98551
 F-NT2RP2004978//Chlamydomonas reinhardtii VSP-3 mRNA, complete cds.//0.22:162:69//L29029
 F-NT2RP2004982//F26D4-Sp6 IGF Arabidopsis thaliana genomic clone F26D4, genomic survey sequence.//0.13:273:61//B12642
 F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds.//1.5e-20:431:65//D63478
 F-NT2RP2004999
 F-NT2RP2005000//R.rattus gene for beta-1 subunit of Na,K-ATPase.//0.019:240:63//X63375
 F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//6.0e-159:782:97//AB014515
 F-NT2RP2005003//H.sapiens Staf50 mRNA.//3.1e-42:430:75//X82200
 F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds.//1.4e-98:501:96//AF100141
 F-NT2RP2005018//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, complete sequence.//1.0:209:63//AC004849
 F-NT2RP2005020
 F-NT2RP2005022//Human Chromosome 3 pac pDJ7011, WORKING DRAFT SEQUENCE, 2 unordered pieces.//3.0e-43:98:93//AC000380
 F-NT2RP2005031//HS_2052_B2_G10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=20 Row=M, genomic survey sequence.//0.019:363:61//AQ231464
 F-NT2RP2005037//Human 3' of immunoglobulin heavy chain locus (IGHA2) gene.//0.70:174:65//U64454
 F-NT2RP2005038//Homo sapiens chromosome 17, clone hRPK.74_E_22, complete sequence.//0.20:519:57//AC005696
 F-NT2RP2005108
 F-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds.//2.0e-103:495:98//AB014564
 F-NT2RP2005126//H.sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//2.9e-27:157:98//X98743
 F-NT2RP2005139//Amycolatopsis mediterranei genes encoding rifamycin polyketide synthases, ORFs 1 to 5.//0.00024:547:59//AJ223012
 F-NT2RP2005140//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete sequence.//0.95:191:62//AC004527
 F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, complete cds.//2.6e-89:447:96//AF045583
 F-NT2RP2005147//HS_3184_A1_E01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=1 Row=I, genomic survey sequence.//0.10:294:60//AQ252226
 F-NT2RP2005159//H.sapiens CpG island DNA genomic MseI fragment, clone 132g6, forward read cpg132g6.rta.//1.1e-13:93:97//Z59162
 F-NT2RP2005162//Caenorhabditis elegans cosmid F01F1.//2.6e-20:394:64//U13070
 F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein 1.//1.4e-125:633:96//AJ007509
 F-NT2RP2005204//Arabidopsis thaliana ubiquitin activating enzyme (UBA1) gene, complete cds.//0.00016:316:60//U80808
 F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.51:52:92//AC005189
 F-NT2RP2005239//S.pombe chromosome II cosmid c21D10.//1.3e-22:356:67//AL031536
 F-NT2RP2005254
 F-NT2RP2005270//H.sapiens genomic DNA (chromosome 3: clone NL197).//0.58:132:65//X87513

【0741】

【表442】

F-NT2RP2005276//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//9.0e-103:656:85//D30666

F-NT2RP2005287//Cavia porcellus zinc finger protein (zfoc1) mRNA, complete cds.//3.4e-37:302:84//L26335

F-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLC mRNA, complete cds.//7.1e-122:604:96//AF060219

F-NT2RP2005289//Homo sapiens mRNA for XRP2 protein.//4.0e-140:670:98//AJ007590

F-NT2RP2005293//HS_3245_B1_E10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3245 Col=19 Row=J, genomic survey sequence.//8.2e-37:223:92//AQ217454

F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds.//1.1e-95:483:96//AB014576

F-NT2RP2005325//Human LIM-homeobox domain protein (LIM-2) mRNA, complete cds.//8.2e-22:166:90//U11701

F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190k D subunit (SNAP190) mRNA, complete cds.//0.39:353:62//AF032387

F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cds.//8.8e-29:456:66//AB011138

F-NT2RP2005354//Human DNA sequence from PAC 435C23 on chromosome X. Contains ESTs.//0.72:431:61//Z92844

F-NT2RP2005358//Homo sapiens methyl-CpG binding protein MB03 (MBD3) mRNA, complete cds.//4.7e-99:489:96//AF072247

F-NT2RP2005360//Pan troglodytes huntingtin gene, partial exon.//0.93:105:67//L49358

F-NT2RP2005393//Rat parathyroid hormone receptor mRNA, complete cds.//2.4e-08:97:83//M77184

F-NT2RP2005407

F-NT2RP2005436//Homo sapiens chromosome 16, cosmid clone 2H2 (LAN U), complete sequence.//0.014:235:62//AC005346

F-NT2RP2005441//CIT-HSP-2338PS, TR CIT-HSP Homo sapiens genomic clone 2338PS, genomic survey sequence.//4.0e-107:532:97//AQ055548

F-NT2RP2005453//F21C16TFC IGF Arabidopsis thaliana genomic clone F21C16, genomic survey sequence.//1.0:239:61//B97865

F-NT2RP2005457//B. taurus C1-B14.5b mRNA for NADH dehydrogenase (ubiquinone).//4.7e-25:245:79//X68647

F-NT2RP2005464//Human DNA sequence from clone 836E8 on chromosome 20p12 Contains EST, CA repeat, STS, GSS, retroviral sequence, complete sequence.//4.6e-111:724:86//AL031679

F-NT2RP2005465//Homo sapiens chromosome 19, BAC CIT-B-393115 (BC301323), complete sequence.//5.5e-18:152:75//AC006116

F-NT2RP2005472//Human DNA sequence from clone 118D24 on chromosome 1p36.11-36.33. Contains part of a novel gene similar to worm genes T08G11.1 and C25H3.9, part of a 60S Ribosomal Protein L10 LIKE (pseudo) gene and two 3' exons of the TNFR2 gene for Tumor Necrosis Factor Receptor 2 (75 kd) (TNF Binding Protein 2, TBP11, TNF-R2, CD120B, TNFR2). Contains ESTs, STSs, GSSs, genomic marker D15434 and a ca repeat polymorphism, complete sequence.//4.4e-12:89:97//AL031276

F-NT2RP2005476//Homo sapiens BAC clone RC293F17 from Tpl5-p21, complete sequence.//4.3e-40:463:73//AC004130

F-NT2RP2005490//Homo sapiens clone RH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//3.2e-115:228:99//AC006030

F-NT2RP2005491//HS_2253_A2_G10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=20 Row=M, genomic survey sequence.//4.6e-23:234:80//AQ116847

F-NT2RP2005495

F-NT2RP2005496//HS_3064_A1_F08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=15 Row=K, genomic survey sequence.//5.3e-90:436:98//AQ143097

F-NT2RP2005498//Rabbit protein phosphatase 2A beta subunit mRNA, complete cds.//1.4e-63:503:78//M64931

F-NT2RP2005501//Homo sapiens chromosome 10 clone CIT987SK-1143A11 map 10q25, complete sequence.//0.86:183:63//AC005880

F-NT2RP2005509//Homo sapiens cosmid LM1937 from Xq28.//1.0:160:65//U82695

F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//3.9e-81:444:92//AF092563

F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete cds.//6.9e-18:112:99//AB018307

F-NT2RP2005531//Human structural protein 4.1 mRNA, complete cds.//1.1e-05:282:60//M14993

F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.9e-153:747:97//AJ012449

F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//5.9e-130:618:98//AB007963

F-NT2RP2005549//Mus musculus clone OST142, genomic survey sequence.//3.1e-43:277:89//AF046734

F-NT2RP2005555//HS_2188_A2_D04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2188 Col=8 Row=G, genomic survey sequence.//8.0e-05:195:65//AQ086723

F-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds.//2.5e-44:473:71//AF062529

F-NT2RP2005581//Homo sapiens BAC clone GS180J15 from Tq31, complete sequence.//0.99:213:65//AC005016

F-NT2RP2005600//H. sapiens CpG island DNA genomic MseI fragment, clone 172d12, reverse read cpg172d12.rta.//0.32:134:63//Z57359

F-NT2RP2005605

F-NT2RP2005620//Homo sapiens epsilon 2a mRNA, complete cds.//9.8e-91:447:97//AF062085

F-NT2RP2005622

F-NT2RP2005635//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//8.6e-17:411:61//U10556

F-NT2RP2005637//NAT1 (NAT10)=acetyltransferase 1 (3' region, polyadenylation polymorphism) [human, unrelated Caucasians, mRNA Partial Mutant, 300 nt].//0.22:156:65//S78829

F-NT2RP2005640//Mouse US RNA gene.//5.5e-19:249:76//X06980

F-NT2RP2005645//HS_2201_B2_D07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2201 Col=14 Row=H, genomic survey sequence.//0.30:159:65//AQ066763

F-NT2RP2005651//H. sapiens DNA sequence.//0.00037:150:66//Z22493

F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds.//4.7e-07:351:62//AB006626

F-NT2RP2005669//Homo sapiens KE05 protein mRNA, complete cds.//8.2e-98:472:98//AF064605

F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//2.4e-94:462:98//AF089814

F-NT2RP2005683//HS-1024-B1-H05-MF, abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 803 Col=9 Row=P, genomic survey sequence.//0.99:156:64//B34405

F-NT2RP2005690//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//7.7e-10:328:61//M77836

F-NT2RP2005694

F-NT2RP2005701//Homo sapiens 12p13.3 BAC RPC111-288K12 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.72:160:65//AC005183

F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//1.6e-124:599:97//AB018342

F-NT2RP2005719//R. norvegicus mRNA for metallothionein-III.//0.86:17:64//X89603

F-NT2RP2005722//Human zinc finger protein ZNF136.//2.6e-44:415:77//U09367

F-NT2RP2005723//Human BAC clone GS542D18 from Tq31-q32, complete sequence.//6.9e-15:153:81//AC002528

F-NT2RP2005726//Homo sapiens clone DJ0577P23, WORKING DRAFT SEQUENCE, 28 unordered pieces.//5.1e-41:138:95//AC005627

F-NT2RP2005732//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 291J10, WORKING DRAFT SEQUENCE.//0.61:303:60//Z93017

F-NT2RP2005741//Homo sapiens PALM gene, exon 1 and joined CDS.//0.52:116:67//Y16270

F-NT2RP2005748//Human Kox11 mRNA for zinc finger protein, partial.//0.11:136:66//X52342

F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//7.8e-22:134:96//AF088868

F-NT2RP2005753//Homo sapiens l-1 receptor candidate protein mRNA, complete cds.//1.2e-100:486:98//AF082516

F-NT2RP2005763//Human mRNA for KIAA0111 gene, complete cds.//0.00073:425:56//D21853

F-NT2RP2005767//G. gallus PB1 gene.//2.1e-73:544:80//X90849

F-NT2RP2005773//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//6.2e-15:153:82//M77836

F-NT2RP2005775//Sus scrofa mRNA for soluble angiotensin-binding protein, complete cds.//1.2e-121:649:88//D11336

F-NT2RP2005781//Pseudomonas aeruginosa gene for MexX and MexY, complete cds.//0.96:184:60//AB015853

F-NT2RP2005784//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE.//1.9e-63:222:96//AL034423

F-NT2RP2005804//Oryza sativa glycine-rich protein (OSGRP1) mRNA, complete cds.//2.6e-07:232:64//AF010579

F-NT2RP2005812

F-NT2RP2005815//Streptomyces sp. gene for alkaline serine protease 1.//0.031:358:59//X74103

F-NT2RP2005835//Rattus norvegicus mRNA for p47, complete cds.//2.5e-107:449:91//AB002086

F-NT2RP2005841//Human DNA sequence from cosmid U209G1 on chromosome X.//5.1e-05:144:73//Z68873

F-NT2RP2005853//RPC111-24D4, TKBF RPC1-11 Homo sapiens genomic clone RPC1-11-24D4, genomic survey sequence.//6.4e-13:130:85//AQ013490

【0742】

【表443】

F-NT2RP2005857//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds.//1.7e-174:829:98//AF092564
 F-NT2RP2005859//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 914P20, WORKING DRAFT SEQUENCE.//0.25:174:62//AL034553
 F-NT2RP2005868//Fugu rubripes GSS sequence, clone 103124aF4, genomic survey sequence.//7.8e-06:92:79//AL027276
 F-NT2RP2005886//HS_3187_A2_008_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3187 Col=16 Row=G, genomic survey sequence.//7.1e-95:494:95//AQ155885
 F-NT2RP2005890//Mouse oncogene (ect2) mRNA, complete cds.//2.7e-32:660:66//L11316
 F-NT2RP2005901//H.sapiens CpG island DNA genomic MseI fragment, clone 15b5, reverse read cpg15b5.rta.//0.0026:66:84//Z54729
 F-NT2RP2005908//Homo sapiens l2q13.1 PAC RPC13-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.4e-49:481:75//AC004241
 F-NT2RP2005933//Rattus norvegicus nucleoporin p54 mRNA, complete cds.//6.6e-61:657:73//U63840
 F-NT2RP2005942//H.sapiens PAP mRNA.//1.6e-46:618:67//X76770
 F-NT2RP2005980//Homo sapiens chromosome 17, clone hRPC.1081_P_3, complete sequence.//1.0e-48:533:71//AC005207
 F-NT2RP2006023//HS_3048_A1_A11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3048 Col=21 Row=A, genomic survey sequence.//2.1e-25:167:91//AQ126553
 F-NT2RP2006038//CIT-HSP-384K4, TR CIT-HSP Homo sapiens genomic clone 384K4, genomic survey sequence.//3.9e-06:102:74//B51912
 F-NT2RP2006043//Human intercrine-alpha (hIRH) mRNA, complete cds.//1.9e-05:418:59//U19495
 F-NT2RP2006052//Peromyscus polionotus ammobates dinucleotide microsatellite Ppa55.//0.0035:226:65//AF016861
 F-NT2RP2006069//Human HepG2 partial cDNA, clone hmd3g02m5.//3.9e-11:121:85//D17047
 F-NT2RP2006071
 F-NT2RP2006098//Homo sapiens chromosome 21q22.2, cosmid D13C2, complete sequence.//0.46:264:59//AF027207
 F-NT2RP2006100//Human Chromosome X, complete sequence.//3.2e-94:488:95//AC004073
 F-NT2RP2006103//HS_2254_A2_002_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2254 Col=4 Row=G, genomic survey sequence.//5.7e-27:156:96//AQ129602
 F-NT2RP2006106//Human Chromosome 11 pac pDJ1173a5, complete sequence.//1.2e-62:655:71//AC000378
 F-NT2RP2006141//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SEQUENCE.//1.2e-69:316:98//AL034405
 F-NT2RP2006166//Homo sapiens chromosome 4 clone B3218, complete sequence.//3.1e-45:387:81//AC004063
 F-NT2RP2006184//Cricetulus griseus beta-1,6-N-acetylglucosaminyltransferase Lec4A cell line point mutant mRNA, complete cds.//0.99:111:73//U62587
 F-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds.//7.8e-113:567:96//AB014554
 F-NT2RP2006196//Homo sapiens clone DJ1189D06, complete sequence.//2.8e-28:718:62//AC005232
 F-NT2RP2006200//Homo sapiens chromosome 12p13.3 clone RPC11-96H9, WORKING DRAFT SEQUENCE. 66 unordered pieces.//6.5e-83:239:94//AC006057
 F-NT2RP2006219//H.sapiens mRNA for DGCR6 protein.//1.4e-116:618:93//X96484
 F-NT2RP2006237//CIT-HSP-2300P9, TR CIT-HSP Homo sapiens genomic clone 2300P9, genomic survey sequence.//2.0e-18:118:97//AQ012480
 F-NT2RP2006238//Rattus norvegicus CTD-binding SR-like protein RAB mRNA, complete cds.//7.6e-102:635:86//U49055
 F-NT2RP2006258//RPC11-9N9, TP RPC1-11 Homo sapiens genomic clone R PC1-11-9N9, genomic survey sequence.//8.6e-05:181:63//B71615
 F-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase ENK.//0.44:111:71//X97630
 F-NT2RP2006275//Pseudorabies virus UL[5,6,7,8,8.5,9,10,11,12,13] genes.//2.0e-05:501:59//X97257
 F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.7e-138:679:97//AF035262
 F-NT2RP2006320//P.falciparum pfmdr1 gene.//0.00013:425:60//X56851
 F-NT2RP2006321//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//4.1e-19:545:62//AC003973
 F-NT2RP2006323//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 745114, WORKING DRAFT SEQUENCE.//8.9e-18:131:90//AL033532
 F-NT2RP2006333//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//6.2e-125:602:98//AC004893
 F-NT2RP2006334//Homo sapiens chromosome 19, cosmid R27139, complete sequence.//2.1e-06:241:65//AC005514
 F-NT2RP2006365//Fugu rubripes GSS sequence, clone 171K15aC5, genomic survey sequence.//7.8e-06:148:70//AL029590
 F-NT2RP2006393//Human DNA sequence from clone 80119 on chromosome 6p21.31-22.2 Contains genes and pseudogenes for olfactory receptor-like proteins, STS, GSS, complete sequence.//6.8e-06:167:70//AL027277
 F-NT2RP2006436//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//4.2e-92:363:84//AL023808
 F-NT2RP2006441
 F-NT2RP2006454//Sequence 8 from Patent W09517522.//2.9e-06:180:66//A45338
 F-NT2RP2006456
 F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//3.4e-148:545:98//AJ006266
 F-NT2RP2006467//Sus scrofa IgM heavy chain gene, switch region and exons encoding chl-ch4 and secretion domains, partial cds.//0.061:201:66//U50149
 F-NT2RP2006472
 F-NT2RP2006534//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to MDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism. complete sequence.//8.8e-10:273:66//Z93929
 F-NT2RP2006554//Human DNA mismatch repair protein homolog (hMLH1) gene, exon 6.//0.71:174:59//U40965
 F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds.//6.6e-114:669:90//AF038966
 F-NT2RP2006571//Rabbit cytochrome P-450 isozyme 2 (type B2) mRNA, complete cds, clone B2-1.//6.0e-26:503:63//M20855
 F-NT2RP2006573//Molluscum contagiosum virus subtype 1, complete genome.//0.44:134:71//U60315
 F-NT2RP2006598//Human BRCA2 region, mRNA sequence CG033.//5.0e-16:140:85//U50537
 F-NT2RP3000002//***ALU WARNING: Human Alu-Sc subfamily consensus sequence.//3.8e-32:214:89//U14571
 F-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//5.8e-136:637:98//AJ011972
 F-NT2RP3000046//Bovine herpesvirus type 1-early-intermediate transcription control protein (BICP4) gene, complete cds.//5.4e-05:571:60//L14320
 F-NT2RP3000047
 F-NT2RP3000050//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//1.0e-67:626:74//M27877
 F-NT2RP3000055//Genomic sequence from Human 9q34, complete sequence.//3.5e-10:394:64//AC001227
 F-NT2RP3000058
 F-NT2RP3000072//Homo sapiens BAC clone RG290G13 from 7q21, complete sequence.//1.0:301:61//AC004746
 F-NT2RP3000080//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 102D24, WORKING DRAFT SEQUENCE.//1.9e-44:297:79//AL021391
 F-NT2RP3000085//Arabidopsis thaliana 3-methylcrotonyl-CoA carboxylase precursor mRNA, complete cds.//4.5e-33:528:65//U12536
 F-NT2RP3000092//RPC11-22M5, TV RPC1-11 Homo sapiens genomic clone RPC1-11-22M5, genomic survey sequence.//3.3e-27:157:97//B84237
 F-NT2RP3000109//Arabidopsis thaliana l-aminocyclopropanecarboxylate synthase (ACS5) gene, complete cds.//0.92:185:64//L29260
 F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//1.2e-112:286:89//AC005189
 F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//9.0e-181:849:98//AB011164
 F-NT2RP3000149//Homo sapiens chromosome 17, clone hRPC.264_B_14, complete sequence.//4.2e-24:155:94//AC005884
 F-NT2RP3000186//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 500L14, WORKING DRAFT SEQUENCE.//7.2e-43:269:81//AL023583
 F-NT2RP3000197//Homo sapiens interleukin 9 receptor (IL9R) pseudogene, exons 1-9.//0.098:405:57//L39063
 F-NT2RP3000207//Drosophila melanogaster DNA sequence (P1 D500164 (D269)), complete sequence.//0.96:608:55//AC004716
 F-NT2RP3000220
 F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.0e-18:509:58//AF059569
 F-NT2RP3000235//Mouse Cosmid ma53a016 from 14D1-02, complete sequence.//3.5e-05:224:65//AC004101
 F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds.//2.1e-109:691:86//D86972
 F-NT2RP3000251//Caenorhabditis elegans cosmid ZK930, complete sequence.//0.20:119:68//Z70213

【0743】

【表444】

F-NT2RP3000252//Homo sapiens cosmid IF1, complete sequence.//9.8e-78:174:88//AF065393
 F-NT2RP3000255
 F-NT2RP3000267
 F-NT2RP3000289//Mus musculus Crk-associated substrate (Cas-b) mRNA, complete cds.//5.9e-48:374:82//U48853
 F-NT2RP3000312//Fruit fly (D.melanogaster) Glued mRNA, complete cds.//4.9e-22:583:63//J02932
 F-NT2RP3000320//RPC111-36J1, TP RPC1-11 Homo sapiens genomic clone RPC1-11-36J1, genomic survey sequence.//4.4e-06:87:88//AQ047107
 F-NT2RP3000324//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//5.5e-26:283:79//U78090
 F-NT2RP3000333//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 973M2, WORKING DRAFT SEQUENCE.//1.0:309:60//AL033533
 F-NT2RP3000341//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXST locus with GT and GTG repeat polymorphisms, complete sequence.//6.7e-42:465:74//Z97181
 F-NT2RP3000348
 F-NT2RP3000350//Homo sapiens cosmid IF1, complete sequence.//3.4e-79:174:88//AF065393
 F-NT2RP3000359//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//2.2e-127:816:85//M25757
 F-NT2RP3000361//Schizosaccharomyces pombe DNA for pre-mRNA splicing factor, complete cds.//0.0075:288:58//D83743
 F-NT2RP3000366//Mus musculus ras-related protein (rab18) mRNA, complete cds.//7.1e-134:693:94//U4966
 F-NT2RP3000393//Rattus norvegicus mRNA for GABA-B R2 receptor.//0.049:308:60//AJ011318
 F-NT2RP3000397//S.cerevisiae chromosome VII reading frame ORF YGL120c.//0.00012:441:58//Z72642
 F-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//5.0e-174:841:97//AF071185
 F-NT2RP3000418//Homo sapiens chromosome 17, clone hRPK.1053_B_8, complete sequence.//7.9e-53:817:68//AC006083
 F-NT2RP3000433//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE.//6.1e-31:590:63//AL031681
 F-NT2RP3000439//Fugu rubripes GSS sequence, clone 075E22aB10, genomic survey sequence.//4.0e-19:169:81//AL026471
 F-NT2RP3000441//Human DNA sequence from PAC 93H18 on chromosome 6 contains ESTs heterochromatin protein HP1s-gamma pseudogene, STS and CpG island.//2.4e-41:459:65//Z84488
 F-NT2RP3000449//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE.//1.1e-100:365:87//AL031650
 F-NT2RP3000451//HS_2024_A1_E10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2024 Col=19 Row=1, genomic survey sequence.//0.011:367:57//AQ229420
 F-NT2RP3000456//CIT-HSP-2338P5, TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence.//1.5e-89:458:96//AQ055548
 F-NT2RP3000484//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 90L6, WORKING DRAFT SEQUENCE.//0.043:147:70//Z97353
 F-NT2RP3000487//H.sapiens CpG island DNA genomic MseI fragment, clone 11b11, forward read cpg11b11.ftla.//1.7e-11:96:92//Z64440
 F-NT2RP3000512//Human HOX2G mRNA from the Hox2 locus.//9.7e-17:109:97//X16667
 F-NT2RP3000526//Homo sapiens full length insert cDNA clone Y238E04.//4.1e-30:283:76//AF086071
 F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds.//2.5e-34:706:63//D86966
 F-NT2RP3000531//Mus musculus immunosuperfamily protein B12 mRNA, complete cds.//1.9e-14:220:70//AF061260
 F-NT2RP3000542//Human Chromosome 11p11.2 PAC clone pD1404m15, complete sequence.//0.00019:361:60//AC002554
 F-NT2RP3000561//Homo sapiens PAC clone D0942116 from Tq11, complete sequence.//9.0e-171:827:98//AC006012
 F-NT2RP3000562
 F-NT2RP3000578//F.rubripes GSS sequence, clone 013G07cE7, genomic survey sequence.//1.7e-25:284:74//AL011271
 F-NT2RP3000582//CIT1978SK-A-56H4, TP CIT1978SK Homo sapiens genomic clone A-56H4, genomic survey sequence.//5.8e-07:239:66//B73597
 F-NT2RP3000584
 F-NT2RP3000590//H.sapiens CpG island DNA genomic MseI fragment, clone 17047, forward read cpg17047.ftla.//3.0e-22:128:100//Z59723
 F-NT2RP3000592//CIT-HSP-2288J7, TR CIT-HSP Homo sapiens genomic clone 2288J7, genomic survey sequence.//2.2e-78:382:98//B98868
 F-NT2RP3000596//CIT-HSP-2375J10, TR CIT-HSP Homo sapiens genomic clone 2375J10, genomic survey sequence.//0.00076:143:67//AQ109305
 F-NT2RP3000599//Caenorhabditis elegans cosmid T19B10, complete sequence.//1.2e-13:295:66//Z74043
 F-NT2RP3000603//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.37:520:57//L14320
 F-NT2RP3000605//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//8.8e-155:526:97//AC006128
 F-NT2RP3000622//HS_3213_A2_002_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=4 Row=G, genomic survey sequence.//4.1e-29:238:85//AQ175104
 F-NT2RP3000624//Homo sapiens clone DJ0800G07, complete sequence.//0.47:75:80//AC004890
 F-NT2RP3000628//Human DNA sequence from clone 581F12 on chromosome 1q21. Contains Eukaryotic Translation Initiation Factor EIF3 P35 Subunit and 60S Ribosomal protein L22 pseudogenes. Contains ESTs, complete sequence.//0.078:393:58//AL031313
 F-NT2RP3000632//Human zinc finger protein zfp6 (ZF6) mRNA, partial cds.//1.4e-96:541:79//U71363
 F-NT2RP3000644//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//5.2e-46:421:77//AC005089
 F-NT2RP3000661
 F-NT2RP3000665//Human DNA sequence from clone 1191B2 on chromosome 22q13.2-13.3. Contains part of the BIK (NBK, BP4, BIP1) gene for BCL2-interacting killer (apoptosis-inducing), a 40S Ribosomal Protein S25 pseudogene and part of an alternatively spliced novel Act1 Transferase gene similar to C. elegans C5002.7. Contains ESTs, STSs, GSSs, two putative CpG islands and genomic marker D22S1151, complete sequence.//1.7e-11:292:65//AL022237
 F-NT2RP3000685//H.sapiens mRNA for novel protein.//2.4e-80:460:92//X99961
 F-NT2RP3000690//H.sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA10F6.//1.0:141:65//Z77872
 F-NT2RP3000736//Human mRNA for KIAA0140 gene, complete cds.//6.1e-20:127:96//D50930
 F-NT2RP3000739//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//1.1e-46:622:67//AF015264
 F-NT2RP3000742//Rattus norvegicus phospholipase C delta-4 mRNA, complete cds.//4.7e-37:429:70//U16655
 F-NT2RP3000753
 F-NT2RP3000759//Caenorhabditis elegans cosmid Y57G11C, complete sequence.//2.8e-38:519:69//Z99281
 F-NT2RP3000815//HS_2237_A2_D12_WF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2237 Col=24 Row=G, genomic survey sequence.//0.79:151:61//AQ067252
 F-NT2RP3000825//Campanula ramosa chloroplast NADH dehydrogenase (ndhF) gene, complete cds.//0.36:378:58//L39387
 F-NT2RP3000826//Suid herpesvirus 1 Kaplan glycoprotein L (UL1) and uracil-DNA glycosylase (UL2) genes, complete cds, and (UL3) gene, partial cds.//0.0025:291:62//U02513
 F-NT2RP3000836//Mouse complement factor H-related protein mRNA, complete cds, clone 9C4.//0.69:563:57//M29009
 F-NT2RP3000841//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs, polymorphic CA repeat, CpG island, CpG island genomic fragments.//2.1e-46:666:68//Z86062
 F-NT2RP3000845//Homo sapiens chromosome 19, cosmid R31237, complete sequence.//3.4e-92:193:93//AC005581
 F-NT2RP3000847//Human HepG2 3' region cDNA, clone hmd5d02.//3.4e-32:261:81//D16938
 F-NT2RP3000850//Homo sapiens clone RG271G13, WORKING DRAFT SEQUENCE, 7 unordered pieces.//5.1e-44:358:81//AC005082
 F-NT2RP3000852//Homo sapiens DNA sequence from PAC 117P20 on chromosome 1q24. Contains the LMHR (SELL) gene coding for Lymph Node Homing Receptor (L-Selectin precursor, LAM-1 Leukocyte Adhesion Molecule, Leukocyte surface antigen Leu-8, TQ1, GP90-MEL, LECAM1 Leukocyte-Endothelial Cell Adhesion Molecule 1, CD62L). Contains the SELE gene coding for E-Selectin precursor (CD62E, ELAM-1 Endothelial Leukocyte Adhesion Molecule 1, LECAM-2 Leukocyte-Endothelial Cell Adhesion Molecule 2). Contains an unknown gene with homology to predicted yeast, plant and worm proteins. Contains ESTs and STSs, complete sequence.//4.4e-123:150:98//AL021940
 F-NT2RP3000859//T19M2TF TAMU Arabidopsis thaliana genomic clone T19M2, genomic survey sequence.//0.016:185:65//B60831
 F-NT2RP3000865
 F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//2.0e-29:766:60//U53445
 F-NT2RP3000869//H.sapiens gene for plectin.//1.1e-12:700:60//Z54367
 F-NT2RP3000875//HS_2236_B1_G10_WF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2236 Col=19 Row=N, genomic survey sequence.//0.98:153:68//AQ154007
 F-NT2RP3000901//Human herpesvirus 2 glycoprotein B precursor (UL2

【0744】

【表445】

7) gene, complete cds.//0.44:213:65//AF021340	ds.//3.8e-47:761:64//AB018269
F-NT2RP3000904//Rat Nat channel mRNA, 3' end.//3.6e-106:505:99//M27223	F-NT2RP3001268//Homo sapiens zinc finger protein (ZNF6) mRNA, 5' UTR and partial cds.//2.3e-64:618:72//AF027513
F-NT2RP3000917//Mouse mRNA for Ohal protein, complete cds.//3.1e-132:691:93//D38517	F-NT2RP3001272//Mus musculus mRNA for macrophage actin-associated-tyrosine-phosphorylated protein.//2.6e-99:669:83//Y18101
F-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//3.2e-97:585:88//AF015264	F-NT2RP3001274//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//0.99:400:58//U07561
F-NT2RP3000968//Human Chromosome 16 BAC clone C1T987SK-A-234F9, complete sequence.//5.8e-70:181:89//U91326	F-NT2RP3001281//Homo sapiens chromosome 17, clone hRPK.318_A_15, complete sequence.//5.9e-39:304:70//AC005837
F-NT2RP3000980//R. norvegicus CYP3A1 gene, 5' flanking region.//6.1e-26:507:66//X98335	F-NT2RP3001297//Human mRNA for KIAA0281 gene, complete cds.//7.6e-47:544:69//D87457
F-NT2RP3000994//HS-1049-B2-F03-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 771 Col=6 Row=L, genomic survey sequence.//1.5e-22:128:100//B39529	F-NT2RP3001307//Ambystoma tigrinum RPE65 protein mRNA, complete cds.//2.4e-27:547:63//AF047465
F-NT2RP3001004//H. sapiens CpG island DNA genomic MseI fragment, clone 39c1, reverse read cpg39c1.r1a.//5.9e-27:150:99//Z60925	F-NT2RP3001318//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0022:624:60//AC004709
F-NT2RP3001007//Homo sapiens clone MH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.11:610:57//AC006039	F-NT2RP3001325//Caenorhabditis elegans cosmid F36H12.//0.25:523:59//AF078790
F-NT2RP3001055//Drosophila melanogaster: Chromosome 2R: Region 47F1-47F7; P1 clone DS02304, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-23:352:67//AC005653	F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds.//5.1e-29:345:73//D86966
F-NT2RP3001057//H. sapiens HZF4 mRNA for zinc finger protein.//1.4e-49:437:77//X78927	F-NT2RP3001339//Rattus norvegicus myotonic dystrophy kinase-related Cdc42-binding kinase (MRCK) mRNA, complete cds.//1.2e-151:821:91//AF021935
F-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds.//8.4e-50:534:74//AF060219	F-NT2RP3001340//Homo sapiens MGC box factor SOX-13 mRNA, complete cds.//5.3e-27:247:81//AF083105
F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 protein, partial cds.//1.2e-14:474:60//AB018325	F-NT2RP3001355//Homo sapiens Chromosome 22q11.2 BAC Clone 77h2 in CES Region, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-16:130:76//AC000052
F-NT2RP3001096//CIT-HSP-230SP8.TF CIT-HSP Homo sapiens genomic clone 230SP8, genomic survey sequence.//3.4e-37:222:93//AQ021278	F-NT2RP3001356
F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds.//8.5e-33:712:64//D86969	F-NT2RP3001374
F-NT2RP3001109//Human Chromosome 15q26.1 PAC clone pDJ45711 containing DNA polymerase gamma (polg) gene, complete sequence.//2.7e-116:186:99//AC005317	F-NT2RP3001383//Homo sapiens DNA sequence from PAC 140C12 on chromosome 6q26-q27.//0.0082:365:61//AL008628
F-NT2RP3001111	F-NT2RP3001384//Homo sapiens HRHFB2018 mRNA, partial cds.//6.4e-157:743:98//AB015332
F-NT2RP3001113//Human DNA sequence from cosmid U157D4, between markers DXS366 and DXS87 on chromosome X.//2.4e-05:702:58//Z68871	F-NT2RP3001392//Human DNA sequence from PAC 302D9 on chromosome 22 q11.2-qter. Contains STS, complete sequence.//0.045:359:61//Z82198
F-NT2RP3001115//Homo sapiens PAC clone DJ0905J08 from Tpl2-pl4, complete sequence.//1.9e-170:821:98//AC005189	F-NT2RP3001396//Drosophila melanogaster DNA sequence (P1 DS08860 (D181)), complete sequence.//1.3e-16:336:65//AC004296
F-NT2RP3001116//HS_3075_A1_F01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=1 Row=K, genomic survey sequence.//7.3e-49:290:92//AQ120581	F-NT2RP3001398//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//3.1e-100:711:82//U49046
F-NT2RP3001119//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein n, first coding exon of dynamin 2 (DYN11). ESTs, STS, GSS, CpG island, complete sequence.//1.4e-121:598:97//AL031864	F-NT2RP3001399//Homo sapiens PAC clone DJ1106E03 from Tq31.3-Tq3, complete sequence.//5.4e-20:245:73//AC005521
F-NT2RP3001120//Human zinc finger protein ZNF136.//7.4e-76:687:75//U09367	F-NT2RP3001407//RPC111-41A20.TP RPC1-11 Homo sapiens genomic clone RPC1-11-41A20, genomic survey sequence.//0.051:306:59//AQ029031
F-NT2RP3001126//Bovine herpesvirus type 1 DNA for UL36, UL37, UL38, UL39, UL40 and UL41.//6.8e-05:344:64//Z49078	F-NT2RP3001420//Human DNA sequence from PAC 12409 on chromosome 6q21. Contains DNAJ2 (HDJ1) like pseudogene, ESTs, STSs and GSSs.//0.90:170:65//AL021327
F-NT2RP3001133//Nephila clavipes minor ampullate silk protein MiSp1 mRNA, partial cds.//0.00021:529:60//AF027735	F-NT2RP3001426//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE.//2.9e-89:138:98//AL031447
F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//3.6e-179:851:98//AB018305	F-NT2RP3001427//CIT-HSP-230Z24.TF CIT-HSP Homo sapiens genomic clone 230Z24, genomic survey sequence.//8.1e-36:212:94//AQ020997
F-NT2RP3001147//RPC111-3M16.TP RPC1-11 Homo sapiens genomic clone RPC1-11-3M16, genomic survey sequence.//2.1e-15:106:96//B48859	F-NT2RP3001428//Human nuclear pore complex-associated protein TPR (tpr) mRNA, complete cds.//8.5e-73:431:91//U6966B
F-NT2RP3001150//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//2.0e-159:418:95//AL034379	F-NT2RP3001432//HS_3032_B1_A03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=5 Row=B, genomic survey sequence.//0.00024:111:76//AQ096619
F-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//5.1e-190:89:1:98//AJ006266	F-NT2RP3001447
F-NT2RP3001176//Human DNA sequence from clone 879K22 on chromosome 1q32.1-41 Contains GSS, complete sequence.//1.1e-59:207:97//AL034351	F-NT2RP3001449//Human DNA sequence from clone 283E3 on chromosome 1p36.21-36.33. Contains the alternatively spliced gene for Matrix Metalloproteinase in the Female Reproductive tract MIFR1, -2, MMP21, 22A, -B and -C, a novel gene, the alternatively spliced CDC2L2 gene for Cell Division Cycle 2-Like 2 (PITSLRE, p58/GTA, Galactosyl transferase Associated Protein Kinase) beta 1, beta 2-1, beta 2-2 and alpha 2-4, a 40S Ribosomal Protein S7 pseudogene, part of the KIAA0447 gene, a novel alternatively spliced gene similar to many (archae) bacterial, worm and yeast hypothetical genes, and the GMB1 gene for Guanine Nucleotide Binding Protein (G protein). Beta polypeptide 1 (Transducin Beta chain 1). Contains putative CpG island s, ESTs, STSs and GSSs, complete sequence.//2.1e-105:223:99//AL031282
F-NT2RP3001214//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-628 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.16:475:58//AC005507	F-NT2RP3001453//Ralstonia sp. E2 positive phenol-degradative gene regulator (poxR), phenol hydroxylase components (poxA, poxB, poxC, poxD, poxE, poxF), and ferredoxin-like protein (poxG) genes, complete cds.//0.75:349:59//AF026065
F-NT2RP3001216//Homo sapiens clone DJ0635005, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.3e-05:561:56//AC004845	F-NT2RP3001457
F-NT2RP3001221	F-NT2RP3001459
F-NT2RP3001232//Mouse mRNA for serine protease PC6, complete cds.//1.0e-11:120:87//D12619	F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA, complete cds.//1.3e-08:168:70//AF072836
F-NT2RP3001236	
F-NT2RP3001239//Mouse MAP1B mRNA for MAP1B microtubule-associated protein.//3.9e-19:501:61//X13396	
F-NT2RP3001245//CITB1-EI-250SC1.TF.1 CITB1-EI Homo sapiens genomic clone 250SC1, genomic survey sequence.//8.5e-70:337:100//AQ242007	
F-NT2RP3001253//CITB1-EI-250SN14.TR CITB1-EI Homo sapiens genomic clone 250SN14, genomic survey sequence.//0.83:235:60//AQ260430	
F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete c	

【0745】

【表446】

- F-NT2RP3001490
F-NT2RP3001495//Human oxidoreductase (HMCMA56) mRNA, complete cds. //1.0e-26:191:90//U13395
F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor 1 RC8 (TRC8) mRNA, complete cds. //8.5e-171:804:98//AF064801
F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-A) mRNA, complete cds. //8.9e-140:743:91//U35499
F-NT2RP3001529//Streptomyces griseus DNA for ribosome protein L21, ribosomal protein L27, Obg, complete cds. //2.1e-14:517:59//D87916
F-NT2RP3001538//Capra hircus hircus clone 12 RAPD PCR sequence, genomic survey sequence. //4.7e-05:217:63//AF078176
F-NT2RP3001554//Rattus norvegicus microtubule-associated protein 1 A MAP1A (Map-1) mRNA, complete cds. //4.3e-17:332:67//M83196
F-NT2RP3001580//RPC111-91E19. TV RPC111 Homo sapiens genomic clone R-91E19, genomic survey sequence. //4.2e-15:110:91//AQ281332
F-NT2RP3001587//S.pombe chromosome 11 cosmid c16H5. //6.6e-28:491:64//AL022104
F-NT2RP3001589//RPC111-68M15. TX RPC111 Homo sapiens genomic clone R-68M15, genomic survey sequence. //8.7e-108:517:98//AQ237629
F-NT2RP3001607//Homo sapiens Xp22 BAC GSHB-600G8 (Genome Systems Human BAC library) complete sequence. //1.0e-09:257:65//AC004674
F-NT2RP3001608//Methylococcus capsulatus methane monooxygenase component A alpha chain, methane monooxygenase A beta chain and methane monooxygenase component C genes, complete cds. //0.59:450:57//M90050
F-NT2RP3001621//Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VMD-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence. //1.8e-42:278:79//AL021808
F-NT2RP3001629
F-NT2RP3001634//Homo sapiens mRNA for Ariadne-2 protein. //1.5e-63:276:97//AJ130978
F-NT2RP3001642//Caenorhabditis elegans cosmid F45E6, complete sequence. //0.018:127:66//Z68117
F-NT2RP3001646
F-NT2RP3001671//Homo sapiens mRNA for NS1-binding protein (NS1-BP). //3.4e-171:816:98//AJ012449
F-NT2RP3001672//Drosophila melanogaster transcriptional repressor protein (Scm) mRNA, complete cds. //1.6e-38:542:66//U49793
F-NT2RP3001676//HS_3090_B1_B04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3090 Col=7 Row=D, genomic survey sequence. //3.1e-07:333:64//AQ123250
F-NT2RP3001678//Drosophila melanogaster: Chromosome 3L: Region 53C 5-6303: PI clone DS01859, WORKING DRAFT SEQUENCE, 6 unordered pieces. //1.0:539:57//AC004358
F-NT2RP3001679//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11. //2.8e-130:355:96//AB020860
F-NT2RP3001688//Rattus norvegicus glucocorticoid modulatory element binding protein 2 mRNA, complete cds. //2.1e-37:512:70//AF059273
F-NT2RP3001690//CIT-HSP-2300P9. TR CIT-HSP Homo sapiens genomic clone 2300P9, genomic survey sequence. //2.8e-19:123:95//AQ012480
F-NT2RP3001698//Rat mRNA for RhoGAP, complete cds. //9.4e-11:167:74//D31962
F-NT2RP3001708//H. sapiens CpG island DNA genomic MseI fragment, clone 4g7, reverse read cpg4g7.rtd. //1.3e-17:113:97//Z61312
F-NT2RP3001712//M. musculus mRNA for HP1-BP74 protein. //2.2e-95:601:88//X99642
F-NT2RP3001716
F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds. //1.4e-159:565:97//AF054177
F-NT2RP3001727//Rattus norvegicus implantation-associated protein (IAG2) mRNA, partial cds. //1.7e-132:786:88//AF008554
F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds. //3.9e-104:811:78//D50918
F-NT2RP3001739//Homo sapiens Chromosome 22q11.2 PAC Clone p201m18 In DGCR Region, complete sequence. //6.5e-07:178:69//AC000097
F-NT2RP3001752//Human DNA sequence from clone 10S016 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence. //5.2e-31:111:77//AL031311
F-NT2RP3001753//Sequence 29 from patent US 5658882. //0.11:513:58//162381
F-NT2RP3001764//Sequence 6 from Patent WO9706245. //6.4e-47:673:66//A59888
F-NT2RP3001777//Caenorhabditis elegans cosmid T10E10. //0.078:290:63//U39644
F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds. //2.8e-151:710:98//AB007928
F-NT2RP3001792//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds. //1.2e-26:213:85//U13262
F-NT2RP3001799//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 469D22, WORKING DRAFT SEQUENCE. //8.4e-51:168:95//AL031284
F-NT2RP3001819//S. glaucus genes strU, strX, strV and strW for 5'-hydroxystreptomycin production and transport polypeptides. //0.084:526:58//X89010
F-NT2RP3001844//HS_3110_B1_E10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3110 Col=19 Row=J, genomic survey sequence. //1.5e-40:232:82//AQ140433
F-NT2RP3001854//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces. //0.14:452:58//AC005505
F-NT2RP3001855//Mus musculus homeobox protein PKNOX1 (Pknol1) mRNA, complete cds. //2.7e-39:575:67//AF061270
F-NT2RP3001857//M. musculus tex292 mRNA (5' region). //8.7e-07:106:81//X80434
F-NT2RP3001896
F-NT2RP3001898//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 163G9, WORKING DRAFT SEQUENCE. //0.094:456:60//AL008733
F-NT2RP3001915//Caenorhabditis elegans cosmid C12D8, complete sequence. //0.58:482:56//Z73969
F-NT2RP3001926//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE. //0.42:401:58//AL034557
F-NT2RP3001929//Homo sapiens chromosome 16, cosmid clone RT102 (LA ML), complete sequence. //3.1e-28:263:77//AC004651
F-NT2RP3001931
F-NT2RP3001938//CIT-HSP-2165E8. TR CIT-HSP Homo sapiens genomic clone 2165E8, genomic survey sequence. //3.6e-24:182:91//B95475
F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete cds. //1.8e-165:815:96//AB014575
F-NT2RP3001944
F-NT2RP3001969//Homo sapiens chromosome 12p13.3 clone RPC111-350L7, WORKING DRAFT SEQUENCE, 72 unordered pieces. //4.8e-62:304:89//AC005844
F-NT2RP3001989//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds. //8.2e-10:564:60//AF030694
F-NT2RP3002002//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs. //2.5e-57:361:80//Z83822
F-NT2RP3002004//Sequence 3 from patent US 5798245. //1.6e-26:104:100//AR025386
F-NT2RP3002007//Human Chromosome 15q11-q13 PAC clone pJ223c9 from the Prader-Willi/Angelman Syndrome region, complete sequence. //0.0053:633:58//AC004137
F-NT2RP3002014//Drosophila melanogaster DNA sequence (Pis DS07528 (D169) and DS06665 (D220)), complete sequence. //1.3e-32:334:68//AC004640
F-NT2RP3002033//H. sapiens DNA sequence. //0.012:214:63//Z22493
F-NT2RP3002045//Rat mRNA for alpha-c large chain of the protein complex AP-2 associated with clathrin. //8.7e-116:713:86//K53773
F-NT2RP3002054//Mycobacterium tuberculosis H37Rv complete genome: segment 143/162. //1.6e-12:613:60//AL021841
F-NT2RP3002056//Human DNA sequence from PAC 358H7 on chromosome X. //0.17:566:59//Z77249
F-NT2RP3002057//Homo sapiens clone M00084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces. //3.3e-24:167:82//AC005682
F-NT2RP3002062
F-NT2RP3002063//Rickettsia prowazekii strain Madrid E, complete genome: segment 3/4. //0.24:508:58//AJ235272
F-NT2RP3002081//HS_2001_B1_E06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2001 Col=11 Row=J, genomic survey sequence. //9.7e-22:155:90//AQ218494
F-NT2RP3002097//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence. //9.6e-66:562:77//AC006210
F-NT2RP3002102//CIT-HSP-2307B10. TR CIT-HSP Homo sapiens genomic clone 2307B10, genomic survey sequence. //5.9e-16:214:74//AQ018040
F-NT2RP3002108
F-NT2RP3002142//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence. //7.6e-29:414:68//AC004020
F-NT2RP3002146//Pseudomonas fluorescens polyketide synthase type I (pltB) and polyketide synthase type I (pltC) genes, complete cds. //0.96:434:60//AF003370
F-NT2RP3002147//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 329F2, WORKING DRAFT SEQUENCE. //1.3e-63:380:91//AL031710
F-NT2RP3002151//Human chromosome 16p13.1 BAC clone CIT987SK-551G9 complete sequence. //9.9e-60:315:80//U95742

【0746】

【表447】

F-NT2RP3002163	sequence. //3.3e-22:407:67//AC006129
F-NT2RP3002165// <i>M. musculus</i> HCNPG mRNA. //1.4e-142:867:87//X68061	F-NT2RP3002671// <i>S. pombe</i> chromosome III cosmid c553. //1.0e-12:336:66//AL023704
F-NT2RP3002166// <i>Homo sapiens</i> chromosome X, clone hCIT.200_L_4, complete sequence. //0.090:394:59//AC006121	F-NT2RP3002682// <i>Caenorhabditis elegans</i> cosmid F17C11, complete sequence. //1.3e-21:448:64//Z72507
F-NT2RP3002173// <i>HS_3062_B1_G05_MF</i> CIT Approved Human Genomic Sperm Library D <i>Homo sapiens</i> genomic clone Plate=3062 Col=9 Row=N, genomic survey sequence. //3.3e-101:509:96//AQ193219	F-NT2RP3002687//CIT978SK-A-78981.TP CIT978SK <i>Homo sapiens</i> genomic clone A-78981, genomic survey sequence. //2.5e-25:173:91//B51656
F-NT2RP3002181// <i>Human</i> DNA sequence from clone 24ol8 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VNO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, GSS, complete sequence. //4.5e-106:432:84//AL021808	F-NT2RP3002688// <i>Mouse</i> mRNA for kinesin-like protein (Kif1b), complete cds. //1.2e-73:728:74//D17577
F-NT2RP3002244// <i>Homo sapiens</i> chromosome 19, cosmid R27377, complete sequence. //0.63:353:60//AC005321	F-NT2RP3002701//CITBI-E1-2507L14.TF CITBI-E1 <i>Homo sapiens</i> genomic clone 2507L14, genomic survey sequence. //0.0012:55:92//AQ263530
F-NT2RP3002248// <i>HS_3029_A1_D10_MIR</i> CIT Approved Human Genomic Sperm Library D <i>Homo sapiens</i> genomic clone Plate=3029 Col=19 Row=G, genomic survey sequence. //3.5e-10:125:79//AQ094880	F-NT2RP3002713
F-NT2RP3002255// <i>Bovine</i> herpesvirus type 1 immediate-early transcriptional control protein (BICP4) gene, 5' end. //5.6e-09:629:59//L14321	F-NT2RP3002763// <i>Caenorhabditis elegans</i> cosmid T20F10, complete sequence. //0.98:209:63//Z81594
F-NT2RP3002273//cSRL-165E12-u cSRL flow sorted Chromosome 11 specific cosmid <i>Homo sapiens</i> genomic clone cSRL-165E12, genomic survey sequence. //4.9e-35:366:74//B03004	F-NT2RP3002770
F-NT2RP3002276// <i>B. taurus</i> mRNA for B15 subunit of NADH: ubiquinone oxidoreductase complex. //0.023:326:60//X64898	F-NT2RP3002785// <i>Homo sapiens</i> laminin beta-4 chain precursor (LAMB4) mRNA, alternatively spliced short variant, partial cds. //0.78:515:57//AF029325
F-NT2RP3002303// <i>Methanobacterium thermoautotrophicum</i> from bases 172512 to 182957 (section 16 of 148) of the complete genome. //3.8e-12:643:57//AE000810	F-NT2RP3002799// <i>Human</i> DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acidic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4 LIKE gene. Contains ESTs and GSSs, complete sequence. //1.9e-21:167:79//AL022718
F-NT2RP3002304// <i>Plasmodium falciparum</i> 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces. //1.6e-09:490:60//AC005504	F-NT2RP3002810// <i>Homo sapiens</i> chromosome 17, clone hRKC.215_E_13, complete sequence. //0.32:187:66//AC005549
F-NT2RP3002330// <i>Human</i> DNA sequence from cosmid L58b6, Huntington's Disease Region, chromosome 4p16.3, containing STS matches. //1.9e-93:572:88//Z49862	F-NT2RP3002818// <i>Homo sapiens</i> jerky gene product homolog mRNA, complete cds. //6.9e-54:615:70//AF004715
F-NT2RP3002343// <i>HS_3010_A2_B08_T7</i> CIT Approved Human Genomic Sperm Library D <i>Homo sapiens</i> genomic clone Plate=3010 Col=16 Row=C, genomic survey sequence. //9.0e-75:373:97//AQ119068	F-NT2RP3002861// <i>Caenorhabditis elegans</i> cosmid W03F4. //4.2e-05:226:65//U64601
F-NT2RP3002351// <i>Human</i> mRNA for NAD-dependent methylene tetrahydrofolate dehydrogenase cyclohydrolase (EC 1.5.1.15). //4.9e-64:588:75//X16396	F-NT2RP3002869// <i>Mus musculus</i> semaphorin 11a mRNA, complete cds. //2.0e-93:638:83//AF030430
F-NT2RP3002352// <i>Homo sapiens</i> mRNA for protein encoded by cxorf5 (71-7A) gene, alternatively spliced form. //1.3e-164:770:98//Y16355	F-NT2RP3002876// <i>Homo sapiens</i> mRNA for B120, complete cds. //8.5e-89:557:88//AB001895
F-NT2RP3002377// <i>Homo sapiens</i> mRNA for KIAA0788 protein, partial cds. //1.4e-190:911:98//AB018331	F-NT2RP3002877// <i>Homo sapiens</i> chromosome 12p13.3 clone RPC111-433J, WORKING DRAFT SEQUENCE, 100 unordered pieces. //7.9e-12:160:78//AC006087
F-NT2RP3002399	F-NT2RP3002909// <i>Homo sapiens</i> mRNA for KIAA0771 protein, partial cds. //5.7e-180:853:98//AB018314
F-NT2RP3002402// <i>Rattus norvegicus</i> mRNA for dipeptidyl peptidase II, complete cds. //7.2e-25:249:79//D89340	F-NT2RP3002911//RPC111-24N15.TPC RPC111-11 <i>Homo sapiens</i> genomic clone RPC111-24N15, genomic survey sequence. //2.3e-13:442:61//B88815
F-NT2RP3002455// <i>Homo sapiens</i> mRNA for KIAA0678 protein, partial cds. //1.2e-138:649:99//AB014578	F-NT2RP3002948//, complete sequence. //2.2e-110:637:91//AC005500
F-NT2RP3002484//CIT-HSP-367N3.TP.1 CIT-HSP <i>Homo sapiens</i> genomic clone 367N3, genomic survey sequence. //5.0e-18:115:95//B78927	F-NT2RP3002953// <i>Homo sapiens</i> chromosome 5, BAC clone 34j15 (LEML H169), complete sequence. //1.7e-166:793:98//AC005754
F-NT2RP3002501// <i>Caenorhabditis elegans</i> cosmid X01C8, complete sequence. //0.00020:170:65//Z49068	F-NT2RP3002955// <i>Human</i> HepG2 partial cDNA, clone hcd3c02e5. //0.00011:61:95//D17024
F-NT2RP3002512// <i>Homo sapiens</i> clone 664 unknown mRNA, partial sequence. //1.6e-59:308:97//AF091088	F-NT2RP3002969// <i>Rat</i> mRNA for brain acyl-CoA synthetase II, complete cds. //1.2e-128:808:85//D30666
F-NT2RP3002529// <i>Human</i> vacuolar protein sorting homolog h-vps45 mRNA, complete cds. //1.4e-144:763:93//U35246	F-NT2RP3002972// <i>H. sapiens</i> (xsl68) mRNA, 381bp. //1.5e-43:312:85//Z36820
F-NT2RP3002545// <i>Homo sapiens</i> mRNA for KIAA0729 protein, partial cds. //1.8e-178:833:98//AB018272	F-NT2RP3002978// <i>Plasmodium falciparum</i> 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces. //0.0044:527:57//AC005505
F-NT2RP3002549// <i>Homo sapiens</i> clone DJ0098022, WORKING DRAFT SEQUENCE, 5 unordered pieces. //4.7e-26:123:72//AC004821	F-NT2RP3002985//Genomic sequence from Human 9q34, complete sequence. //0.92:341:60//AC001644
F-NT2RP3002566// <i>Streptomyces viridifaciens</i> sigma factor (hrdD) gene, complete cds. //0.76:459:59//U60418	F-NT2RP3002988// <i>HS_3015_A1_B07_T7</i> CIT Approved Human Genomic Sperm Library D <i>Homo sapiens</i> genomic clone Plate=3015 Col=13 Row=C, genomic survey sequence. //4.4e-05:379:58//AQ091708
F-NT2RP3002587// <i>Homo sapiens</i> chromosome Y, clone 264.M.20, complete sequence. //4.6e-13:199:76//AC004617	F-NT2RP3003008// <i>Mus musculus</i> major histocompatibility locus class III regions Hsc70t gene, partial cds: snRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds: and unknown genes. //1.4e-72:197:79//AF109905
F-NT2RP3002590// <i>Porphyra purpurea</i> chloroplast, complete genome. //0.88:284:60//U38804	F-NT2RP3003032// <i>Plasmodium falciparum</i> DNA *** SEQUENCING IN PROGRESS *** from contig 3-80, complete sequence. //1.6e-08:809:58//AL010153
F-NT2RP3002602//CIT978SK-A-441H11-2.TP CIT978SK <i>Homo sapiens</i> genomic clone A-441H11, genomic survey sequence. //2.0e-22:140:95//B68331	F-NT2RP3003059// <i>Rattus norvegicus</i> potassium channel regulator 1 mRNA, complete cds. //4.1e-111:804:81//U78090
F-NT2RP3002603	F-NT2RP3003061// <i>Human</i> mRNA for ankyrin (variant 2.1). //1.4e-12:633:59//X16609
F-NT2RP3002628// <i>C. acetobutylicum</i> dnaJ and oriB genes. //2.0e-05:333:60//X69050	F-NT2RP3003068// <i>Human</i> BAC clone RG264L19 from 7p15-p21, complete sequence. //0.034:282:60//AC002410
F-NT2RP3002631	F-NT2RP3003071// <i>H. sapiens</i> CpG island DNA genomic MseI fragment, clone 13d12, reverse read cpg13d12.rtlc. //6.8e-15:95:100//Z64565
F-NT2RP3002650// <i>Mus musculus</i> mRNA for cartilage-associated protein (CASP). //1.5e-20:41:62//AJ006469	F-NT2RP3003078
F-NT2RP3002659// <i>Bovine</i> herpesvirus type 1 UL22-35 genes. //5.2e-05:621:59//Z78205	F-NT2RP3003101// <i>Mouse</i> mRNA for tetracycline transporter-like protein, complete cds. //8.1e-72:732:71//D88315
F-NT2RP3002660// <i>Homo sapiens</i> PAC clone DJ1006K12 from 7q31.2-q31, complete sequence. //0.98:453:57//AC004946	F-NT2RP3003121
F-NT2RP3002663// <i>Homo sapiens</i> chromosome 19, cosmid F6697, complete	F-NT2RP3003133// <i>Homo sapiens</i> chromosome 19, cosmid R30385, complete sequence. //3.5e-12:168:76//AC004510
	F-NT2RP3003138// <i>Mouse</i> kif4 mRNA for microtubule-based motor protein

【0747】

【表448】

n KIF4, complete cds.//4.0e-148:908:87//D12646
 F-NT2RP3003139//Rattus norvegicus kappa opioid receptor gene, exon 4 and complete cds.//2.0e-31:658:63//U17995
 F-NT2RP3003145//Mus musculus carboxypeptidase X2 mRNA, complete cds.//3.5e-22:430:63//AF017639
 F-NT2RP3003150
 F-NT2RP3003157//HS_3055_B1_G05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=9 Row=N, genomic survey sequence.//1.9e-92:493:94//AQ155489
 F-NT2RP3003185//Rattus norvegicus brain-enriched guanylate kinase-associated protein 1 mRNA, complete cds.//8.6e-06:228:65//AF064868
 F-NT2RP3003193//H.sapiens HZF10 mRNA for zinc finger protein.//7.4e-73:737:71//X78933
 F-NT2RP3003197
 F-NT2RP3003203//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//4.1e-48:640:67//AF015264
 F-NT2RP3003204//Human Mermaid LINE-1 element mRNA sequence.//0.0033:69:81//U31059
 F-NT2RP3003210//Homo sapiens SYBL1 gene.//1.1e-34:430:70//AJ004799
 F-NT2RP3003212//Rattus norvegicus lamina associated polypeptide 1C (LAPIC) mRNA, complete cds.//6.3e-75:776:74//U20286
 F-NT2RP3003230//Rattus norvegicus mRNA for coronin-like protein.//1.8e-62:575:74//AJ006064
 F-NT2RP3003242//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.//3.7e-128:617:98//AF055460
 F-NT2RP3003251//H.sapiens Stat50 mRNA.//3.5e-67:651:76//X82200
 F-NT2RP3003264//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.015:473:58//AC004153
 F-NT2RP3003278//H.sapiens CpG island DNA genomic MseI fragment, clone 28b4, forward read cpg28b4.ftla.//4.0e-27:174:93//Z60555
 F-NT2RP3003282//Homo sapiens nckin (DNM) mRNA, complete cds.//1.3e-131:694:93//L36983
 F-NT2RP3003290//Homo sapiens nickel-specific induction protein (Cap43) mRNA, complete cds.//1.7e-64:662:71//AF084162
 F-NT2RP3003301//Spinacia oleracea mRNA for ATP-dependent protease Lon, complete cds.//4.9e-37:682:64//D85610
 F-NT2RP3003302//Homo sapiens, clone hRPK.15_A.1, complete sequence.//4.6e-95:680:82//AC006213
 F-NT2RP3003311//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete sequence.//1.0:191:62//AC004527
 F-NT2RP3003313//Streptomyces coelicolor cosmid SAT.//0.0084:403:61//AL031107
 F-NT2RP3003327//H.sapiens Stat50 mRNA.//2.5e-29:253:67//X82200
 F-NT2RP3003330
 F-NT2RP3003344
 F-NT2RP3003346//Homo sapiens chromosome 17, clone hRPK.795_F.17, complete sequence.//9.0e-41:296:84//AC005284
 F-NT2RP3003353//Human DNA sequence from PAC 97D01 on chromosome 1q24. Contains ESTs, STSs and a BAC end-sequence (GSS).//0.047:404:60//AL021069
 F-NT2RP3003377//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//8.3e-122:632:96//AC005519
 F-NT2RP3003384//Homo sapiens Chromosome 2 BAC Clone 376a1, WORKING DRAFT SEQUENCE, 17 unordered pieces.//0.0036:127:74//AC000360
 F-NT2RP3003385//Mus musculus SKD3 mRNA, complete cds.//2.0e-110:843:79//U09874
 F-NT2RP3003403//Human Chromosome X, complete sequence.//7.5e-21:647:61//AC002407
 F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds.//1.0e-20:430:63//U90653
 F-NT2RP3003411//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//4.2e-139:524:90//AF071317
 F-NT2RP3003427//HS-1051-A1-D03-MF, abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 773 Col=5 Row=G, genomic survey sequence.//8.8e-18:111:97//B40173
 F-NT2RP3003433//HS_2219_B2_A11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=22 Row=B, genomic survey sequence.//1.2e-57:410:83//AQ145866
 F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds.//5.2e-181:853:98//AF004828
 F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds.//1.6e-173:826:98//AB018268
 F-NT2RP3003491//CIT-HSP-234401, TR CIT-HSP Homo sapiens genomic clone 234401, genomic survey sequence.//1.2e-39:213:97//AQ057124
 F-NT2RP3003500//HS_3000_B1_C07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3000 Col=13 Row=F, genomic survey sequence.//0.025:253:60//AQ090347
 F-NT2RP3003543//Homo sapiens chromosome 16, cosmid clone 399H11 (L ANL), complete sequence.//0.95:279:60//AC004234
 F-NT2RP3003552//Homo sapiens clone UBCG:y54c222 from 6p21, complete sequence.//1.8e-88:166:84//AC006049
 F-NT2RP3003555//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 228H13, WORKING DRAFT SEQUENCE.//8.9e-17:245:72//AL031985
 F-NT2RP3003564//HS_3141_B1_G10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3141 Col=19 Row=N, genomic survey sequence.//2.7e-79:442:93//AQ187798
 F-NT2RP3003572
 F-NT2RP3003576//Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE, 1 unordered pieces.//5.8e-55:275:84//AC005632
 F-NT2RP3003589//Canine rab10 mRNA for ras-related GTP-binding protein.//1.1e-94:488:95//X56387
 F-NT2RP3003621//Homo sapiens chromosome 16, cosmid clone 432A1 (LA ML), complete sequence.//6.0e-88:463:84//AC004235
 F-NT2RP3003625//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 390E6, WORKING DRAFT SEQUENCE.//0.98:307:60//AL031600
 F-NT2RP3003656
 F-NT2RP3003659//F.rubripes GSS sequence, clone 013G07cE7, genomic survey sequence.//1.7e-25:284:74//AL011271
 F-NT2RP3003665//Homo sapiens chromosome 9q34, clone 63G10, complete sequence.//0.011:279:65//AC002096
 F-NT2RP3003672
 F-NT2RP3003680//Drosophila melanogaster: Chromosome 2R: Region 39B 1-39B3: P1 clone DSO5527, WORKING DRAFT SEQUENCE, 9 unordered pieces.//3.4e-16:425:64//AC005811
 F-NT2RP3003686//HS_3064_B2_A04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=8 Row=B, genomic survey sequence.//3.1e-27:153:98//AQ136993
 F-NT2RP3003701
 F-NT2RP3003716//Rattus norvegicus Shal-related potassium channel K v4.3 mRNA, complete cds.//4.6e-107:788:82//U42975
 F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete cds.//2.3e-148:700:98//AB018300
 F-NT2RP3003746//CIT-HSP-2306A10, TF CIT-HSP Homo sapiens genomic clone 2306A10, genomic survey sequence.//0.39:212:61//AQ015785
 F-NT2RP3003795//Human DNA sequence from clone 333H23 on chromosome 22q12.1-12.3. Contains the (possibly alternatively spliced) RPL3 gene for 60S Ribosomal Protein L3 and the threefold alternatively spliced gene for Synaptogyrin 1A, 1B and 1C (SYNGR1A, SYNGR1B, SYNGR1C), both genes downstream of a putative CpG island. Contains ESTs, an STS, GSSs, genomic marker D2S1155 and a ca repeat polymorphism, complete sequence.//4.2e-21:445:66//AL022326
 F-NT2RP3003799//Homo sapiens DNA from chromosome 19-cosmids R3115 B, R31874, and R28125, genomic sequence, complete sequence.//1.0:257:63//AF038458
 F-NT2RP3003800//Mouse neuronal proto-oncogene c-src mRNA encoding tyrosine-specific protein kinase, complete cds.//1.2e-63:484:81//M17031
 F-NT2RP3003805//Homo sapiens chromosome 19, cosmid R27377, complete sequence.//0.96:353:60//AC005321
 F-NT2RP3003809//Bovine herpesvirus 1 complete genome.//7.2e-12:615:60//AJ004801
 F-NT2RP3003819
 F-NT2RP3003825
 F-NT2RP3003828//Human rRNA primary transcript internal transcribed spacer 2 (ITS2).//6.2e-16:543:62//X17626
 F-NT2RP3003831//RPC111-SON15, TJ RPC111 Homo sapiens genomic clone R-SON15, genomic survey sequence.//1.1e-21:174:85//AQ082633
 F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence.//8.0e-47:242:98//AF070611
 F-NT2RP3003842//RPC111-44E5, TJ RPC111 Homo sapiens genomic clone R-44E5, genomic survey sequence.//9.7e-25:143:97//AQ195884
 F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cds.//4.2e-36:335:68//AB018268
 F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete cds.//4.1e-174:805:99//AB018343
 F-NT2RP3003876//Rattus norvegicus Rabin3 mRNA, complete cds.//2.7e-109:709:84//U19181
 F-NT2RP3003914//Drosophila melanogaster UDP-glucose:glycoprotein g lucosyltransferase mRNA, complete cds.//8.9e-11:193:70//U20554
 F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VA P-33) mRNA, complete cds.//2.6e-47:404:77//AF057358
 F-NT2RP3003932//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.68:597:55//AC005504
 F-NT2RP3003989//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 404H4, WORKING DRAFT SEQUENCE.//0.37:548:56//AL031661
 F-NT2RP3003992//Human cGMP-gated cation channel beta subunit (CNCG 2) mRNA, complete cds.//0.021:433:58//U58837

【0748】

【表449】

F-NT2RP3004013//M.musculus Spnr mRNA for RNA binding protein.//1.4 e-164:838:94//X84692
 F-NT2RP3004016//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018K9, WORKING DRAFT SEQUENCE.//0.00042:356:62//AL031726
 F-NT2RP3004041//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 809F4, WORKING DRAFT SEQUENCE.//6.8e-112:627:82//AL022400
 F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds.//2.2e-61:774:67//AB002317
 F-NT2RP3004070//Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family protein. Contains ESTs, STSs and GSSs, complete sequence.//7.9e-17:484:62//AL021939
 F-NT2RP3004078//M.musculus (BALB/c) MRF2 mRNA.//1.9e-102:684:83//X76089
 F-NT2RP3004093//F24P17-Sp6 IGF Arabidopsis thaliana genomic clone F24P17, genomic survey sequence.//0.021:207:63//B09433
 F-NT2RP3004095//Homo sapiens clone NH0486122, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.5e-25:272:77//AC005038
 F-NT2RP3004110//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//8.6e-28:223:73//AC003973
 F-NT2RP3004125//Homo sapiens TTF-1 interacting peptide 20 mRNA, partial cds.//2.2e-28:637:63//AF000560
 F-NT2RP3004145
 F-NT2RP3004148
 F-NT2RP3004155//Homo sapiens timing protein CLK-1 mRNA, complete cds.//6.5e-120:578:98//AF032900
 F-NT2RP3004189//M.musculus tex292 mRNA (5' region).//1.1e-06:102:82//X80434
 F-NT2RP3004206//D.melanogaster crn mRNA.//7.3e-69:715:71//X58374
 F-NT2RP3004207//Mouse mRNA for seizure-related gene product 6 type 2 precursor, complete cds.//4.8e-42:650:66//D64009
 F-NT2RP3004209//Human cosmid Q7A10 (D215246) insert DNA, complete sequence.//8.4e-55:184:84//D42052
 F-NT2RP3004215//Homo sapiens chromosome 5, Pac clone 9c13 (LBNI H127), complete sequence.//0.22:458:60//AC006084
 F-NT2RP3004242//Caenorhabditis elegans cosmid ZK632, complete sequence.//1.6e-29:409:69//Z22181
 F-NT2RP3004246//Homo sapiens chromosome 10 clone C178B7SK-1010K1 map 10q25, complete sequence.//3.6e-117:242:100//AC005385
 F-NT2RP3004253//H.sapiens 28S rRNA V8 region (LAN5-6).//2.6e-12:589:59//X69353
 F-NT2RP3004258//Rattus norvegicus Zis mRNA, complete cds.//1.2e-8:489:97//AF013967
 F-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, complete cds.//3.1e-153:733:98//AF088982
 F-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds.//1.3e-24:597:61//AF007871
 F-NT2RP3004332
 F-NT2RP3004334//L.esculentum gene for fruit ripening polygalacturonase.//0.23:501:57//X80908
 F-NT2RP3004341//Human DNA sequence from clone 503G16 on chromosome 6p23 Contains EST, CpG island, complete sequence.//0.0014:198:66//Z93020
 F-NT2RP3004348//R.norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//1.4e-103:600:82//X67877
 F-NT2RP3004349//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//5.1e-49:480:75//AC004025
 F-NT2RP3004378//Drosophila melanogaster: Chromosome 2R: Region 47F 1-47F7; Pl clone DS02304, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.8e-23:352:67//AC005653
 F-NT2RP3004399//H.sapiens mRNA for leucine-rich primary response protein 1.//7.2e-140:804:90//X97249
 F-NT2RP3004424//Mus musculus mRNA for nuclear protein SA3.//6.8e-53:413:81//AJ005678
 F-NT2RP3004428//Salmo salar DNA for a cryptic repeat.//3.2e-07:270:63//AJ012206
 F-NT2RP3004451//RPC111-51J15.TK RPC111 Homo sapiens genomic clone R-51J15, genomic survey sequence.//8.8e-19:180:82//AQ052326
 F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds.//6.2e-123:583:99//AB007917
 F-NT2RP3004466//HS_3038_B2_F08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3038 Col=16 Row=L, genomic survey sequence.//0.41:172:59//AQ102458
 F-NT2RP3004470//H.sapiens CpG island DNA genomic MseI fragment, clone Blal1, reverse read cpg81a11.r11a.//7.0e-25:148:96//Z56029
 F-NT2RP3004472//RPC111-42M5.TJ RPC111 Homo sapiens genomic clone R-42M5, genomic survey sequence.//1.6e-20:143:92//AQ052792
 F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds.//3.0e-150:715:98//AB007925
 F-NT2RP3004480//Mus musculus maternal-embryonic 3 (Mem3) mRNA, complete cds.//1.0e-119:679:90//U47024
 F-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds.//7.1e-155:752:97//AB012851
 F-NT2RP3004498//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//4.0e-67:265:84//AC006023
 F-NT2RP3004503//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//1.2e-55:415:78//AC004673
 F-NT2RP3004504//M.musculus mRNA for CPB protein.//2.0e-110:618:91//X08260
 F-NT2RP3004507//Homo sapiens chromosome 19, cosmid.R26660, complete sequence.//9.3e-46:433:76//AC005328
 F-NT2RP3004527//Homo sapiens mRNA; transcriptional unit N144, 5' end.//1.1e-100:508:97//AJ002574
 F-NT2RP3004534//Mouse oncogene (ect2) mRNA, complete cds.//2.0e-93:442:84//L11316
 F-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds.//8.5e-145:679:98//AB014532
 F-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds.//2.8e-169:793:98//AB011126
 F-NT2RP3004566//Mus musculus kruppel-related zinc finger protein (Ezfl1) mRNA, complete cds.//6.9e-18:433:64//AF031955
 F-NT2RP3004569//CITB1-E1-2522H6.TF CITB1-E1 Homo sapiens genomic clone 2522H6, genomic survey sequence.//5.3e-15:138:84//AQ280780
 F-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF15) mRNA, complete cds.//1.0e-179:860:97//AF026445
 F-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//4.2e-150:711:98//AB007946
 F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein.//1.1e-158:796:95//AJ006266
 F-NT2RP3004617//Homo sapiens clone DJ1152C17, WORKING DRAFT SEQUENCE, 1 unordered piece.//9.3e-14:360:65//AC004977
 F-NT2RP3004618//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.9e-52:539:73//AF005355
 F-NT2RP3004669//Brn-3a=class V POU transcription factor [mice, CD/CD, embryo fibroblast cells, Genomic, 2160 nt].//0.046:437:57//S69350
 F-NT2RP3004670//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 35688, WORKING DRAFT SEQUENCE.//1.9e-05:625:59//Z98882
 F-NT2RP4000008//Homo sapiens chromosome X, clone hCIT.200.L4, complete sequence.//1.5e-155:844:92//AC006121
 F-NT2RP4000023//Arabidopsis thaliana genomic DNA, chromosome 5, TA clone: K24G6, complete sequence.//0.012:417:59//AB012242
 F-NT2RP4000035//Homo sapiens BAC clone NH0353P23 from 2, complete sequence.//8.0e-18:242:74//AC005035
 F-NT2RP4000049//Homo sapiens decoy receptor 2 mRNA, complete cds.//2.1e-81:556:85//AF029761
 F-NT2RP4000051//Mus musculus mRNA for cartilage-associated protein (CASP).//1.6e-19:654:63//AJ006469
 F-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.5e-149:720:97//AJ012449
 F-NT2RP4000102//Plasmodium falciparum MAL3P2, complete sequence.//0.28:336:57//AL034558
 F-NT2RP4000109//Homo sapiens mRNA for MECF5, partial cds.//4.4e-166:774:99//AB011538
 F-NT2RP4000111//B.taurus mRNA for cleavage and polyadenylation specificity factor.//2.6e-137:678:91//X75931
 F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds.//3.3e-114:548:98//AB007952
 F-NT2RP4000147//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//1.2e-104:677:85//U35776
 F-NT2RP4000150//Rat proto-oncogene (Ets-1) mRNA, complete cds.//7.2e-54:327:74//L20681
 F-NT2RP4000151//Homo sapiens clone 664 unknown mRNA, partial sequence.//2.2e-62:360:92//AF091088
 F-NT2RP4000159//RPC111-75N16.TJ RPC111 Homo sapiens genomic clone R-75N16, genomic survey sequence.//2.6e-19:119:98//AQ267551
 F-NT2RP4000167//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//3.3e-49:683:67//AC006210
 F-NT2RP4000185//Homo sapiens clone DTIPIE11 mRNA, CAG repeat region.//1.1e-99:543:93//U92989
 F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//4.4e-174:825:98//AB014600
 F-NT2RP4000212//, complete sequence.//4.0e-131:233:94//AC005300
 F-NT2RP4000214//Homo sapiens chromosome 19, CIT-HSP-444n24, complete

【0749】

【表450】

te sequence.//1.8e-161:751:99//AC005261	DNA binding protein and Myc-associated zinc finger protein, complete cds.//1.9e-11:104:85//AB017335
F-NT2RP4000218//RPC111-6987.TJ RPC111 Homo sapiens genomic clone R-6987, genomic survey sequence.//1.7e-84:413:98//AQ268504	F-NT2RP4000657//Mus musculus bone morphogenetic factor 11 (Bmp11) gene, exon 1.//0.34:350:62//AF100904
F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//2.6e-156:771:97//AJ006470	F-NT2RP4000704//Homo sapiens mRNA expressed in 19week fetal lung, clone IMAGE:300856.//3.3e-167:785:99//AB004852
F-NT2RP4000246//Mus musculus neural variant menatt+ protein (Mena) mRNA, complete cds.//2.1e-120:707:87//U72523	F-NT2RP4000713//Gallus gallus atonal homolog 1 (Cath1) gene, complete cds.//3.7e-07:261:65//U61149
F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence.//2.8e-128:604:99//AF091092	F-NT2RP4000724//Human endogenous retrovirus env mRNA.//9.2e-136:474:89//X82272
F-NT2RP4000263//CIT-HSP-2336M24.TF CIT-HSP Homo sapiens genomic clone 2336M24, genomic survey sequence.//0.27:124:69//AQ043515	F-NT2RP4000728//Homo sapiens mRNA for KIAA0606 protein, partial cds.//3.1e-41:350:71//AB011178
F-NT2RP4000290//S.cerevisiae chromosome XIV reading frame ORF YNL132w.//8.6e-32:619:63//Z71408	F-NT2RP4000737//Myxococcus xanthus ATP-dependent protease (hsaA) gene, complete cds.//1.0:504:58//L19301
F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds.//4.7e-41:685:63//D63481	F-NT2RP4000739//CIT-HSP-2010022.TR CIT-HSP Homo sapiens genomic clone 2010022, genomic survey sequence.//1.1e-24:161:93//B57903
F-NT2RP4000321//Mus musculus transcription factor HOXA13 (Hoxa13) gene, complete cds.//6.9e-05:756:59//U59322	F-NT2RP4000781//Homo sapiens clone DJ0892G19, complete sequence.//0.052:493:58//AC004917
F-NT2RP4000323	F-NT2RP4000787//Cricetulus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mRNA, complete cds.//9.6e-18:259:68//U22818
F-NT2RP4000355	F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds.//1.5e-174:816:98//AB007939
F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//2.0e-140:654:99//AB018281	F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.97:52:92//AC005189
F-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//2.6e-135:649:97//AF044195	F-NT2RP4000837//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1112F19, WORKING DRAFT SEQUENCE.//2.1e-128:644:97//AL034420
F-NT2RP4000370//Rickettsia prowazekii strain Madrid E, complete genome: segment 3/4.//2.0e-23:524:62//AJ235272	F-NT2RP4000839//RPC111-608.TP RPC111 Homo sapiens genomic clone R-608, genomic survey sequence.//1.5e-44:281:91//B48216
F-NT2RP4000376//Sequence 1 from patent US 5580968.//1.6e-115:716:87//J30536	F-NT2RP4000855//Rattus norvegicus mRNA for aminopeptidase-B, complete cds.//9.5e-43:722:64//D87515
F-NT2RP4000381//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain: BALB/c.//4.3e-05:450:58//D63850	F-NT2RP4000865//Human zinc finger protein ZNF136.//6.8e-95:415:78//U09367
F-NT2RP4000398//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//9.2e-37:336:69//AC006116	F-NT2RP4000878//Mus musculus mRNA for myeloid associated differentiation protein.//7.0e-87:646:80//AJ001616
F-NT2RP4000415//Caenorhabditis elegans cosmid C4208.//0.30:222:60//U56966	F-NT2RP4000879//N.tabacum mRNA for ubiquitin activating enzyme E1.//9.0e-17:806:58//Y10804
F-NT2RP4000417//Drosophila melanogaster cosmid clone 86E4.//1.8e-48:580:69//AL021086	F-NT2RP4000907//Mouse NLRR-1 mRNA for leucine-rich-repeat protein, complete cds.//6.8e-153:934:86//U45913
F-NT2RP4000424//Homo sapiens chromosome 17, clone HRP41C23, complete sequence.//1.6e-42:265:81//AC003101	F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein.//9.4e-79:584:78//AJ224901
F-NT2RP4000448//CIT-HSP-2370F8.TF CIT-HSP Homo sapiens genomic clone 2370F8, genomic survey sequence.//2.0e-56:287:98//AQ110194	F-NT2RP4000918//Drosophila melanogaster DNA sequence (P1 D504106 (D172)), complete sequence.//2.0e-08:609:58//AC004290
F-NT2RP4000449//CIT-HSP-2366M18.TR CIT-HSP Homo sapiens genomic clone 2366M18, genomic survey sequence.//2.4e-42:236:95//AQ076183	F-NT2RP4000925//Rattus norvegicus Shal-related potassium channel Kv4.3 mRNA, complete cds.//3.5e-64:415:87//U42975
F-NT2RP4000455//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//0.17:158:67//AC003982	F-NT2RP4000927//H. sapiens genomic DNA (Chromosome 3: clone NRL062 R).//0.75:175:62//X87547
F-NT2RP4000457//H. sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP).//0.00034:532:57//Z72499	F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//3.5e-163:781:97//AF069532
F-NT2RP4000480//Rhodothermus marinus R-21 DNA ligase gene, complete cds.//0.0094:616:58//X740483	F-NT2RP4000929//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.94:763:56//AC004608
F-NT2RP4000481	F-NT2RP4000955//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUENCE, 34 unordered pieces.//1.0e-128:673:96//AC005519
F-NT2RP4000498//S.cerevisiae chromosome IX cosmid 9150.//5.7e-24:633:60//Z38125	F-NT2RP4000973//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//1.6e-15:255:69//AL032657
F-NT2RP4000500//G.gallus mRNA for LRP/alpha-2-macroglobulin receptor.//2.4e-62:667:73//X74904	F-NT2RP4000975//CIT-HSP-230716.TF CIT-HSP Homo sapiens genomic clone 230716, genomic survey sequence.//6.5e-31:317:79//AQ015742
F-NT2RP4000515	F-NT2RP4000979//Human bullous pemphigoid antigen mRNA, 3' end.//0.88:54:90//W22942
F-NT2RP4000517//Homo sapiens chromosome 18, clone hRPK.474_N_24, complete sequence.//1.6e-179:851:98//AC006238	F-NT2RP4000984//Rhodobacter sphaeroides mRNA.//0.76:214:64//M83823
F-NT2RP4000518//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//6.7e-33:203:93//AJ010840	F-NT2RP4000989//F.rubripes GSS sequence, clone 011A11aE12, genomic survey sequence.//1.0:149:65//AL010911
F-NT2RP4000519//Mus musculus tyrosine kinase growth factor receptor (Etk2/tyro3) gene, alternative 5' coding exon 2C.//0.26:162:61//U23720	F-NT2RP4000996//Penaeus setiferus microsatellite Pse017 repeat region.//3.3e-08:139:74//AF047358
F-NT2RP4000524//Rattus norvegicus rsec8 mRNA, partial cds.//1.2e-139:809:89//U32498	F-NT2RP4000997//Rattus norvegicus RNA polymerase I 127 kDa subunit mRNA, complete cds.//3.6e-126:824:84//AF025424
F-NT2RP4000528//Caenorhabditis elegans cosmid F59E12.//1.0e-06:404:59//AF003386	F-NT2RP4001004
F-NT2RP4000541//Drosophila melanogaster DNA sequence (P1 D502109 (D53)), complete sequence.//1.3e-05:498:58//AC002443	F-NT2RP4001006//Mus musculus ROSA 26 transcription AS ROSA26AS mRNA, complete cds.//1.4e-110:861:78//U83176
F-NT2RP4000556//Sequence 1 from Patent EP 0285405.//1.2e-18:586:61//I05465	F-NT2RP4001010//Rattus norvegicus PSD-95/SAP90-associated protein-4 mRNA, complete cds.//2.0e-135:789:89//U67140
F-NT2RP4000560//Murine genomic DNA: partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence.//2.5e-53:183:82//AF059580	F-NT2RP4001029//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//3.7e-120:718:88//U20086
F-NT2RP4000588//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 41407, WORKING DRAFT SEQUENCE.//0.00062:253:65//AL033543	F-NT2RP4001041//Schizosaccharomyces pombe mRNA, partial cds, clone: SY 0717.//4.1e-22:452:64//D89170
F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//3.2e-138:666:98//AF067730	F-NT2RP4001057
F-NT2RP4000638//HS_3042_82_005_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3042 Col=10 Row=M, genomic survey sequence.//3.0e-06:78:89//AQ099333	F-NT2RP4001064//Mus musculus mRNA for cartilage-associated protein (CASP).//1.2e-20:639:62//AJ006469
F-NT2RP4000648//Homo sapiens KNSL4 and MAZ genes for kinesin-like	

【0750】

【表451】

F-NT2RP4001078//Streptomyces coelicolor cosmid IC2.//0.0025:474:59//AL031124	F-NT2RP4001407//P.falci-parum glutamic acid-rich protein gnen, complete cds.//0.00079:686:57//J03998
F-NT2RP4001079//Rat alternatively spliced mRNA.//1.4e-141:832:88//M93018	F-NT2RP4001414//Human mRNA for KIAA202 gene, partial cds.//2.0e-7 6:818:71//D86957
F-NT2RP4001080//H.sapiens PTB-4 gene for polypirimidine tract binding protein.//9.0e-64:628:70//X65372	F-NT2RP4001433//H.sapiens HZF10 mRNA for zinc finger protein.//3.5 e-87:839:73//X78933
F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds.//4.7e-84:604:86//AB011164	F-NT2RP4001442
F-NT2RP4001095	F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds.//0.21:218:63//AB018326
F-NT2RP4001100//CITBI-EI-2503J7.TR CITBI-EI Homo sapiens genomic clone 2503J7, genomic survey sequence.//9.4e-17:185:79//AQ263402	F-NT2RP4001474//Human NotI linking clone 924A058R, genomic survey sequence.//7.6e-14:109:90//U49884
F-NT2RP4001117//Canis familiaris secB1 homologue mRNA, complete cds.//1.0e-143:760:87//M96629	F-NT2RP4001483//Human mRNA for 2-oxoglutarate dehydrogenase, complete cds.//2.5e-59:480:75//D10523
F-NT2RP4001122	F-NT2RP4001498//Homo sapiens huntingtin interacting protein HYPH mRNA, partial cds.//9.7e-39:392:72//AF049612
F-NT2RP4001126//Homo sapiens shox gene, alternatively spliced products, complete cds.//4.2e-17:636:61//U82668	F-NT2RP4001502//H.sapiens (DBS135) DNA segment containing GT repeat.//2.7e-24:147:96//X61693
F-NT2RP4001138//Homo sapiens PAC clone DJ1121E10 from 7q21.1-q2, complete sequence.//2.5e-23:408:60//AC004969	F-NT2RP4001507//Plasmid pSB24.2 (from S.cyanogenus) neomycin resistance protein gene, complete cds.//0.87:583:58//W32513
F-NT2RP4001143//Sequence 5 from patent US 5753432.//1.8e-39:276:86//A0008079	F-NT2RP4001524//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.9 3:394:58//AC005308
F-NT2RP4001148//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.7e-116:684:89//AC005095	F-NT2RP4001529//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//3.1e-143:820:89//U20086
F-NT2RP4001149//Mouse mRNA for thymic epithelial cell surface antigen, complete cds.//3.0e-48:581:66//D67067	F-NT2RP4001547//S.cerevisiae chromosome XIV reading frame ORF YNR04Bw.//2.2e-05:319:61//Z71663
F-NT2RP4001150//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.4e-25:193:67//AC004952	F-NT2RP4001551//S.pombe chromosome 11 pl p8B7.//0.64:335:60//AL032684
F-NT2RP4001159//Human FMR1 gene, 5' end.//0.28:130:66//L19476	F-NT2RP4001555//Homo sapiens 12q24.2 BAC RPC111-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.0:30 9:58//AC004806
F-NT2RP4001174//FMR1 (CCG repeats) [human, Fragile X syndrome patient, Genomic, 429 nt].//0.0014:187:67//S74494	F-NT2RP4001567//HS_2166_B1_C07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2166 Col=13 Row=F, genomic survey sequence.//0.99:188:59//AQ086290
F-NT2RP4001206//Dictyostelium discoideum random slug cDNA19 protein (rsc19) mRNA, partial cds.//0.032:453:58//U82511	F-NT2RP4001568//Human mRNA for KIAA0167 gene, complete cds.//7.0e-53:566:72//D79989
F-NT2RP4001207//HS_2248_A1_C03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2248 Col=5 Row=E, genomic survey sequence.//0.00018:58:94//AQ192358	F-NT2RP4001571//RPC111-21F20.TP RPC11-11 Homo sapiens genomic clone RPC11-11-21F20, genomic survey sequence.//2.8e-19:119:97//B85885
F-NT2RP4001210//Homo sapiens chromosome 10 clone C17987SK-1019018 map 10p11.2-10p12.1, complete sequence.//0.93:515:58//AC005877	F-NT2RP4001574//B.primigenius mRNA for coat protein gamma-cop.//5.8e-129:813:85//X92987
F-NT2RP4001213//Human KRAB zinc finger protein (ZNF177) mRNA, splicing variant, complete cds.//3.6e-44:187:74//U37251	F-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein.//3.4e-13 1:795:86//AJ223830
F-NT2RP4001219//Caenorhabditis elegans cosmid Y47H9C, complete sequence.//1.3e-15:288:67//AL032657	F-NT2RP4001592//S.aureus gene for isoleucyl-tRNA synthetase.//1.3 e-14:663:59//X74219
F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//2.2e-26:855:60//AF059569	F-NT2RP4001610//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12, U11589 (Lawrence Livermore human cosmid library) complete sequence.//6.4e-10:135:73//AC002364
F-NT2RP4001235//RPC111-18E11.TVB RPC11-11 Homo sapiens genomic clone a RPC11-11-18E11, genomic survey sequence.//2.7e-15:101:98//B88081	F-NT2RP4001614//HS_3042_B2_D05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3042 Col=10 Row=H, genomic survey sequence.//3.4e-06:78:89//AQ099333
F-NT2RP4001256//Amycolatopsis mediterranei 3-amino-5-hydroxy benzoic acid synthase (rifD) gene, complete cds.//1.0:459:59//U33061	F-NT2RP4001634
F-NT2RP4001260//Sequence 2 from Patent W09601901.//0.0018:246:63//A48324	F-NT2RP4001638//cSRL-161F1-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-161F1, genomic survey sequence.//4.9e-12:144:76//B02870
F-NT2RP4001274//Homo sapiens, complete sequence.//2.5e-05:201:67//AC005854	F-NT2RP4001644//M.musculus mRNA for map kinase interacting kinase, Mnk2.//3.8e-69:437:86//Y11092
F-NT2RP4001276//CIT-HSP-2324B15.TF CIT-HSP Homo sapiens genomic clone 2324B15, genomic survey sequence.//3.5e-18:138:92//AQ040728	F-NT2RP4001656//HS_2013_A1_D01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2013 Col=1 Row=G, genomic survey sequence.//2.0e-30:207:89//AQ224793
F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//7.4e-30:535:65//AF043250	F-NT2RP4001677//Hylobates lar huntingtin gene, partial exon.//0.2 3:105:71//L49362
F-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5.//3.5e-145:795:91//AJ001119	F-NT2RP4001679//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 462023, WORKING DRAFT SEQUENCE.//2.7e-45:351:84//AL031431
F-NT2RP4001336//CIT-HSP-2169F21.TR CIT-HSP Homo sapiens genomic clone 2169F21, genomic survey sequence.//8.4e-16:109:94//B89870	F-NT2RP4001696//Human chromosome 8 BAC clone C17987SK-2A8 complete sequence.//1.8e-30:163:88//U96629
F-NT2RP4001339//HS_3205_B1_E08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3205 Col=15 Row=J, genomic survey sequence.//7.1e-24:305:73//AQ183725	F-NT2RP4001725//Drosophila melanogaster DNA sequence (P1 DS08860 (D181)), complete sequence.//1.1e-13:402:63//AC004296
F-NT2RP4001343//Homo sapiens PAC clone DJ0894A10 from 7q32-q32, complete sequence.//1.9e-17:106:91//AC004918	F-NT2RP4001730//RPC111-37M21.TK RPC11-11 Homo sapiens genomic clone RPC11-11-37M21, genomic survey sequence.//0.88:177:67//AQ029840
F-NT2RP4001345//G.gallus mRNA for lecithin-cholesterol acyltransferase.//7.6e-40:631:66//X91011	F-NT2RP4001739
F-NT2RP4001351//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 184J9, WORKING DRAFT SEQUENCE.//2.7e-30:608:64//AL031428	F-NT2RP4001753//H.sapiens telomeric DNA sequence, clone 12QTEL023, read 12QTEL00023.seq.//4.9e-36:192:98//Z96232
F-NT2RP4001353//Streptomyces coelicolor cosmid 5A7.//0.23:540:57//AL031107	F-NT2RP4001760//Mouse oncogene (ect2) mRNA, complete cds.//2.3e-14 0:866:86//L11316
F-NT2RP4001372//RPC111-49L11.TJ RPC111 Homo sapiens genomic clone R-49L11, genomic survey sequence.//8.5e-23:129:100//AQ051701	F-NT2RP4001790//Homo sapiens clone NH0569124, complete sequence.//1.4e-29:327:74//AC005678
F-NT2RP4001373//G.gallus genomic DNA repeat region, clone 16E1.//0.15:213:61//X78609	F-NT2RP4001803
F-NT2RP4001375	F-NT2RP4001822//Homo sapiens tetraspan TM4SF (TSPAN-4) mRNA, complete cds.//1.0e-16:576:60//AF054841
F-NT2RP4001379//Homo sapiens chromosome 17, clone hRPK.311_F_12, complete sequence.//7.3e-28:153:88//AC005722	
F-NT2RP4001389//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//7.2e-47:518:73//AC004961	

【0751】

【表452】

F-NT2RP4001823//Human DNA sequence from clone 181C9 on chromosome 22q13.2-13.33. Contains a PHAP12 Leucine Rich Acidic Nuclear Protein in pseudogene, part of a putative novel gene. ESTs, STSs and GSSs, complete sequence.//2.1e-08:601:59//Z98743

F-NT2RP4001828

F-NT2RP4001838//Human mRNA for KIAA0071 gene, partial cds.//2.2e-5 3:555:73//D31888

F-NT2RP4001841

F-NT2RP4001849//Homo sapiens mRNA for KIAA0672 protein, complete cds.//1.7e-55:813:65//AB014572

F-NT2RP4001861//Human simple repeat polymorphism.//0.0014:145:66//M87691

F-NT2RP4001889//HS_2052_B1_H06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=11 Row=P, genomic survey sequence.//1.0e-23:187:86//AQ270425

F-NT2RP4001893//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//7.3e-76:178:95//AC005014

F-NT2RP4001896//T384TFC TAMU Arabidopsis thaliana genomic clone T3 B4, genomic survey sequence.//0.99:354:61//B26193

F-NT2RP4001901//Streptomyces griseus genes for Orf2, Orf3, Orf4, Orf5, AfsA, Orf8, partial and complete cds.//0.031:409:60//AB011413

F-NT2RP4001927//HS_2216_B1_D03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2216 Col=5 Row=M, genomic survey sequence.//4.9e-32:216:89//AQ184677

F-NT2RP4001938//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//1.2e-83:709:79//U49046

F-NT2RP4001946//HS_3021_B1_H10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3021 Col=20 Row=P, genomic survey sequence.//7.6e-09:120:76//AQ133185

F-NT2RP4001950//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SMARCA1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.1e-18:421:65//AL022577

F-NT2RP4001953//CIT-HSP-2294D14.TR CIT-HSP Homo sapiens genomic clone 2294D14, genomic survey sequence.//0.030:358:61//AQ005028

F-NT2RP4001966//Mus musculus Doc4 (Doc4) mRNA, complete cds.//2.5e-68:812:68//AF059485

F-NT2RP4001975//Homo sapiens chromosome 17, clone hCIT.91_J_4, complete sequence.//1.9e-57:555:75//AC003976

F-NT2RP4002018//cSRL-143G4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-143G4, genomic survey sequence.//8.9e-21:123:98//B01950

F-NT2RP4002047//Saccharomyces cerevisiae chromosome XII cosmid 800 3, //1.6e-29:520:64//U17243

F-NT2RP4002052//CIT-HSP-2045A15.TF CIT-HSP Homo sapiens genomic clone 2045A15, genomic survey sequence.//2.8e-22:137:96//B80243

F-NT2RP4002058//T20L11-77 TAMU Arabidopsis thaliana genomic clone T20L11, genomic survey sequence.//0.019:141:65//AQ248640

F-NT2RP4002071//CIT-HSP-2314J9.TF CIT-HSP Homo sapiens genomic clone 2314J9, genomic survey sequence.//0.99:163:63//AQ027223

F-NT2RP4002075//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y57G11, WORKING DRAFT SEQUENCE.//0.15:506:59//Z92841

F-NT2RP4002078//RPC111-73M20.TJ RPC111 Homo sapiens genomic clone R-73M20, genomic survey sequence.//4.8e-21:130:96//AQ269030

F-NT2RP4002081//F. rubripes GSS sequence, clone 190022689, genomic survey sequence.//0.0024:350:60//Z92062

F-NT2RP4002083//M. musculus tex27 mRNA.//8.2e-77:456:89//X80437

F-NT2RP4002408//Caenorhabditis elegans serine/threonine kinase LEY-502 (let-502) mRNA, complete cds.//3.7e-18:541:62//U85515

F-NT2RP4002791

F-NT2RP4002888//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//4.7e-39:385:75//AC002383

F-NT2RP4002905//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence.//6.5e-91:672:83//AC004662

F-NT2RP5003459//Human glyceraldehyde-3-phosphate dehydrogenase (GAPDH) mRNA, complete cds.//2.9e-37:193:99//M33197

F-NT2RP5003461//Human DNA sequence from PAC 506G2 contains ESTs.//7.9e-51:300:80//Z82901

F-NT2RP5003477//Human Chromosome 3 pac pJ70111, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.7e-77:150:100//AC000380

F-NT2RP5003492

F-NT2RP5003500//Human DNA sequence from cosmid 97K10, between markers DXS6791 and DXS8038 on chromosome X contains STSs and CpG island.//1.7e-111:623:93//Z81365

F-NT2RP5003506//H. sapiens CpG island DNA genomic MseI fragment, clone 71h2, reverse read cpg71h2, rta.//1.4e-49:283:93//Z62703

F-NT2RP5003512//HS_3084_A1_D04_MF CIT Approved Human Genomic Sperm

Library D Homo sapiens genomic clone Plate=3084 Col=7 Row=G, genomic survey sequence.//7.7e-18:117:95//AQ186312

F-NT2RP5003522//Homo sapiens clone NHD479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.8e-101:211:96//AC005236

F-NT2RP5003524//Homo sapiens beta-spectrin (HSPB1) gene, exon 14 and partial cds.//0.00056:650:57//AF013178

F-NT2RP5003534//H. sapiens CpG island DNA genomic MseI fragment, clone 14c10, forward read cpg14c10, rta.//0.00013:70:91//Z54631

F-OVARI1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds.//1.2e-67:373:94//AB007934

F-OVARI1000004//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//5.8e-93:518:81//AC005510

F-OVARI1000006//Gallus gallus histone H2A (H2A-VIII) gene, complete cds.//9.1e-56:392:84//U38933

F-OVARI1000013

F-OVARI1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//5.6e-170:815:98//AF058922

F-OVARI1000017//Streptomyces glaucescens tcm operon.//0.37:347:60//M80674

F-OVARI1000035//Homo sapiens GAI7 protein mRNA, complete cds.//6.8e-36:238:89//AF064603

F-OVARI1000058

F-OVARI1000060//Homo sapiens ribonuclease 6 precursor, mRNA, complete cds.//2.5e-36:192:98//U85625

F-OVARI1000068//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 404K8, WORKING DRAFT SEQUENCE.//0.14:554:57//AL023883

F-OVARI1000071//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 596C15, WORKING DRAFT SEQUENCE.//5.3e-104:197:100//AL031387

F-OVARI1000085//Human DNA sequence from clone 191N21 on chromosome 6q27 Contains genes for PDCD2 (PROGRAMMED CELL DEATH-2/RP8 HOMOLOG), TATA factor (TFIID), proteasome subunit HC5, EST, STS, GSS, complete sequence.//1.6e-116:588:96//AL031259

F-OVARI1000087//HS_2004_B2_E11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2004 Col=22 Row=J, genomic survey sequence.//7.1e-11:94:94//AQ221037

F-OVARI1000091//nxbx0020P17r CUGI Rice BAC Library Oryza sativa genomic clone nxbx0020P17r, genomic survey sequence.//5.2e-05:238:64//AQ258489

F-OVARI1000092//Homo sapiens chromosome Y, clone 254.M.20, complete sequence.//1.1e-10:720:58//AC004617

F-OVARI1000106//HS_3212_B2_G12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3212 Col=24 Row=N, genomic survey sequence.//9.9e-05:141:73//AQ175369

F-OVARI1000109

F-OVARI1000113//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//1.6e-133:663:96//AF069250

F-OVARI1000114//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1111N9, WORKING DRAFT SEQUENCE.//2.3e-51:547:70//AL022574

F-OVARI1000133//Homo sapiens clone G5512121, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.62:349:61//AC005027

F-OVARI1000139//Caenorhabditis elegans cosmid F09D1.//2.5e-18:314:64//AF040640

F-OVARI1000145//HS_2257_B2_D11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2257 Col=22 Row=H, genomic survey sequence.//5.8e-30:203:90//AQ304854

F-OVARI1000148//CIT-HSP-2345A22.TR CIT-HSP Homo sapiens genomic clone 2345A22, genomic survey sequence.//1.1e-26:146:100//AQ056703

F-OVARI1000151//Sequence 1 from patent US 5665588.//2.6e-61:677:70//164695

F-OVARI1000168//Homo sapiens chromosome 19, cosmid R31343, complete sequence.//4.9e-19:381:63//AC005764

F-OVARI1000191//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//1.3e-06:745:57//AL034557

F-OVARI1000198//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0366H07: HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//6.4e-161:781:97//AC004604

F-OVARI1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//9.2e-33:511:65//AF068332

F-OVARI1000212//F. rubripes GSS sequence, clone 185L11aC1, genomic survey sequence.//1.1e-13:139:79//AL019910

F-OVARI1000240//Sequence 1 from patent US 5710024.//1.4e-129:623:98//181226

F-OVARI1000241//Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//1.1e-112:697:87//AF060194

F-OVARI1000288

2.2e-22:181:83//J00345

F-OVARI1000302//A-192A9.TP CIT978SK Homo sapiens genomic clone A-1

【表453】

92A9, genomic survey sequence.//4.8e-18:110:99//B18003
 F-OVARC1000304//Mouse mRNA from Mov10 locus.//5.5e-100:631:85//X52574
 F-OVARC1000309
 F-OVARC1000321//Homo sapiens clone NH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.1e-122:325:95//AC005236
 F-OVARC1000326//Rattus norvegicus lamina-associated polypeptide IC (LAPIC) mRNA, complete cds.//4.0e-46:339:84//U19614
 F-OVARC1000335//Caenorhabditis elegans cosmid F15B10.//0.020:545:57//AF036696
 F-OVARC1000347//Homo sapiens clone GS051M12, complete sequence.//0.71:252:59//AC005007
 F-OVARC1000384//Homo sapiens expanded SCAT CAG repeat.//2.2e-09:276:64//AF020275
 F-OVARC1000408//Human Chromosome 11p15.5 PAC clone pDJ915f1 containing KvLQT1 gene, complete sequence.//0.61:343:59//AC003693
 F-OVARC1000411//S. cerevisiae chromosome XI reading frame ORF YKL202w.//0.075:242:60//Z28201
 F-OVARC1000414//Homo sapiens PAC clone DJ0905M06 from 7q31, complete sequence.//0.00088:285:62//AC005166
 F-OVARC1000420//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 371H6, WORKING DRAFT SEQUENCE.//0.14:487:60//AL031718
 F-OVARC1000427//Homo sapiens clone UMCC:rg04la03 from 7p14-15, complete sequence.//4.9e-30:195:84//AC005826
 F-OVARC1000431//Plasmodium falciparum MAL3P2, complete sequence.//1.3e-05:651:59//AL034558
 F-OVARC1000437//Chicken tensin mRNA, complete cds.//9.6e-54:296:78//M74165
 F-OVARC1000440//Human PINCH protein mRNA, complete cds.//2.7e-19:116:99//U09284
 F-OVARC1000442//Human DNA sequence from clone 81GK17 on chromosome 20p12.2-13 Contains TGM3 (PROTEIN-GLUTAMINE GLUTAMYLTRANSFERASE E3 PRECURSOR (EC 2.3.2.13) (TGASE E3) (TRANSGlutAMINASE 3), and another member of the Transglutaminase family, complete sequence.//1.0e-21:202:79//AL031678
 F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete cds.//1.0e-138:566:99//AB014583
 F-OVARC1000461
 F-OVARC1000465//Bos taurus guanine nucleotide-exchange protein (ARF-GEF1) mRNA, complete cds.//4.7e-124:650:93//AF023451
 F-OVARC1000466//Homo sapiens DNA from chromosome 19, cosmid R29144, complete sequence.//1.0e-15:510:59//AC004221
 F-OVARC1000473//Ciona intestinalis genomic fragment, clone 3F4, genomic survey sequence.//2.5e-06:272:62//AJ227191
 F-OVARC1000479//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).//1.1e-117:652:90//E12829
 F-OVARC1000486//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neuronection, Myotendinous antigen)-LIKE gene and a mitochondrial/c chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker DIS2691 and STSs.//1.7e-13:709:60//Z99297
 F-OVARC1000496//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 455J7, WORKING DRAFT SEQUENCE.//6.0e-23:316:72//AL031713
 F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.1e-113:539:99//AF051850
 F-OVARC1000526//Homo sapiens clone GS438P06, WORKING DRAFT SEQUENCE, 17 unordered pieces.//8.0e-149:716:98//AC005024
 F-OVARC1000533//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//5.8e-137:545:97//AC004510
 F-OVARC1000543//HS_3055_A2_F10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=20 Row=K, genomic survey sequence.//0.19:104:71//AQ102820
 F-OVARC1000556//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS, CpG island, complete sequence.//4.4e-136:670:97//AL022069
 F-OVARC1000557//Human DNA from chromosome 19-specific cosmid R27090, genomic survey sequence, complete sequence.//1.3e-15:262:69//AC002985
 F-OVARC1000564//Mus musculus clone OST7314, genomic survey sequence.//1.9e-41:476:70//AF046733
 F-OVARC1000573//HS_3241_B1_H03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=5 Row=P, genomic survey sequence.//2.2e-101:530:95//AQ211942
 F-OVARC1000576//Human Chromosome X, WORKING DRAFT SEQUENCE, 2 unordered pieces.//9.7e-97:445:90//AC002414
 F-OVARC1000578//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//9.1e-27:354:72//AC003973
 F-OVARC1000588//Human DNA sequence from clone 497J21 on chromosome 6q26-27. Contains a KOC (KH-domain containing transcript overexpressed in cancer) pseudogene, genomic marker O6S193, ESTs, STSs and GSSs, and a ca repeat polymorphism, complete sequence.//0.97:276:62//AL023775
 F-OVARC1000605
 F-OVARC1000622//Homo sapiens (subclone 2_d8 from P1 H42) DNA sequence, complete sequence.//7.2e-60:457:82//L81648
 F-OVARC1000640//Human BAC clone RG326K09 from 7q21, complete sequence.//6.2e-58:499:80//AC002069
 F-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, complete cds.//5.1e-77:424:93//D43772
 F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds.//4.8e-99:536:94//AB011162
 F-OVARC1000678//cSRL-29c7-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-29c7, genomic survey sequence.//2.5e-57:336:91//B04244
 F-OVARC1000679//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//1.6e-81:291:84//AJ001713
 F-OVARC1000681//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 257E24, WORKING DRAFT SEQUENCE.//8.2e-158:782:96//AL034424
 F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase 1B mRNA, complete cds.//1.5e-151:549:99//AF027156
 F-OVARC1000689//nbxb0003aC01f CUG1 Rice BAC Library Oryza sativa genomic clone nbxb0003M01f, genomic survey sequence.//0.17:499:60//AQ050003
 F-OVARC1000700
 F-OVARC1000703//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds.//3.5e-26:425:65//U34925
 F-OVARC1000722//Homo sapiens chromosome 1q21-1q23 beta-1,4-galactosyltransferase mRNA, complete cds.//3.7e-109:451:91//AF038661
 F-OVARC1000730
 F-OVARC1000746
 F-OVARC1000769//HS_2056_B2_C06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2056 Col=12 Row=N, genomic survey sequence.//8.8e-19:147:86//AQ245905
 F-OVARC1000771//M. musculus mRNA for GTP-binding protein.//2.2e-62:305:78//X95403
 F-OVARC1000781//Sequence 5 from Patent W09722695.//1.9e-89:705:78//A63552
 F-OVARC1000787//Homo sapiens PAC clone DJ430N08 from 22q12.1-qter, complete sequence.//3.0e-131:631:98//AC004542
 F-OVARC1000800//Human Chromosome 11q23 PAC clone pDJ254e13, complete sequence.//1.7e-32:295:80//AC003691
 F-OVARC1000802//Homo sapiens chromosome Xp22-67-68, WORKING DRAFT SEQUENCE, 99 unordered pieces.//3.2e-55:356:88//AC004469
 F-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CALC.//9.5e-27:163:94//Y17711
 F-OVARC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds.//6.0e-150:432:100//AB014543
 F-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//1.0e-135:632:99//AF045584
 F-OVARC1000862//M. musculus mRNA for FT1.//2.6e-109:769:83//Z67963
 F-OVARC1000876//S. cerevisiae chromosome IX cosmid 9150.//7.4e-21:541:61//Z38125
 F-OVARC1000883//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//2.2e-08:98:88//U20086
 F-OVARC1000885//B. subtilis 25 kb genomic DNA segment (from sspE to kata).//0.25:231:61//Z82044
 F-OVARC1000886//CIT-HSP-2171H6, TR CIT-HSP Homo sapiens genomic clone 2171H6, genomic survey sequence.//0.00035:139:69//B89721
 F-OVARC1000890
 F-OVARC1000891
 F-OVARC1000897//Human DNA sequence from clone 215F16 on chromosome 22q12.1-12.3. Contains part of a Homeobox domain containing gene and GSSs, complete sequence.//1.4e-18:473:64//AL024494
 F-OVARC1000912//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//8.9e-08:378:63//L14320
 F-OVARC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds.//7.7e-85:440:95//AB011172
 F-OVARC1000924//HS_2022_A1_C01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2022 Col=1 Row=E, genomic survey sequence.//5.7e-21:122:99//AQ269493
 F-OVARC1000936//Human PAC clone DJ0093103 from Xq23, complete sequence.//1.2e-113:476:91//AC003983
 F-OVARC1000937//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20208, WORKING DRAFT SEQUENCE.//0.00066:436:61//AL03184

【0753】

【表454】

8	F-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//5.0e-89:556:86//AB005549	plate genome.//1.0:265:59//AE001141
	F-OVARC1000948//P. falciparum complete gene map of plastid-like DNA (IR-B).//0.98:160:64//X95276	F-OVARC1001170//H.sapiens (xsl70) mRNA, 350bp.//4.6e-58:355:90//Z36823
	F-OVARC1000959//CIT-HSP-2348016, TR CIT-HSP Homo sapiens genomic clone 2348016, genomic survey sequence.//0.99:270:59//AQ062850	F-OVARC1001171//CIT-HSP-2285E22, TF CIT-HSP Homo sapiens genomic clone 2285E22, genomic survey sequence.//1.5e-25:152:83//AQ002315
	F-OVARC1000960//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-p35. Contains delta opiate receptor, CpG island, CA repeat.//3.9e-41:577:72//AL009181	F-OVARC1001173//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//0.0024:94:80//AL022323
	F-OVARC1000964//P. falciparum malaria antigen (M26-32-2) gene, partial cds.//0.19:83:73//M63270	F-OVARC1001176//Streptomyces plicatus B-N-acetylhexosaminidase (hex) gene, complete cds.//1.0:356:60//AF063001
	F-OVARC1000971//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y57G11, WORKING DRAFT SEQUENCE.//0.013:670:57//Z92841	F-OVARC1001180//G.gallus DNA for polyubiquitin gene Ub 11.//0.0062:275:60//X58195
	F-OVARC1000984//Leishmania major chromosome 1, complete sequence.//0.80:345:58//AE001274	F-OVARC1001188//Homo sapiens full length insert cDNA clone ZD93F03.//1.8e-32:180:97//AF086486
	F-OVARC1000996//M2025 gene [mice, embryos, mRNA, 2322 nt].//2.6e-55:403:82//S51858	F-OVARC1001200
	F-OVARC1000999//Synthetic construct galanin receptor type 3 (GALR3) gene, complete cds.//0.33:105:69//AF042785	F-OVARC1001232//Caenorhabditis elegans cosmid F1085, complete sequence.//0.013:128:67//Z48334
	F-OVARC1001000//HS_2247_A1_H05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2247 Col=9 Row=0, genomic survey sequence.//3.1e-60:315:96//AQ153910	F-OVARC1001240//Human Chromosome 11 pac pDJ360p17, WORKING DRAFT SEQUENCE, 44 unordered pieces.//3.7e-131:811:87//AC001235
	F-OVARC1001004//Homo sapiens from UMGCC:yl8c282 from 6p21, complete sequence.//3.1e-124:595:98//AC004190	F-OVARC1001243//Human BAC clone GS117010 from 7q21-q22, complete sequence.//0.044:457:59//AC003078
	F-OVARC1001010//CIT-HSP-203483, TF CIT-HSP Homo sapiens genomic clone 203483, genomic survey sequence.//1.0:151:60//B74290	F-OVARC1001244//Human homolog of Drosophila female sterile homeotic mRNA, complete cds.//8.4e-18:118:95//M80613
	F-OVARC1001011//Human DNA sequence from cosmid U85A3, between markers DXS366 and DXS87 on chromosome X contains rad21 and T-cell cyclophorin pseudogenes, STS.//3.0e-08:149:79//Z78021	F-OVARC1001261//Mus musculus putative membrane-associated guanylate kinase 1 (Magi-1) mRNA, alternatively spliced c form, partial cds.//1.4e-95:649:84//AF027505
	F-OVARC1001032//Yeast (S. cerevisiae) mitochondrial Tyr-tRNA gene.//3.2e-13:667:60//M12451	F-OVARC1001268//Rattus norvegicus ADP-ribosylation factor-directed GTPase activating protein mRNA, complete cds.//0.00051:72:83//U35776
	F-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//2.5e-119:73:7:86//AF001533	F-OVARC1001270
	F-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds.//2.7e-150:733:97//AF099149	F-OVARC1001271//Homo sapiens mRNA for KIAA0643 protein, partial cds.//2.1e-142:644:96//AB014543
	F-OVARC1001040//Homo sapiens clone RC270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//9.8e-297:77:76//AC005081	F-OVARC1001282//RPC111-60K8, TK RPC111 Homo sapiens genomic clone R-60K8, genomic survey sequence.//0.0089:285:58//AQ195857
	F-OVARC1001044//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 36411, WORKING DRAFT SEQUENCE.//0.0017:387:61//AL031319	F-OVARC1001296//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//3.0e-20:263:73//U97018
	F-OVARC1001051//Rattus norvegicus brain specific cortactin-binding protein CDP90 mRNA, partial cds.//0.012:112:74//AF053768	F-OVARC1001306//nxb0002M13r CUG1 Rice BAC Library Oryza sativa genomic clone nxb0002M13r, genomic survey sequence.//0.98:170:66//AQ156061
	F-OVARC1001055//Sequence 1 from patent US 5580754.//3.3e-45:381:81//I30292	F-OVARC1001329//Homo sapiens BAC clone RC370M10 from 7p15, complete sequence.//1.3e-05:432:61//AC003986
	F-OVARC1001062//nxb0026H08r CUG1 Rice BAC Library Oryza sativa genomic clone nxb0026H08r, genomic survey sequence.//0.018:344:59//AQ271878	F-OVARC1001330//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.027:444:59//AC005504
	F-OVARC1001065//S.pombe chromosome 1 cosmid c29E6.//0.86:338:59//Z66525	F-OVARC1001339//Homo sapiens chromosome 17, clone hCIT.124_H.2, complete sequence.//0.76:89:74//AC006071
	F-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//2.0e-130:620:98//AF082657	F-OVARC1001341//CITB1-E1-2503J7, TR CITB1-E1 Homo sapiens genomic clone 2503J7, genomic survey sequence.//0.99:45:86//AQ263402
	F-OVARC1001072//Homo sapiens glypican 3 (GPC3) gene, partial cds and flanking repeat regions.//9.3e-24:285:65//AF003529	F-OVARC1001342
	F-OVARC1001074//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//2.0e-07:652:59//AL022153	F-OVARC1001344//HS-1059-A2-H02-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 781 Col=4 Row=0, genomic survey sequence.//1.5e-07:254:67//B44456
	F-OVARC1001085//Homo sapiens c-syn protooncogene mRNA, complete cds.//5.0e-35:187:99//M14333	F-OVARC1001357//Homo sapiens Xp22-149 BAC RPC111-46604 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.83:376:61//AC005297
	F-OVARC1001092//Homo sapiens mRNA for JMS protein, complete CDS (clone IMAGE 53337, LLNLc110F1857Q7 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).//4.0e-74:289:95//AJ005897	F-OVARC1001360
	F-OVARC1001107//Homo sapiens SKB1Hs mRNA, complete cds.//3.6e-72:351:86//AF015913	F-OVARC1001369//Homo sapiens clone 162B15, complete sequence.//0.0066:99:76//AC004811
	F-OVARC1001113//Homo sapiens diaphanous 1 (DIA1) mRNA, complete cds.//6.4e-150:710:98//AF051782	F-OVARC1001372//Homo sapiens liprin-alpha4 mRNA, partial cds.//2.7e-142:683:98//AF034801
	F-OVARC1001117//Homo sapiens chromosome 5, Pl clone 328E3 (LBML HS3), complete sequence.//0.99:148:67//AC005178	F-OVARC1001376//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 850H21, WORKING DRAFT SEQUENCE.//1.9e-52:382:73//AL031680
	F-OVARC1001118//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.5e-35:302:74//AC000382	F-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL.//1.2e-147:683:99//AJ224819
	F-OVARC1001129//CIT-HSP-647P20, TP CIT-HSP Homo sapiens genomic clone 647P20, genomic survey sequence.//0.94:106:66//B79052	F-OVARC1001391//S.coelicolor whiB gene.//0.018:454:59//X62287
	F-OVARC1001154//R.norvegicus mRNA for epithelin 1 and 2.//1.8e-95:462:79//X62322	F-OVARC1001399//CIT-HSP-229118, TR CIT-HSP Homo sapiens genomic clone 229118, genomic survey sequence.//1.7e-11:104:87//AQ007611
	F-OVARC1001161//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//2.9e-90:496:84//AC004059	F-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds.//3.9e-149:707:98//AB006651
	F-OVARC1001162	F-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds.//4.9e-48:586:69//U52426
	F-OVARC1001167//Homo sapiens clone DJ1098J04, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00090:219:64//AC004961	F-OVARC1001425//Human DNA sequence from clone 1048E9 on chromosome 22q11.2-12.2 Contains pseudogene similar to ribosomal protein S3A and part of a gene similar to C.elegans protein CE02118, ESTs, STS, GSS, complete sequence.//0.0019:96:78//Z99714
	F-OVARC1001169//Borrelia burgdorferi (section 27 of 70) of the com	F-OVARC1001436//Caenorhabditis elegans mitotic chromosome and X-chromosome associated MIX-1 protein (mix-1) mRNA, complete cds.//0.77:519:59//U96387
		F-OVARC1001442//Human DNA sequence *** SEQUENCING IN PROGRESS ***

【0754】

【表455】

from clone 998H6. WORKING DRAFT SEQUENCE. //1.0:167:64//AL031687
 F-OVARC1001453//Human DNA sequence from PAC 453D15 on chromosome 6 contains STS. //4.4e-64:376:79//Z84482
 F-OVARC1001476//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y24F12. WORKING DRAFT SEQUENCE. //0.20:107:71//AL022277
 F-OVARC1001480
 F-OVARC1001489//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-42 0 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces. //0.20:281:63//AC005140
 F-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds. //8.1e-85:479:92//AF016507
 F-OVARC1001506//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-13 F4 complete genomic sequence, complete sequence. //1.2e-98:503:83//AC002039
 F-OVARC1001525//Human beta-hexosaminidase alpha chain (HEXA) gene, exon 1. //1.7e-13:87:100//M16411
 F-OVARC1001542//H.sapiens polymorphic repeat associated with glutamate dehydrogenase pseudogene 5. //0.43:190:68//X69219
 F-OVARC1001547//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-42 0 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces. //0.017:533:56//AC005140
 F-OVARC1001555//Homo sapiens clone MH0469W07. WORKING DRAFT SEQUENCE. 7 unordered pieces. //7.4e-159:416:99//AC005037
 F-OVARC1001577//Homo sapiens Srp46 splicing factor transcribed rat pseudogene. //2.4e-115:540:99//AF031165
 F-OVARC1001600//Homo sapiens chromosome 21q22.3 PAC 39C17, complete sequence. //5.5e-13:529:62//AF043945
 F-OVARC1001610//, complete sequence. //1.4e-12:152:77//AC005409
 F-OVARC1001611
 F-OVARC1001615//Human DNA sequence from clone 873P14 on chromosome 20p12 Contains STS, GSS. complete sequence. //0.022:146:70//AL031682
 F-OVARC1001668//Homo sapiens mRNA for MCM3 import factor, complete cds. //6.5e-109:358:96//AB005543
 F-OVARC1001702//Homo sapiens mRNA for hSOX20 protein, complete cds. //1.8e-47:393:81//AB006867
 F-OVARC1001703//CIT-HSP-2164L6.TF CIT-HSP Homo sapiens genomic clone 2164L6, genomic survey sequence. //0.94:85:69//B92840
 F-OVARC1001711//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 317C6. WORKING DRAFT SEQUENCE. //1.9e-06:489:61//Z97651
 F-OVARC1001713//Rattus norvegicus neuroigin 2 mRNA, complete cds. //1.0:262:59//U41662
 F-OVARC1001726//Human telomere associated repeat sequence, complete sequence. //7.5e-08:283:65//M57752
 F-OVARC1001731//Mus musculus gene for beta-tropomyosin. //2.6e-83:606:81//X12650
 F-OVARC1001745//HS_3007_B2_C09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=18 Row=N, genomic survey sequence. //0.00020:269:50//AQ164522
 F-OVARC1001762//S.pombe chromosome III cosmid c338. //3.0e-17:624:61//AL023781
 F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds. //4.2e-149:708:98//U97670
 F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds. //3.0e-115:580:96//AB014575
 F-OVARC1001768
 F-OVARC1001791//Homo sapiens BAC clone RG118P15 from Bq21, complete sequence. //5.7e-64:477:78//AC005066
 F-OVARC1001795//Homo sapiens chromosome 4 clone B341C20 map 4Q25, complete sequence. //6.5e-11:171:76//AC004704
 F-OVARC1001802//CITB1-E1-2502A17.TR CITB1-E1 Homo sapiens genomic clone 2502A17, genomic survey sequence. //0.98:214:61//AQ264481
 F-OVARC1001805//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence. //9.5e-151:712:99//AL023694
 F-OVARC1001809//Mus musculus sphingosine kinase (SPHK1a) mRNA, partial cds. //2.7e-56:522:75//AF068748
 F-OVARC1001812//Homo sapiens chromosome 17, clone HC1T104N19, complete sequence. //1.7e-63:526:81//AC003662
 F-OVARC1001813//Human DNA sequence from cosmid U144A10, between markers DXS366 and DXS87 on chromosome X contains STS. //0.17:214:65//Z70224
 F-OVARC1001820//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 445N2. WORKING DRAFT SEQUENCE. //3.2e-55:379:82//AL031779
 F-OVARC1001828//Homo sapiens chromosome 5, BAC clone 203o13 (LBML H155), complete sequence. //2.8e-17:509:62//AC005609
 F-OVARC1001846//Human DNA sequence from cosmid U73E8, between markers DXS366 and DXS87 on chromosome X. //0.35:403:58//Z73361
 F-OVARC1001861//CIT-HSP-2165M3.TR CIT-HSP Homo sapiens genomic clone 2165M3, genomic survey sequence. //2.4e-25:148:96//B94622
 F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence. //1.2e-18:122:95//AF070611
 F-OVARC1001879//HS_3026_B1_F09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026 Col=17 Row=L, genomic survey sequence. //4.9e-29:204:87//AQ207748
 F-OVARC1001880//Human interferon regulatory factor 5 (Hmif5) mRNA, complete cds. //3.5e-05:489:60//U51127
 F-OVARC1001883//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE. 4 unordered pieces. //1.9e-29:350:74//AC005020
 F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds. //8.5e-56:300:96//AF061749
 F-OVARC1001901//Human DNA sequence from clone 103M22 on chromosome 6p24. Contains STSs and GSSs, complete sequence. //2.3e-10:253:66//AL031904
 F-OVARC1001911//HS_2196_B2_H11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2196 Col=22 Row=P, genomic survey sequence. //3.4e-09:123:78//AQ294069
 F-OVARC1001916//HS_3054_B1_C11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=21 Row=F, genomic survey sequence. //1.2e-31:126:97//AQ099979
 F-OVARC1001928
 F-OVARC1001942//H.sapiens CpG island DNA genomic MseI fragment, clone 21d7, forward read cpq21d7.tlta. //7.2e-12:83:98//Z60390
 F-OVARC1001943//Aplysia californica potassium channel modulatory factor mRNA, complete cds. //3.5e-50:535:69//AF059179
 F-OVARC1001949//Human KRAB zinc finger protein (ZNF177) mRNA, complete cds. //1.7e-16:294:67//U37263
 F-OVARC1001950//Homo sapiens *** SEQUENCING IN PROGRESS *** WORKING DRAFT SEQUENCE. //1.5e-20:261:68//AJ011929
 F-OVARC1001987//D.melanogaster G6PD gene, exons 2-4. //0.99:447:57//Z19021
 F-OVARC1001989//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE. 20 unordered pieces. //2.9e-19:178:83//AC005995
 F-OVARC1002044//Plasmodium falciparum MAL3P7, complete sequence. //0.17:232:62//AL034559
 F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds. //2.1e-158:739:98//AB007934
 F-OVARC1002066//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE. //3.0e-17:781:59//AP000011
 F-OVARC1002082//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE. 6 unordered pieces. //5.4e-136:683:96//AC006015
 F-OVARC1002107//Homo sapiens BAC clone RG276003 from 7q22-q31.1, complete sequence. //1.0:220:61//AC004668
 F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds. //6.1e-115:557:98//AF041483
 F-OVARC1002127//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence. //0.013:461:57//AC006241
 F-OVARC1002138//Caenorhabditis elegans cosmid F32D1. //1.0e-29:545:64//AF016427
 F-OVARC1002143//CIT-HSP-2343H20.TR CIT-HSP Homo sapiens genomic clone 2343H20, genomic survey sequence. //2.3e-11:258:67//AQ055576
 F-OVARC1002156
 F-OVARC1002158//F1707-T7 IGF Arabidopsis thaliana genomic clone F1707, genomic survey sequence. //1.8e-16:383:66//B11616
 F-OVARC1002165//H.sapiens BOP1 mRNA for protein-tyrosine-phosphatase. //0.0041:300:64//X79568
 F-OVARC1002182//F.rubripes GSS sequence, clone 123123a7, genomic survey sequence. //1.4e-10:240:66//AL017241
 F-PLACE1000004//CIT-HSP-2294H13.TF CIT-HSP Homo sapiens genomic clone 2294H13, genomic survey sequence. //8.2e-10:158:75//AQ003859
 F-PLACE1000005//Mouse alpha-1 antitrypsin gene, segment 1. //4.8e-15:89:93//M12585
 F-PLACE1000007//Homo sapiens ubiquitin hydrolyzing enzyme 1 (UBH1) mRNA, partial cds. //3.8e-51:550:72//AF022789
 F-PLACE1000014
 F-PLACE1000031//Homo sapiens clone DJ0098022, WORKING DRAFT SEQUENCE. 5 unordered pieces. //0.91:333:61//AC004821
 F-PLACE1000040//Homo sapiens DNA sequence from PAC 95893 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island. //2.6e-20:279:67//Z93023
 F-PLACE1000048//Homo sapiens chromosome 17, clone HC1T462L7, complete sequence. //3.6e-63:488:82//AC005177
 F-PLACE1000050//Mus musculus chromosome 14 marker um-m24 GA dinucleotide DNA sequence. //2.3e-10:141:75//U31508
 F-PLACE1000061//Human ribosomal protein L37a mRNA sequence. //1.9e-

【表456】

30:190:94//L22154	Library D Homo sapiens genomic clone Plate=2056 Col=19 Row=G, genomic survey sequence.//5.3e-24:188:87//AQ235967
F-PLACE1000065//Homo sapiens PAC clone DJ1106E03 from 7q31.3-7q3, complete sequence.//6.0e-63:597:74//AC005521	F-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2.4e-47:687:66//AF044201
F-PLACE1000078//Homo sapiens chromosome 11 clone C1T987SK-1012F4, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.2e-09:143:73//AC005848	F-PLACE1000636
F-PLACE1000081//Human DNA from chromosome 19 specific cosmid R2846 1, genomic sequence, complete sequence.//0.52:390:60//AC002389	F-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//1.5e-152:747:96//AF102265
F-PLACE1000094	F-PLACE1000656//Homo sapiens mRNA for JMA protein, complete CDS (clone IMAGE 546750 and LMLC110F1857Q7 (RZPD Berlin)).//2.3e-156:775:97//AJ005896
F-PLACE1000133//Human DNA sequence from clone 372K1 on chromosome 6q24 Contains EST, STS, GSS and CpG Island, complete sequence.//4.4e-129:731:92//AL023580	F-PLACE1000706//nuclear protein TIF1 (mice, mRNA, 3951 nt).//8.0e-60:675:70//S78219
F-PLACE1000142//H. sapiens ALN mRNA.//6.4e-09:328:62//X79888	F-PLACE1000712
F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds.//7.7e-150:737:97//AF058291	F-PLACE1000716//HS-1057-A1-A03-MR. abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 779 Col=5 Row=A, genomic survey sequence.//2.7e-42:266:82//B43026
F-PLACE1000185//Sequence 15 from patent US 5691147.//5.7e-106:558:94//I76211	F-PLACE1000748//CIT-HSP-2372J8.TR CIT-HSP Homo sapiens genomic clone 2372J8, genomic survey sequence.//0.023:157:68//AQ113109
F-PLACE1000213	F-PLACE1000749//Plasmodium falciparum MAL3P7, complete sequence.//0.099:664:57//AL034559
F-PLACE1000214//Plasmodium falciparum 307 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-06:644:57//AC005504	F-PLACE1000755//H. sapiens DNA 3' flanking simple sequence region clone wg2c3.//0.00068:206:62//X76589
F-PLACE1000236//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 695020, WORKING DRAFT SEQUENCE.//2.6e-39:191:83//AL032818	F-PLACE1000769//RPC111-3J18.TPB RPC1-11 Homo sapiens genomic clone RPC1-11-3J18, genomic survey sequence.//6.5e-08:93:89//B63806
F-PLACE1000246//HS_2008_A2_D04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=8 Row=G, genomic survey sequence.//0.96:153:61//AQ269813	F-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//3.5e-138:663:98//AB014548
F-PLACE1000292//Drosophila melanogaster Oregon-R mitochondrial A+T region.//5.1e-12:571:60//U11584	F-PLACE1000786//Drosophila melanogaster cosmid 80HT.//1.4e-43:589:68//AL031027
F-PLACE1000308//D. teissieri mitochondrial DNA for tRNA- ^{met} , tRNA-Ile, tRNA-Gln & tRNA-Val.//0.00013:369:59//X54011	F-PLACE1000793//H. sapiens CpG island DNA genomic MseI fragment, clone 13d12, reverse read cpq13d12.rtlc.//4.6e-09:71:100//Z64565
F-PLACE1000332//HS_2016_B2_D08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=16 Row=H, genomic survey sequence.//7.5e-83:424:96//AQ232106	F-PLACE1000798//Human Chromosome 16 BAC clone CIT987SK-A-635H12, complete sequence.//5.0e-14:235:72//AC002310
F-PLACE1000347//CIT-HSP-2326A16.TV CIT-HSP Homo sapiens genomic clone 2326A16, genomic survey sequence.//0.13:46:100//AQ047350	F-PLACE1000841//Homo sapiens clone RH0441G08, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.013:404:60//AC006158
F-PLACE1000374//Mus musculus putative CCAAT binding factor 1 (mCBF) mRNA, alternatively spliced transcript mCBF1, complete cds.//0.00048:84:83//U19891	F-PLACE1000849//H. sapiens CpG island DNA genomic MseI fragment, clone 72a10, reverse read cpq72a10.rtlc.//3.3e-09:82:92//Z62712
F-PLACE1000380//F. rubripes GSS sequence, clone 047P21a10, genomic survey sequence.//0.43:198:62//Z88163	F-PLACE1000856//Hydra vulgaris HT4 mRNA for collagen-like protein, partial cds.//1.0:317:59//AB008935
F-PLACE1000383//Homo sapiens myotubularin related protein 1 (MTNR1) mRNA, partial cds.//8.7e-149:740:96//U58032	F-PLACE1000863//H. sapiens CpG island DNA genomic MseI fragment, clone 53d2, forward read cpq53d2.ftlb.//7.3e-37:199:98//Z55621
F-PLACE1000401//Pinctada fucata mRNA for insoluble protein, complete cds.//0.22:484:56//D86074	F-PLACE1000909//H. sapiens CpG island DNA genomic MseI fragment, clone 173f8, reverse read cpq173f8.rtlc.//1.5e-17:128:92//Z57391
F-PLACE1000406//Human nuclear matrix protein 55 (nmt55) mRNA, complete cds.//3.3e-19:372:65//U89867	F-PLACE1000931//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-1p35. Contains delta opiate receptor, CpG island, CA repeat.//8.1e-55:647:72//AL009181
F-PLACE1000420//Homo sapiens chromosome 17, clone hRPK.227.G_15, complete sequence.//1.6e-85:421:87//AC005899	F-PLACE1000948
F-PLACE1000421//Human GT334 protein (GT334) gene, exons 16 and 17.//0.88:145:68//U61515	F-PLACE1000972//RPC111-61B1.TJ RPC111 Homo sapiens genomic clone R-61B1, genomic survey sequence.//1.0e-26:148:99//AQ194348
F-PLACE1000424//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//0.076:196:66//AC005189	F-PLACE1000977//Homo sapiens mRNA for KIAA0672 protein, complete cds.//6.1e-08:413:61//AB014572
F-PLACE1000435//HS_3217_A2_A12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3217 Col=24 Row=A, genomic survey sequence.//2.2e-47:438:76//AQ181698	F-PLACE1000979//H. sapiens CpG island DNA genomic MseI fragment, clone 76e8, reverse read cpq76e8.rtlc.//2.7e-10:84:94//Z55963
F-PLACE1000444//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-15 ZES, complete sequence.//6.9e-61:616:71//AC004382	F-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete cds.//8.0e-140:694:96//AB018267
F-PLACE1000453//Murine genomic DNA: partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence.//5.8e-18:314:69//AF059580	F-PLACE1001000//Herpetomonas muscarum muscarum kinetoplast 12S rRNA gene.//0.0056:443:58//U01011
F-PLACE1000481//Homo sapiens Chromosome 22q11.2 Cosmid Clone 94a 1 n DGCR Region, complete sequence.//1.1e-33:349:76//AC002491	F-PLACE1001007//CIT-HSP-2013L15.TF CIT-HSP Homo sapiens genomic clone 2013L15, genomic survey sequence.//0.99:277:58//B58681
F-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA A, complete cds.//1.1e-34:256:83//U35245	F-PLACE1001010//Human cosmid g1572c101, complete sequence.//3.6e-55:294:88//AC000357
F-PLACE1000540//P. falciparum complete gene map of plastid-like DNA (IR-B).//0.099:336:58//X95276	F-PLACE1001015//Homo sapiens PAC clone DJ0754J18 from 7p21, complete sequence.//7.2e-33:333:73//AC004741
F-PLACE1000541//Arabidopsis thaliana GDP-mannose pyrophosphorylase (GMP1) mRNA, complete cds.//5.4e-11:279:63//AF076484	F-PLACE1001024
F-PLACE1000564	F-PLACE1001036//CIT-HSP-2373110.TF CIT-HSP Homo sapiens genomic clone 2373110, genomic survey sequence.//1.1e-80:393:98//AQ108662
F-PLACE1000583//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//3.3e-46:631:68//M27877	F-PLACE1001054//Arabidopsis thaliana genomic DNA, chromosome 5, TA C clone: K919, complete sequence.//8.8e-40:483:66//AB013390
F-PLACE1000588//Human guanylate binding protein isoform 1 (GBP-2) mRNA, complete cds.//7.3e-84:503:88//M55542	F-PLACE1001062//Mus musculus mRNA encoding lysine-ketoglutarate reductase/saccharopine dehydrogenase.//1.2e-23:224:80//AJ224761
F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//3.8e-164:798:97//AJ012449	F-PLACE1001076//HS_2195_B1_D05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=9 Row=H, genomic survey sequence.//0.0014:168:66//AQ066659
F-PLACE1000599//P. falciparum complete gene map of plastid-like DNA (IR-B).//0.018:295:61//X95276	F-PLACE1001088
F-PLACE1000610//HS_2056_A1_D10_T7 CIT Approved Human Genomic Sperm	F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//3.1e-95:489:96//AF065485
	F-PLACE1001104//Caprine arthritis-encephalitis virus envelope glycoprotein (env) gene, partial cds.//0.0073:253:62//U81400
	F-PLACE1001118//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds.//2.5e-64:676:71//AF022158
	F-PLACE1001136//Human amphiregulin (AR) gene, exon 5, clones lambd

【0756】

【表457】

a-ARH(6,12).//3.8e-26:174:93//M30702
 F-PLACE1001168
 F-PLACE1001171//Homo sapiens subtelomeric cosmid 11b-1, complete sequence.//7.6e-23:245:68//AC005603
 F-PLACE1001185//Human DNA sequence from clone 889N15 on chromosome Xq22.1-22.3. Contains part of the gene for a novel protein similar to X. laevis Cortical Thymocyte Marker CTX, the possibly alternatively spliced gene for 265 Proteasome subunit p28 (Ankyrin repeat protein), a novel gene and exons 36 through 45 of the COL4A6 for Collagen Alpha 6(IV). Contains ESTs, STSs, GSSs and a putative CpG island, complete sequence.//0.010:102:70//AL031177
 F-PLACE1001238//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//9.3e-82:684:77//D14336
 F-PLACE1001241
 F-PLACE1001257//Caenorhabditis elegans cosmid R12E2.//1.1e-16:480:60//AF067219
 F-PLACE1001272//H. sapiens subunit of coatomer complex.//0.31:50:95//X70476
 F-PLACE1001279//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-62 8 genomic sequence, WORKING DRAFT SEQUENCE. 9 unordered pieces.//0.054:352:60//AC005507
 F-PLACE1001280//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//1.0e-10:620:61//L14320
 F-PLACE1001294//M. musculus GEG-154 mRNA.//5.0e-107:826:80//X71642
 F-PLACE1001304//Mouse Zfp-35 mRNA for zinc finger protein ZFP-35.//1.2e-67:510:77//X71617
 F-PLACE1001311//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE. 4 unordered pieces.//1.6e-47:491:73//AC005282
 F-PLACE1001323//HS-1007-A2-B10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 328 Col=20 Row=C, genomic survey sequence.//9.6e-26:142:100//B31181
 F-PLACE1001351
 F-PLACE1001366//Homo sapiens mRNA for KIAA0799 protein, partial cds.//8.6e-25:155:95//AB018342
 F-PLACE1001377//H. sapiens MADN gene (exon 1).//1.6e-43:393:79//Z48614
 F-PLACE1001383//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//1.5e-119:705:91//AL022324
 F-PLACE1001384//Homo sapiens mRNA for multi PDZ domain protein.//5.7e-08:117:84//AJ001319
 F-PLACE1001387//Sequence 3 from patent US 5610018.//1.7e-06:395:58//I57340
 F-PLACE1001395//Plasmodium falciparum circular DNA rpoB and rpoC genes for beta and beta-prime subunits of RNA polymerase (EC 2.7.7.6).//7.2e-11:620:60//X52177
 F-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22_M.12, WORKING DRAFT SEQUENCE. 2 ordered pieces.//3.0e-145:700:98//AC005412
 F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence.//2.0e-69:365:96//AF091087
 F-PLACE1001414//Homo sapiens chromosome 9, clone hRPK.202_H.3, complete sequence.//8.2e-121:608:97//AC006241
 F-PLACE1001440//Human Chromosome 11 pac pD393015, WORKING DRAFT SEQUENCE. 8 unordered pieces.//1.3e-06:437:61//AC000384
 F-PLACE1001456//Homo sapiens Xp22 GS-52411 (Genome Systems Human BAC library), complete sequence.//0.98:348:60//AC003106
 F-PLACE1001468//Homo sapiens DNA sequence from PAC 435A7 on chromosome Xq22.1-q22.3. Contains STS.//4.4e-05:358:62//AL022148
 F-PLACE1001484//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 387E22, WORKING DRAFT SEQUENCE.//5.7e-31:195:93//AL031660
 F-PLACE1001502//Human fibroblast growth factor receptor 3 (FGFR3) gene, exon 1.//0.00015:333:59//L78720
 F-PLACE1001503//Drosophila melanogaster DNA sequence (P1 DS05273 (DS0)), complete sequence.//0.00016:161:66//AC004373
 F-PLACE1001517//Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs.//3.7e-22:260:76//AL021786
 F-PLACE1001534//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 620E11, WORKING DRAFT SEQUENCE.//1.1e-143:713:97//AL031667
 F-PLACE1001545//Homo sapiens chromosome 3, clone hRPK.165_L.16, complete sequence.//2.7e-139:482:96//AC005669
 F-PLACE1001551//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//6.9e-116:681:89//AC005261
 F-PLACE1001570//HS_3105_A1_F06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3105 Col=11 Row=K, genomic survey sequence.//1.2e-10:137:79//AQ139817
 F-PLACE1001602//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//1.8e-102:217:99//AB020860
 F-PLACE1001603//Homo sapiens nitrilase homolog 1 (NIT1) gene, alternatively spliced product, complete cds.//3.7e-104:501:98//AF069984
 F-PLACE1001608//HS_2189_A1_G07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2189 Col=13 Row=M, genomic survey sequence.//2.9e-60:429:84//AQ221959
 F-PLACE1001610//Homo sapiens clone MH0469M07, WORKING DRAFT SEQUENCE. 7 unordered pieces.//4.4e-114:552:98//AC005037
 F-PLACE1001611//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//0.93:131:71//AL031587
 F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete cds.//1.1e-74:702:75//AB018341
 F-PLACE1001634//Human p190-B (p190-B) mRNA, complete cds.//1.2e-18:114:100//U17032
 F-PLACE1001640//Homo sapiens chromosome 17, clone hRPK.651_L.9, complete sequence.//7.7e-159:788:97//AC005971
 F-PLACE1001672//Human DNA sequence from clone 71L16 on chromosome Xp11. Contains a probable Zinc Finger protein (pseudo) gene, an unknown putative gene, a pseudogene with high similarity to part of a ntigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Contains a predicted CpG island, ESTs, STSs and GSSs and genomic markers DXS1003 and DXS1055, complete sequence.//7.8e-36:365:73//AL022165
 F-PLACE1001691//Homo sapiens chromosome 17, clone hRPK.294_J.22, complete sequence.//9.1e-149:760:96//AC005921
 F-PLACE1001692//Rat medium-chain S-acyl fatty acid synthetase thioester hydrolase (MCH), complete cds.//2.9e-57:643:71//M16200
 F-PLACE1001705//Homo sapiens chromosome 17, clone hRPK.958_E.11, WORKING DRAFT SEQUENCE. 2 ordered pieces.//3.9e-18:284:71//AC005883
 F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds.//6.6e-68:369:73//D83776
 F-PLACE1001720//Homo sapiens Chromosome 22q11.2 Cosmid Clone 31f3 in IGLC Region, complete sequence.//1.0:274:59//AC000051
 F-PLACE1001729//Streptomyces coelicolor cosmid 1C2.//0.22:433:57//AL031124
 F-PLACE1001739//Caenorhabditis elegans cosmid C18H7.//0.049:341:61//AF067607
 F-PLACE1001740//Homo sapiens chromosome 5, P1 clone 1108H7 (LBNL H81), complete sequence.//4.8e-26:372:68//AC005221
 F-PLACE1001745
 F-PLACE1001746//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MALPI, WORKING DRAFT SEQUENCE.//0.018:472:57//AL031744
 F-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//8.8e-159:773:97//AF061243
 F-PLACE1001756//Homo sapiens chromosome 12p13.3 clone RPC111-303E5, WORKING DRAFT SEQUENCE. 65 unordered pieces.//1.9e-54:274:81//AC005842
 F-PLACE1001761//HS_3027_A1_D02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3027 Col=3 Row=G, genomic survey sequence.//0.095:49:93//AQ130972
 F-PLACE1001771//Homo sapiens transient receptor potential protein 6 mRNA, complete cds.//1.0e-146:709:97//AF080394
 F-PLACE1001781
 1.3e-08:238:65//AC005637
 F-PLACE1001799//HS_3075_B1_M03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=5 Row=P, genomic survey sequence.//1.7e-09:166:69//AQ138474
 F-PLACE1001810//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: WRC8, complete sequence.//0.00035:196:66//AB020749
 F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//1.1e-108:546:96//AF058953
 F-PLACE1001821//RPC111-35D17.TK RPC1-11 Homo sapiens genomic clone RPC1-11-35D17, genomic survey sequence.//2.1e-55:300:97//AQ045286
 F-PLACE1001844//Homo sapiens chromosome 17, clone HC1T462L7, complete sequence.//2.8e-67:443:86//AC005177
 F-PLACE1001845//Arabidopsis thaliana chromosome 1 BAC T25B24 genomic sequence, complete sequence.//0.34:219:64//AC005850
 F-PLACE1001869//Klebsiella pneumoniae ribitol kinase (rbtK) and ribitol transporter (rbtT) genes, complete cds.//7.1e-11:505:57//AF045244
 F-PLACE1001897//RPC111-46D15.TJ RPC111 Homo sapiens genomic clone

【0757】

【表458】

R-46015, genomic survey sequence.//9.3e-08:383:63//AQ194408
 F-PLACE1001912
 F-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//7.3e-156:753:98//AF099935
 F-PLACE1001928//HS_2220_B2_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2220 Col=8 Row=N, genomic survey sequence.//2.8e-43:233:97//AQ152361
 F-PLACE1001983//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 745C22, WORKING DRAFT SEQUENCE.//1.6e-07:396:62//AL031596
 F-PLACE1001989//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//1.0e-109:602:93//AL023755
 F-PLACE1002004//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 317E23, WORKING DRAFT SEQUENCE.//1.0e-69:475:87//AL020996
 F-PLACE1002046//Mus musculus ligatin (Lgtn) mRNA, partial cds.//7.2e-97:623:85//US8337
 F-PLACE1002052//HS_2178_B2_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=10 Row=M, genomic survey sequence.//4.8e-22:140:95//AQ307908
 F-PLACE1002066//Apis mellifera NADH dehydrogenase subunit 2 (ND2) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.0063:371:60//U72284
 F-PLACE1002072//Homo sapiens tight junction protein ZO (ZO-2) gene, alternative splice products, promoter and exon A.//0.97:248:60//AF043195
 F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds.//1.3e-37:635:64//AB011178
 F-PLACE1002090//Homo sapiens full length insert cDNA clone ZA85C09.//7.0e-122:583:98//AF086131
 F-PLACE1002115//nxbx0038A20r CUGI Rice BAC Library Oryza sativa genomic clone nxbx0038A20r, genomic survey sequence.//0.039:210:69//AQ291086
 F-PLACE1002119//Mus musculus IERS (Ier5) mRNA, complete cds.//7.1e-61:540:77//AF079527
 F-PLACE1002140//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//2.1e-125:491:98//AL022162
 F-PLACE1002150//Plasmodium falciparum MAL3P5, complete sequence.//0.12:408:61//AL034556
 F-PLACE1002157//Homo sapiens BAC clone MH0335J18 from 2, complete sequence.//1.1e-44:515:71//AC005539
 F-PLACE1002163//Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence.//0.98:210:65//AE000662
 F-PLACE1002170//Homo sapiens Xp22 bins 16-17 BAC GSHB-531117 (Genome Systems Human BAC Library) complete sequence.//1.2e-06:283:60//AC004805
 F-PLACE1002171//Mus musculus interferon alpha/beta receptor (IFNAR) gene, exon 11 and partial cds.//1.0e-24:313:71//U06244
 F-PLACE1002205//Drosophila melanogaster: Chromosome 3L: Region 79F1-80A2: BAC clone BACR48E05, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.6e-05:428:50//AC005720
 F-PLACE1002213//HS_3238_B1_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=5 Row=N, genomic survey sequence.//2.2e-74:371:98//AQ206965
 F-PLACE1002227//HS-1056-B1-CD1-MF, abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 778 Col=1 Row=F, genomic survey sequence.//2.1e-07:174:71//B42800
 F-PLACE1002256//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-72, complete sequence.//0.022:458:59//AL010142
 F-PLACE1002259//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRP5 (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//3.5e-91:637:84//AL022324
 F-PLACE1002319
 F-PLACE1002342//Caenorhabditis elegans cosmid M03A1.//0.47:403:58//U49956
 F-PLACE1002395//Homo sapiens chromosome 19, cosmid R28991, complete sequence.//1.9e-127:487:93//AC004623
 F-PLACE1002399//Homo sapiens chromosome 17, clone hRPK.235_1_10, complete sequence.//5.6e-05:474:59//AC005922
 F-PLACE1002433//Drosophila melanogaster fidiipidine gene, exons 1-7.//1.7e-11:613:58//AJ011928
 F-PLACE1002437//M.musculus abcl mRNA.//5.5e-62:452:85//X75926
 F-PLACE1002438//Dictyostelium discoideum developmental protein DGI098 (DGI098) gene, partial cds.//0.013:372:59//AF081801
 F-PLACE1002450//HS_3233_A1_G01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3233 Col=1 Row=M, genomic survey sequence.//3.1e-07:449:59//AQ204769
 F-PLACE1002465
 F-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//1.5e-110:720:85//U69262
 F-PLACE1002477//Homo sapiens Xp22-171-173 BAC GSHB-31214 (Genome Systems Human BAC Library) complete sequence.//3.9e-05:195:71//AC005926
 F-PLACE1002493//Homo sapiens 3p22-8 PAC RPC14-736H12 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.020:301:60//AC006060
 F-PLACE1002499
 F-PLACE1002500//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//2.1e-58:465:80//U50927
 F-PLACE1002514//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 292E10, WORKING DRAFT SEQUENCE.//3.7e-08:139:76//Z93930
 F-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//9.0e-143:583:95//AB018256
 F-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1, complete sequence.//0.00019:193:65//AC004774
 F-PLACE1002537//Human DNA sequence from clone 127F18 on chromosome Xp11.4-21.3. Contains part of a novel gene with some similarity to parts of chicken Myosin Light Chain and various species' Interleukin-1 Receptor Type 1 (IL1-R-1). Contains GSSs, complete sequence.//4.7e-25:198:84//AL031575
 F-PLACE1002571//Drosophila melanogaster actin-related protein mRNA A, complete cds.//2.0e-13:400:60//L25314
 F-PLACE1002578//Homo sapiens Xq28 BACs 360 F12, GSHB-555C13, complete sequence.//3.5e-11:167:72//AC002523
 F-PLACE1002583//Mus musculus glutamate receptor subunit (GluR6) gene, partial cds.//4.2e-09:370:61//U31443
 F-PLACE1002591//H. sapiens mRNA for coronin.//7.2e-26:279:74//X89109
 F-PLACE1002598//Homo sapiens clone GS308H05, WORKING DRAFT SEQUENCE. 6 unordered pieces.//0.0013:375:64//AC005537
 F-PLACE1002604//Hansenula wingei mitochondrial DNA, complete sequence.//4.7e-05:556:59//D31785
 F-PLACE1002625
 F-PLACE1002655//Homo sapiens PAC clone DJ0722F20 from 7q31.1-q31.3, complete sequence.//1.6e-128:229:92//AC005281
 F-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//3.6e-107:706:84//AF079765
 F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//3.4e-186:804:97//AF068180
 F-PLACE1002714//Mus musculus cathepsin S (CatS) gene, promoter region and exons 1 and 2.//2.3e-16:474:64//AF051726
 F-PLACE1002722//Sequence 1 from patent US 5686597.//1.7e-107:552:95//I73723
 F-PLACE1002768//Human DNA sequence from clone 726F20 on chromosome 1p36.11-36.23. Contains ESTs and a GSS, complete sequence.//0.0076:161:70//AL031273
 F-PLACE1002772//HS_3058_A1_D02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3058 Col=3 Row=G, genomic survey sequence.//0.0046:192:64//AQ134567
 F-PLACE1002775//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//7.6e-14:459:62//AF084259
 F-PLACE1002782//Rattus norvegicus zinc transporter (ZnT-2) mRNA, complete cds.//3.6e-43:385:77//U50927
 F-PLACE1002794//CIT-HSP-2368A17, TR CIT-HSP Homo sapiens genomic clone 2368A17, genomic survey sequence.//1.3e-71:368:96//AQ075879
 F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds.//1.8e-44:567:70//D79994
 F-PLACE1002815//Sequence 25 from patent US 5747660.//2.6e-07:150:73//AR005295
 F-PLACE1002816//Homo sapiens antigen NY-CO-9 (NY-CO-9) mRNA, partial cds.//1.3e-68:687:73//AF039691
 F-PLACE1002834//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//9.3e-41:240:93//M27877
 F-PLACE1002839//Human BAC clone RG205G13 from 7q31, complete sequence.//0.00087:213:63//AC003045
 F-PLACE1002851//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.0032:269:66//AC005140
 F-PLACE1002853//Leishmania tarentolae kinetoplast pre-edited mitochondrial maxicircle DNA complete transcribed region and flanks.//0.032:275:62//M10126
 F-PLACE1002881//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 111B22, WORKING DRAFT SEQUENCE.//4.7e-38:355:76//Z98200
 F-PLACE1002908//Gallus gallus beta-1,4-galactosyltransferase (CK1

【0758】

【表459】

1) mRNA, complete cds.//0.00012:200:64//U19889	(hCLCA1) gene, complete cds.//1.3e-11:746:60//AF039401
F-PLACE1002941//Human BAC clone RG161K23 from 7q21, complete sequence.//1.1e-14:241:70//AC000120	F-PLACE1003493
F-PLACE1002962	F-PLACE1003516//Homo sapiens chromosome 17, clone HRC987K16, complete sequence.//8.2e-41:379:78//AC002994
F-PLACE1002968//Plasmodium falciparum MAL3P2, complete sequence.//0.21:410:59//AL034558	F-PLACE1003519//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23 a.//6.2e-21:247:76//AF064859
F-PLACE1002991//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//6.8e-121:605:93//AL023755	F-PLACE1003521//Human DNA sequence from PAC 257A7 on chromosome 6p24. Contains two unknown genes and ESTs, STSs and a GSS.//4.4e-68:502:78//AL008729
F-PLACE1002993//CIT-HSP-2338116.TF CIT-HSP Homo sapiens genomic clone 2338116, genomic survey sequence.//1.9e-13:100:95//AQ054760	F-PLACE1003528//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxyesterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//1.0:323:58//AL022336
F-PLACE1002996//Mouse U6 RNA gene.//2.0e-13:113:90//X06980	F-PLACE1003537//Homo sapiens multispinning membrane protein mRNA, complete cds.//0.0054:322:59//U94831
F-PLACE1003025//Plasmodium falciparum MAL3P6, complete sequence.//0.84:374:58//Z98551	F-PLACE1003553//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE.//2.9e-78:267:88//AL031297
F-PLACE1003027//Homo sapiens mRNA for KIAA0516 protein, partial cds.//6.1e-130:632:97//AB011088	F-PLACE1003566//Plasmodium falciparum MAL3P3, complete sequence.//0.00026:514:58//Z98547
F-PLACE1003044//cDNA encoding novel rat protein TIP120 which is formed of complex with TBP (TATA binding protein).//1.6e-123:687:91//E12829	F-PLACE1003575//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.079:755:54//AC004688
F-PLACE1003045//H.sapiens CpG island DNA genomic MseI fragment, clone 47g6, forward read cpg47g6.ftta.//0.0064:52:96//Z61200	F-PLACE1003583//Human DNA sequence from clone 246H3 on chromosome 22q11.21-12.2 Contains LRPS (Lipoprotein Receptor Related Protein) pseudogene, EST, CA repeats (D22S414, D22S925, D22S926), STS, GSS and CpG island, complete sequence.//1.1e-41:212:74//AL022324
F-PLACE1003092//CIT-HSP-387P22.TRB CIT-HSP Homo sapiens genomic clone 387P22, genomic survey sequence.//0.0031:249:63//B60158	F-PLACE1003584//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-56, complete sequence.//0.0038:465:57//AL010230
F-PLACE1003100//Human Hep27 protein mRNA, complete cds.//8.9e-65:650:73//U31875	F-PLACE1003592//Homo sapiens chromosome 17, clone 296K1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//0.72:111:71//AC002557
F-PLACE1003108	F-PLACE1003593//Human PAC clone DJ318C15 from Xq23, complete sequence.//0.096:162:66//AC002476
F-PLACE1003136//Homo sapiens chromosome 5, P1 clone 113D11 (LBNI H40), complete sequence.//6.3e-46:606:68//AC004219	F-PLACE1003596//Mus musculus integral membrane protein 1 (Itih) mRNA, complete cds.//1.4e-54:685:68//L34260
F-PLACE1003145	F-PLACE1003602//Homo sapiens mRNA expressed in placenta.//1.1e-13:8:679:97//D83200
F-PLACE1003153//RPC111-13P16.TP RPC1-11 Homo sapiens genomic clone RPC1-11-13P16, genomic survey sequence.//2.7e-63:478:82//B76206	F-PLACE1003605//Homo sapiens chromosome 16, cosmid clone RTB1 (LAN L), complete sequence.//0.0074:265:63//AC005356
F-PLACE1003174//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.61:147:65//Z99495	F-PLACE1003611//HS_2198_B1_D02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2198 Col=3 Row=H, genomic survey sequence.//2.1e-23:137:97//AQ184475
F-PLACE1003176//HS_2255_A2_B01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=2 Row=C, genomic survey sequence.//6.3e-09:137:76//AQ131934	F-PLACE1003618//Homo sapiens chromosome 4 clone C0011C13 map 4p16, complete sequence.//3.0e-122:725:89//AC006226
F-PLACE1003190//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.4e-138:791:90//AC005095	F-PLACE1003625//HS_2238_B2_D11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2238 Col=22 Row=H, genomic survey sequence.//4.8e-12:92:94//AQ065662
F-PLACE1003208//P.falciparum complete gene map of plastid-like DNA (IR-B).//7.8e-06:728:57//X95276	F-PLACE1003638//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MKD10, complete sequence.//0.043:264:63//AB011478
F-PLACE1003205//Human BAC clone RG354L07 from 7q31, complete sequence.//7.5e-05:249:63//AC002466	F-PLACE1003669
F-PLACE1003238//HS_3239_A2_C02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3239 Col=4 Row=M, genomic survey sequence.//0.36:64:87//AQ209954	F-PLACE1003704//RPC111-23H21.TKBF RPC1-11 Homo sapiens genomic clone RPC1-11-23H21, genomic survey sequence.//7.1e-31:199:91//AQ013830
F-PLACE1003249	F-PLACE1003709//Homo sapiens mitotic checkpoint kinase Bub1 (BUB1) mRNA, complete cds.//4.3e-132:669:95//AF053305
F-PLACE1003256	F-PLACE1003711//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1 F1551A pseudogene, ESTs, STS, GSS, complete sequence.//1.5e-31:16:6:99//AL021920
F-PLACE1003258//HS_3223_A1_G10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3223 Col=19 Row=M, genomic survey sequence.//1.4e-07:227:65//AQ190317	F-PLACE1003723//HS_2231_A2_C07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2231 Col=14 Row=E, genomic survey sequence.//1.2e-12:114:90//AQ235672
F-PLACE1003296//CIT-HSP-2337F11.TF CIT-HSP Homo sapiens genomic clone 2337F11, genomic survey sequence.//1.1e-13:97:95//AQ057429	F-PLACE1003738//Human zinc finger protein 42 (ZNF-1) mRNA, complete cds.//5.9e-33:592:67//W58297
F-PLACE1003302//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//2.3e-92:485:95//W27877	F-PLACE1003760//Homo sapiens tetraspan TM4SF (TSPAN-3) mRNA, complete cds.//3.6e-11:92:93//AF054840
F-PLACE1003334	F-PLACE1003762
F-PLACE1003342	F-PLACE1003768//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 7/15, WORKING DRAFT SEQUENCE.//4.8e-77:737:76//AP000014
F-PLACE1003343//Homo sapiens clone DJ1022114, WORKING DRAFT SEQUENCE, 14 unordered pieces.//1.0e-20:179:84//AC004951	F-PLACE1003771//Homo sapiens BAC clone GS164B05 from 7p21-p22, complete sequence.//2.1e-164:793:98//AC004160
F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//8.0e-143:773:92//U92715	F-PLACE1003783//HS_2190_A2_C02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2190 Col=4 Row=E, genomic survey sequence.//1.1e-26:147:100//AQ218757
F-PLACE1003361//Human Cosmid g1248a143 from 7q31.3, complete sequence.//1.9e-30:402:70//AC004095	F-PLACE1003784//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//4.5e-57:706:68//AC006210
F-PLACE1003366	
F-PLACE1003369//Plasmodium falciparum MAL3P2, complete sequence.//7.6e-07:378:60//AL034558	
F-PLACE1003373//Homo sapiens PAC clone DJ0740L10 from 7p13-p14, complete sequence.//6.0e-18:471:61//AC005247	
F-PLACE1003375	
F-PLACE1003383//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 10/10.//2.3e-157:779:96//AB020878	
F-PLACE1003394//Sprague-Dawley (clone LRB13) RAB14 mRNA, complete cds.//1.2e-104:596:91//W83680	
F-PLACE1003401//RPC111-71J5.TJ RPC111 Homo sapiens genomic clone R-71J5, genomic survey sequence.//0.85:140:65//AQ268588	
F-PLACE1003420//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone YIE3, WORKING DRAFT SEQUENCE.//0.0015:286:60//A021388	
F-PLACE1003454//Plasmodium falciparum microsatellite pe63 sequence.//0.0084:219:61//AF015470	
F-PLACE1003478//Homo sapiens calcium-dependent chloride channel-1	

【0759】

【表460】

F-PLACE1003795//Homo sapiens Xq28 genomic DNA in the region of the LICAM locus containing the genes for neural cell adhesion molecule 1 (LICAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyltransferase related protein (TE2), renin-binding protein (RBP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq28lu2 gene.//0.015:296:60//JUS2112

F-PLACE1003833//Homo sapiens DNA sequence from cosmid N75B3 on chromosome 22 Contains EST, exon trap, complete sequence.//0.52:212:64//AL022339

F-PLACE1003850//P. falciparum histidine-rich protein genes.//0.39:330:60//M17028

F-PLACE1003858//Human DNA sequence from PAC 332011 on chromosome 1 q24-lq25. Contains ESTs and STSs.//4.8e-07:461:59//Z98043

F-PLACE1003864//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.026:538:56//AC005139

F-PLACE1003870//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54820, WORKING DRAFT SEQUENCE.//6.5e-06:175:69//Z98304

F-PLACE1003885//Mus musculus poly(A) polymerase VI mRNA, complete cds.//9.4e-75:754:72//U58134

F-PLACE1003886//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.7e-20:432:64//AC006030

F-PLACE1003888//Human mRNA for phospholipase C, complete cds.//2.6e-53:702:67//U42108

F-PLACE1003892//RPC111-24P17.TV RPC1-11 Homo sapiens genomic clone RPC1-11-24P17, genomic survey sequence.//3.3e-20:245:65//B86759

F-PLACE1003900//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 328E19, WORKING DRAFT SEQUENCE.//2.5e-17:260:71//AL022240

F-PLACE1003903//Mus musculus CTP synthetase homolog (CTPsh) mRNA, complete cds.//2.7e-86:533:87//U49385

F-PLACE1003915//Mus musculus clone OST1963, genomic survey sequence.//6.4e-29:251:80//AF046591

F-PLACE1003923//Homo sapiens full length insert cDNA clone ZD40A05.//2.8e-25:316:70//AF086251

F-PLACE1003932//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.6e-05:652:58//AC005505

F-PLACE1003936//CIT-HSP-2387C11.TR.1 CIT-HSP Homo sapiens genomic clone 2387C11, genomic survey sequence.//1.0:223:62//AQ239494

F-PLACE1003968//Rattus norvegicus 5'-AMP-activated protein kinase, gamma-1 subunit mRNA, complete cds.//5.2e-47:505:72//U42413

F-PLACE1004103//Homo sapiens chromosome 19, cosmid R28784, complete sequence.//6.7e-29:241:84//AC005954

F-PLACE1004104//Rattus norvegicus rsec5 mRNA, complete cds.//3.0e-115:719:86//AF032666

F-PLACE1004114//Homo sapiens Chromosome 22q11.2 BAC Clone 77h2 in CES Region, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.5e-22:213:80//AC000052

F-PLACE1004118//Pseudorabies virus with upstream and downstream sequences.//0.87:209:64//M34651

F-PLACE1004128//M. musculus G protein beta-subunit mRNA, complete cds.//2.5e-62:437:84//M63658

F-PLACE1004149//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//1.4e-16:342:65//AF005355

F-PLACE1004156//Homo sapiens DNA sequence from PAC 57E3 on chromosome 6p21.1-21.1. Contains GSSs and an STS with a TATC repeat polymorphism, complete sequence.//1.2e-26:299:74//AL022099

F-PLACE1004161

F-PLACE1004183//Homo sapiens for TOM1-like protein.//1.2e-146:731:96//AJ010071

F-PLACE1004197

F-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds.//4.0e-144:695:98//AF069493

F-PLACE1004242//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.3e-151:772:95//AL021326

F-PLACE1004256//HS_2010_B2_C04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2010 Col=8 Row=N, genomic survey sequence.//1.5e-44:372:79//AQ252434

F-PLACE1004257//Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//0.00011:349:63//AC005034

F-PLACE1004258//Homo sapiens DNA sequence from PAC 779B17 on chromosome 22q13.1. Contains exon trap, complete sequence.//0.77:475:59//AL021806

F-PLACE1004270//Human IgA C alpha 1 switch region (Sal).//1.7e-08:622:61//L19121

F-PLACE1004274//H. sapiens CpG island DNA genomic MseI fragment, clone 18g6, forward read cpg18g6.ft1b.//8.6e-37:196:98//Z57691

F-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, complete cds.//6.0e-156:756:97//AF084830

F-PLACE1004284//Arabidopsis thaliana genomic DNA, chromosome 5, PI clone: NP17, complete sequence.//0.0060:635:57//AB011480

F-PLACE1004289//HS_3023_B1_E04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3023 Col=7 Row=J, genomic survey sequence.//2.4e-12:86:98//AQ094451

F-PLACE1004302//Streptomyces coelicolor cosmid 7H1.//0.26:297:64//AL021411

F-PLACE1004316//H. sapiens mRNA for apoptosis specific protein.//2.9e-150:797:94//Y11588

F-PLACE1004336//Drosophila melanogaster DNA sequence (PI D507968 (D117)), complete sequence.//0.87:206:59//AC004267

F-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//5.9e-139:688:97//AF100153

F-PLACE1004376//Mus musculus clone OST20307, genomic survey sequence.//4.1e-81:498:89//AF046631

F-PLACE1004384//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1121J18, WORKING DRAFT SEQUENCE.//3.6e-41:482:73//AL031653

F-PLACE1004388//Caenorhabditis elegans cosmid K08F11.//8.6e-26:515:62//U70855

F-PLACE1004405//Homo sapiens clone GS512121, WORKING DRAFT SEQUENCE, 9 unordered pieces.//9.2e-150:749:96//AC005027

F-PLACE1004425//Homo sapiens PAC clone DJ0733B09 from 7p14-p13, complete sequence.//2.4e-08:129:76//AC005532

F-PLACE1004428//R. norvegicus mRNA for Pristanoyl-CoA Oxidase.//7.0e-17:549:61//X95188

F-PLACE1004437//Human NAD+-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds.//3.1e-129:536:99//U49283

F-PLACE1004451//Human DNA sequence from PAC 214K23, BRCA2 gene region chromosome 13q12-13 contains BRCA2 exons 1-24, Interferon induced 56kd pseudogene and ESTs.//4.8e-23:231:71//Z74739

F-PLACE1004460//Homo sapiens PAC clone DJ1064B22 from 7q21, complete sequence.//0.96:454:56//AC004954

F-PLACE1004467//HS_2058_B1_C09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=17 Row=F, genomic survey sequence.//2.4e-87:433:98//AQ242700

F-PLACE1004471//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//1.4e-74:665:70//M27877

F-PLACE1004473//CIT-HSP-2045A15.TF CIT-HSP Homo sapiens genomic clone 2045A15, genomic survey sequence.//3.3e-20:140:92//B80243

F-PLACE1004491//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//9.9e-05:794:57//AC004709

F-PLACE1004506//Human Gx-alpha gene.//1.0e-05:231:63//D90150

F-PLACE1004510//Homo sapiens TATA binding protein associated factor 7 (TAF1150) mRNA, complete cds.//3.2e-146:699:98//AF040701

F-PLACE1004516//Human DNA sequence from cosmid SRL9A13, chromosome region 11p13. Contains EST.//1.4e-33:367:71//Z86001

F-PLACE1004518

F-PLACE1004548//Dictyostelium discoideum MigA (migA) gene, complete cds.//2.6e-05:318:62//U86962

F-PLACE1004550//Human FMR1 gene, 5' end.//0.0018:142:66//L19476

F-PLACE1004564//B. taurus mRNA for cleavage and polyadenylation specificity factor.//1.7e-114:513:85//X75931

F-PLACE1004629//Anolis carolinensis Brain-1 gene, complete cds.//0.00013:188:67//AB001868

F-PLACE1004645//Mycobacterium tuberculosis H37Rv complete genome: segment 138/162.//0.66:337:60//Z95120

F-PLACE1004646//Rattus norvegicus retinal pigment epithelium-specific protein (Rpe65) mRNA, complete cds.//1.1e-19:326:63//AF035673

F-PLACE1004658//H. sapiens CpG island DNA genomic MseI fragment, clone 55h1, forward read cpg55h1.ft1a.//2.4e-34:188:98//Z61632

F-PLACE1004664//Caenorhabditis elegans cosmid W10G6, complete sequence.//1.0:148:65//Z81140

F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene, complete cds.//1.9e-101:182:95//U07561

F-PLACE1004674//Homo sapiens calcium binding protein (ALC-2) mRNA, complete cds.//4.3e-109:625:91//AF035606

F-PLACE1004681//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//1.9e-152:759:96//AB020860

F-PLACE1004686//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and

【表461】

two predicted CpG islands, complete sequence.//1.2e-34:320:71//Z95152
 F-PLACE1004691//HS_3044_A1_G01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3044 Col=1 Row=M, genomic survey sequence.//0.018:191:63//AQ098323
 F-PLACE1004693//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily A, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.28:573:57//AL022577
 F-PLACE1004716//Plasmodium falciparum MAL3P6, complete sequence.//0.00081:428:59//Z98551
 F-PLACE1004722//HS_3052_B1_C10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3052 Col=19 Row=F, genomic survey sequence.//2.3e-05:104:75//AQ134959
 F-PLACE1004736//CIT-HSP-2365J21.TF CIT-HSP Homo sapiens genomic clone 2365J21, genomic survey sequence.//1.3e-24:180:88//AQ080498
 F-PLACE1004740//RPC111-58A7.TJ RPC111 Homo sapiens genomic clone R-58A7, genomic survey sequence.//8.6e-26:522:65//AQ195766
 F-PLACE1004743//Mus musculus ubiquitin-protein ligase E3-alpha (Ubr1) mRNA, complete cds.//1.1e-112:711:86//AF061555
 F-PLACE1004751
 F-PLACE1004773//Homo sapiens inversin protein mRNA, complete cds.//5.4e-171:828:97//AF084367
 F-PLACE1004777//Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//4.2e-134:763:90//AJ001713
 F-PLACE1004793//Human DNA sequence from clone 323P24 on chromosome Xp11.21-11.23 Contains SPIN (spindlin homolog (PROTEIN DXF34)), hypothetical protein EST, STS, GSS, complete sequence.//9.3e-132:75:90//AL022157
 F-PLACE1004804
 F-PLACE1004813//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//6.5e-06:403:58//AC004710
 F-PLACE1004814//Homo sapiens chromosome 17, clone hRPK.294_J_22, complete sequence.//9.8e-39:207:99//AC005921
 F-PLACE1004815//Homo sapiens PAC clone DJ0651K02 from 7p21-p22, complete sequence.//8.1e-15:203:73//AC004613
 F-PLACE1004824//G. gallus PB1 gene.//1.1e-103:759:80//X90849
 F-PLACE1004827//HS_2230_A2_A05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2230 Col=10 Row=A, genomic survey sequence.//4.1e-38:330:81//AQ299313
 F-PLACE1004836//H. sapiens nidogen gene (exon 8).//0.97:116:68//X84825
 F-PLACE1004838//HS_3241_A2_A04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=8 Row=A, genomic survey sequence.//1.8e-87:425:98//AQ206740
 F-PLACE1004840//Sequence 2 from patent US 5728819.//6.7e-47:285:91//192819
 F-PLACE1004868
 F-PLACE1004885//Arabidopsis thaliana DNA chromosome 4, ESSA1 contig fragment No. 9.//0.14:465:59//Z97344
 F-PLACE1004900
 F-PLACE1004902//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//3.6e-06:56:100//AQ261184
 F-PLACE1004913//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//2.6e-151:770:91//AC005058
 F-PLACE1004918//Mus musculus signaling molecule (ATTP) mRNA, complete cds.//2.6e-68:459:84//U97571
 F-PLACE1004930//Homo sapiens TNF-induced protein CG2-1 mRNA, complete cds.//4.4e-106:545:95//AF070671
 F-PLACE1004934//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmalipin, ESTs and GSSs, complete sequence.//3.5e-45:226:84//AL020989
 F-PLACE1004937
 F-PLACE1004969
 F-PLACE1004972//Homo sapiens PAC clone DJ0612F12 from 7p12-p14, complete sequence.//0.012:316:61//AC004843
 F-PLACE1004979//Human DNA sequence from clone 142F18 on chromosome Xq26.3-27.2 Contains part of a gene similar to melanoma-associated antigen, EST, GSS and an inverted repeat, complete sequence.//4.7e-39:394:77//AL031073
 F-PLACE1004982//Caenorhabditis elegans cosmid B0507.//0.16:167:65//U64833
 F-PLACE1004985//Plasmodium falciparum chromosome 2, section 10 of 73 of the complete sequence.//8.8e-14:590:61//AE001373
 F-PLACE1005026
 F-PLACE1005027
 F-PLACE1005046
 F-PLACE1005052//Homo sapiens chromosome Xp22-135-136 clone GSHB-56711, WORKING DRAFT SEQUENCE, 35 unordered pieces.//2.1e-135:675:97//AC005867
 F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds.//1.9e-159:761:98//AB011148
 F-PLACE1005066//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//9.2e-10:757:56//AF059569
 F-PLACE1005077
 F-PLACE1005085//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//6.9e-29:253:77//AC004673
 F-PLACE1005086//Homo sapiens chromosome 17, clone HCIT11023, complete sequence.//6.5e-52:446:78//AC002316
 F-PLACE1005101//Homo sapiens clone DJ0414A15, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.0e-146:734:96//AC005225
 F-PLACE1005102//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//9.8e-83:254:95//AC004476
 F-PLACE1005108//Human BAC clone RG009H02 from 7q31, complete sequence.//0.46:179:64//AC003081
 F-PLACE1005111
 F-PLACE1005128//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//0.00051:287:63//U14320
 F-PLACE1005146//HS_3071_A1_E03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=5 Row=1, genomic survey sequence.//7.4e-38:299:82//AQ103361
 F-PLACE1005162//Human BAC clone GS306C12 from 7q21-q22, complete sequence.//2.6e-44:346:82//AC002451
 F-PLACE1005176
 F-PLACE1005181//CIT-HSP-234005.TR CIT-HSP Homo sapiens genomic clone 234005, genomic survey sequence.//0.99:211:63//AQ054651
 F-PLACE1005187//CIT-HSP-2358N6.TR CIT-HSP Homo sapiens genomic clone 2358N6, genomic survey sequence.//2.7e-07:80:90//AQ074445
 F-PLACE1005206//Human BAC clone 133K23 from 7q31.2, complete sequence.//0.98:216:61//AC000061
 F-PLACE1005232//Homo sapiens clone DJ1106H14, WORKING DRAFT SEQUENCE, 42 unordered pieces.//0.70:245:63//AC004965
 F-PLACE1005243
 F-PLACE1005261//Caenorhabditis elegans cosmid T05H10, complete sequence.//0.00041:254:61//Z47812
 F-PLACE1005266//H. sapiens mRNA (fetal brain cDNA a4_2a).//9.6e-33:177:98//Z70695
 F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds.//1.6e-148:706:98//AB011182
 F-PLACE1005287//Plasmodium falciparum (MESA) mRNA exons 1-2, complete cds.//2.8e-15:737:60//M69183
 F-PLACE1005305//Bovine mitochondrial GTP:AMP phosphotransferase mRNA, complete cds.//3.8e-111:728:84//M25757
 F-PLACE1005308//Clostridium glareolus endogenous retroviral sequence ERV-L pol gene, clone ERV-L Vole Cg14.//1.0:128:67//AJ233621
 F-PLACE1005313//Caenorhabditis elegans cosmid D2092.//8.8e-11:342:62//U88167
 F-PLACE1005327//HS_3080_B2_A12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3080 Col=24 Row=B, genomic survey sequence.//4.1e-25:147:96//AQ139116
 F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569, complete sequence.//1.4e-132:399:94//AC004794
 F-PLACE1005335//Human Chromosome 3 pac pDJ70i11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.5e-114:237:92//AC000380
 F-PLACE1005373
 F-PLACE1005374//Homo sapiens chromosome 7 common fragile site, complete sequence.//0.20:305:58//AF017104
 F-PLACE1005409//Human BAC clone RG167B05 from 7q21, complete sequence.//2.5e-148:760:95//AC003991
 F-PLACE1005453//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y48A6, WORKING DRAFT SEQUENCE.//0.00069:582:59//Z92854
 F-PLACE1005467//Rat mRNA.//0.0014:131:70//M59859
 F-PLACE1005471//Human DNA sequence from clone 4514 on chromosome 6 q24.1-24.3. Contains two putative unknown genes, ESTs, STSs and GSSs, complete sequence.//3.0e-23:530:67//AL023581
 F-PLACE1005477//Human DNA sequence from clone J181N11, WORKING DRAFT SEQUENCE.//3.3e-131:814:88//Z82191
 F-PLACE1005480//Homo sapiens DNA sequence from PAC 257120 on chromosome 22q13.1-13.2. Contains cytochrome P450 pseudogenes CYP2D7P, CYP2D8P, CYP2D6(D), TCF20, NADH ubiquinone oxidoreductase B14 subunit, ESTs, CA repeat, STS, GSS.//7.0e-34:246:73//AL021878
 F-PLACE1005481//RPC111-74L17.TJ RPC111 Homo sapiens genomic clone R-74L17, genomic survey sequence.//0.37:403:57//AQ266885
 F-PLACE1005494//Homo sapiens transient receptor potential protein

【0761】

【表462】

6 mRNA, complete cds.//2.1e-67:325:99//AF080394	m46+) mRNA, partial cds.//9.3e-16:638:57//U29892
F-PLACE1005502//Homo sapiens BAC clone NH0161H12 from 7p14-p15, complete sequence.//0.015:403:61//AC005589	F-PLACE1005898//Rattus norvegicus A-kinase anchoring protein AKAP150 mRNA, complete cds.//1.0:178:65//U67136
F-PLACE1005526//H.sapiens CpG island DNA genomic MseI fragment, clone 9f1, reverse read cp9f1.rta.//3.6e-27:159:96//Z66485	F-PLACE1005921//M.musculus mRNA for immunity associated protein 3.8.//6.6e-17:614:59//Y08026
F-PLACE1005528//Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE.//2.6e-28:449:67//AP000038	F-PLACE1005923//RPC111-33G19.TJ RPC111 Homo sapiens genomic clone RPC111-33G19, genomic survey sequence.//4.0e-10:535:57//AQ046151
F-PLACE1005530//Homo sapiens clone DJ0691L07, complete sequence.//6.5e-18:234:72//AC004860	F-PLACE1005925//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SEQUENCE.//0.17:159:65//AL034405
F-PLACE1005550//Fugu rubripes GSS sequence, clone 048A08bH3, genomic survey sequence.//1.2e-14:123:75//AL025925	F-PLACE1005932
F-PLACE1005554//Leishmania tarentolae mitochondrial 12S ribosomal RNA gene.//0.43:209:66//X02354	F-PLACE1005934//H.sapiens CpG island DNA genomic MseI fragment, clone 165g2, forward read cp9165g2.ftta.//8.3e-43:247:93//Z57153
F-PLACE1005557//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence.//9.3e-113:536:97//AC004707	F-PLACE1005936//F.rubripes GSS sequence, clone 069K22aG2, genomic survey sequence.//0.91:116:68//AL014719
F-PLACE1005574//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE. 3 unordered pieces.//1.1e-10:514:59//AC005504	F-PLACE1005951//Rhodobacter sphaeroides DMSO/TMAO-sensor kinase (dors), DMSO/TMAO-response regulator (dorR), DMSO/TMAO-cytochrome c-containing subunit (dorC), DMSO-membrane protein (dorB), and DMSO/TMAO-reductase (dorA) genes, complete cds.//0.0022:495:59//AF016236
F-PLACE1005584//Homo sapiens mRNA for KIAA0617 protein, complete cds.//0.00056:289:63//AB014517	F-PLACE1005953//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//2.9e-05:442:61//AC004081
F-PLACE1005595//Human chromosome 11q12.2 PAC clone pDJ0606g6, complete sequence.//1.2e-111:262:89//AC004126	F-PLACE1005955//Caenorhabditis elegans cosmid F01F1.//4.3e-20:409:64//U13070
F-PLACE1005603	F-PLACE1005966//P.falciparum aarp3 gene, exon.//0.0083:270:64//Y08925
F-PLACE1005611//F1605TFC IGF Arabidopsis thaliana genomic clone F1605, genomic survey sequence.//2.0e-10:209:66//B98589	F-PLACE1005968
F-PLACE1005623	F-PLACE1005990//Homo sapiens chromosome 12p13.3 clone RPC111-407G.6, WORKING DRAFT SEQUENCE, 51 ordered pieces.//1.0e-100:513:96//AC005866
F-PLACE1005630//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.2e-93:230:98//AC005840	F-PLACE1006002//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 229A8, WORKING DRAFT SEQUENCE.//2.5e-54:444:77//Z86090
F-PLACE1005639//HS_3095_B1_A03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3095 Col=5 Row=B, genomic survey sequence.//1.2e-05:220:63//AQ123022	F-PLACE1006003//HS-1059-A2-G01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 781 Col=2 Row=W, genomic survey sequence.//3.4e-05:214:64//B44442
F-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//6.4e-150:721:98//AF083255	F-PLACE1006011//Mus musculus poly-(ADP-ribose)-transferase homolog PARP mRNA, complete cds.//4.3e-71:580:79//AF072521
F-PLACE1005656//H.sapiens RR2 mRNA for small subunit ribonucleotide reductase.//1.3e-51:480:74//X59618	F-PLACE1006017//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-113A6 complete genomic sequence, complete sequence.//8.6e-32:177:83//AC002299
F-PLACE1005666//RPC111-78015.TV RPC111 Homo sapiens genomic clone R-78015, genomic survey sequence.//8.7e-05:243:62//AQ284667	F-PLACE1006037//Mus musculus B6D2F1 clone 2C11B mRNA.//1.8e-34:269:83//U01139
F-PLACE1005698//Human membrane-associated lectin type-C mRNA.//1.9e-63:374:85//M98457	F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//3.4e-14:7:719:97//X99906
F-PLACE1005727//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.69:633:57//AE001422	F-PLACE1006076//Homo sapiens DNA sequence from PAC 79C4 on chromosome 1q24. Contains the PMX1 gene, coding for two alternative forms of the Paired Mesoderm Homeobox protein 1 (PMX-1, PHOX-1). Contains ESTs, STSs and BAC end sequences (GSSs), complete sequence.//0.37:332:62//Z97200
F-PLACE1005730//HS_2026_B1_H11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=21 Row=P, genomic survey sequence.//2.0e-24:286:74//AQ231147	F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.3e-145:679:99//AF039023
F-PLACE1005739//Mus musculus IFN-gamma induced (Mg11) mRNA, complete cds.//2.8e-55:621:71//U15635	F-PLACE1006129
F-PLACE1005755//HS_2213_A2_H11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=22 Row=D, genomic survey sequence.//1.4e-25:290:75//AQ136844	F-PLACE1006139//Saccharomyces cerevisiae chromosome VI cosmid 9965.//4.8e-27:693:60//D44597
F-PLACE1005763//Rat medium-chain 3-acyl fatty acid synthetase thioester hydrolase (MCH), complete cds.//4.5e-40:297:70//M16200	F-PLACE1006143//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 16915, WORKING DRAFT SEQUENCE.//4.7e-46:435:77//Z93015
F-PLACE1005799//R.norvegicus mRNA for mitochondrial isoform of cytochrome b5.//0.91:287:63//Y12517	F-PLACE1006157//Saguinus oedipus mRNA for membrane cofactor protein CD46, complete cds, clone:B2.//0.048:290:60//D85750
F-PLACE1005802//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//5.0e-109:530:98//AC004827	F-PLACE1006159//Homo sapiens chromosome 10 clone CIT987SK-105402 map 10q25, complete sequence.//3.2e-129:466:96//AC005661
F-PLACE1005803//HS_3092_B1_A10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=19 Row=B, genomic survey sequence.//2.4e-08:76:96//AQ103695	F-PLACE1006164//HS_3003_A1_F08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3003 Col=15 Row=K, genomic survey sequence.//1.4e-70:388:93//AQ118200
F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase 1B mRNA, complete cds.//1.4e-126:636:96//AF027156	F-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//4.3e-78:385:86//AC005239
F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//2.6e-154:739:98//AF065482	F-PLACE1006170//Mouse mRNA for alpha-adaptin (C).//3.5e-91:630:84//X14972
F-PLACE1005828//Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.2e-37:355:77//AC004150	F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds.//3.9e-149:694:99//AF091433
F-PLACE1005834//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-105, complete sequence.//0.00080:663:58//AL010283	F-PLACE1006195//Homo sapiens Xp22 BAC GS-60TH18 (Genome Systems Human BAC library) complete sequence.//2.5e-16:283:70//AC003658
F-PLACE1005845//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00015:340:58//AC004153	F-PLACE1006196//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//2.2e-94:648:84//L25125
F-PLACE1005850//Human DNA sequence from clone 465M24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG island s, complete sequence.//1.8e-46:278:85//AL031432	F-PLACE1006205//Human Xp22 cosmid U250A9, complete sequence.//0.15:533:58//U75931
F-PLACE1005851	F-PLACE1006223//F24L20-T7 IGF Arabidopsis thaliana genomic clone F24L20, genomic survey sequence.//0.0068:175:64//B19803
F-PLACE1005876//B.taurus mRNA for cleavage and polyadenylation specificity factor.//5.0e-120:701:89//X75931	F-PLACE1006225//CIT-HSP-2335123.TF CIT-HSP Homo sapiens genomic clone 2335123, genomic survey sequence.//2.1e-19:149:90//AQ039880
F-PLACE1005884//CIT-HSP-2333012, TR CIT-HSP Homo sapiens genomic clone 2333012, genomic survey sequence.//4.6e-78:385:98//AQ039226	F-PLACE1006236//Human chromosome 12p15 BAC clone CIT987SK-9908 complete sequence.//0.51:290:58//U91327
F-PLACE1005890//Schizosaccharomyces pombe bem1/bud5 suppressor (Be	

【0762】

【表463】

F-PLACE1006239//Homo sapiens BAC clone RG118D07 from 7q31, complete sequence.//7.4e-158:452:96//AC004142
 F-PLACE1006246//RPC111-36123.TK RPC1-11 Homo sapiens genomic clone RPC1-11-36123, genomic survey sequence.//2.6e-31:176:97//AQ045400
 F-PLACE1006248//Homo sapiens mRNA for KIAA0548 protein, partial cds.//2.3e-156:791:98//AB014548
 F-PLACE1006262//342E3.TVD CIT978SKA1 Homo sapiens genomic clone A-342E03, genomic survey sequence.//1.0:228:63//B16447
 F-PLACE1006288//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20M2, WORKING DRAFT SEQUENCE.//6.6e-172:809:99//AL031320
 F-PLACE1006318
 F-PLACE1006325//Homo sapiens PAC clone DJ0988L12 from 7q11.23-q21.1, complete sequence.//0.079:396:59//AC004454
 F-PLACE1006335//Mouse Ig third hypervariable region (HCDR3), nonproductively rearranged alpha-chain gene VHSB32-D-JH2 region.//1.0:90:67//M55721
 F-PLACE1006357//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.16:445:56//AC005504
 F-PLACE1006360//Plasmodium falciparum MAL3P7, complete sequence.//6.1e-05:625:57//AL034559
 F-PLACE1006368//X. laevis mRNA for KLP2 protein.//3.0e-25:376:68//X94082
 F-PLACE1006371//Homo sapiens chromosome 16, cosmid clone 36QHG (LANL), complete sequence.//2.0e-146:711:97//AC004232
 F-PLACE1006382
 F-PLACE1006385//Homo sapiens epsilon 2a mRNA, complete cds.//5.1e-110:539:97//AF062085
 F-PLACE1006412//Homo sapiens BAC clone G558G18 from 7p12-p14, complete sequence.//1.3e-23:463:68//AC005029
 F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds.//1.3e-109:525:98//AF069735
 F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds.//6.9e-23:531:65//AB011129
 F-PLACE1006445//HS_3071_A1_C11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=21 Row=E, genomic survey sequence.//4.7e-74:392:95//AQ103347
 F-PLACE1006469//Rhodobacter capsulatus strain SB1003, partial genome.//1.1e-40:686:65//AF010496
 F-PLACE1006470//T. brucei kinetoplast maxicircle variable region DN A.//0.99:250:59//Z15118
 F-PLACE1006482//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 447C4, WORKING DRAFT SEQUENCE.//4.3e-120:328:98//AL021977
 F-PLACE1006488//Canine mRNA for 68kDa subunit of signal recognition particle (SRP68).//6.5e-86:478:91//X53744
 F-PLACE1006492
 F-PLACE1006506
 F-PLACE1006521//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//0.0010:547:58//AC005083
 F-PLACE1006531//Oryctolagus cuniculus translation initiation factor eIF2C mRNA, complete cds.//2.6e-84:625:80//AF005355
 F-PLACE1006534//Caenorhabditis elegans cosmid Y40H7A, complete sequence.//0.00031:671:58//AL033510
 F-PLACE1006540
 F-PLACE1006552//P. falciparum glutamic acid-rich protein gnen, complete cds.//6.0e-10:636:59//J03998
 F-PLACE1006598//Homo sapiens BAC clone MH0539B24 from 7p15.1-p14, complete sequence.//9.8e-25:170:77//AC006044
 F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//6.7e-167:781:99//U97670
 F-PLACE1006617//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence.//0.98:514:59//AC004470
 F-PLACE1006626//H. sapiens DNA 3' flanking simple sequence region clone wg2c3.//0.00079:206:62//X76589
 F-PLACE1006629//Human BAC clone RG333F24 from 7q11.2-q21, complete sequence.//0.0012:576:57//AC004015
 F-PLACE1006640//P. falciparum complete gene map of plastid-like DNA (IR-B).//0.0018:588:59//X95276
 F-PLACE1006673//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0028:469:58//AC004688
 F-PLACE1006678//Mus musculus UDP-Gal:betaGlcNAc beta 1,3-galactosyl transferase-I (B3GT1) gene, complete cds.//0.00011:184:64//AF029790
 F-PLACE1006704//Mus musculus dentin sialophosphoprotein precursor (DSPP) mRNA, complete cds.//0.0013:380:62//U67916
 F-PLACE1006731//Human DNA sequence from PAC 408N23 on chromosome 2 2q13. Contains HIP, HSC70-INTERACTING PROTEIN (PROGESTERONE RECEPTOR-ASSOCIATED P48 PROTEIN). ESTs and STS.//1.5e-78:520:86//Z98048
 F-PLACE1006754//Homo sapiens chromosome 19, cosmid R29124, complete sequence.//1.9e-135:378:99//AC005626
 F-PLACE1006760//CIT-HSP-2336013.TR CIT-HSP Homo sapiens genomic clone 2336013, genomic survey sequence.//0.018:147:66//AQ039246
 F-PLACE1006779//Plasmodium falciparum chromosome 2, section 63 of 73 of the complete sequence.//2.6e-08:823:58//AE001426
 F-PLACE1006782//Homo sapiens clone NH0005N18, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.043:252:65//AC005487
 F-PLACE1006792//HS_3165_B1_H01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3165 Col=1 Row=P, genomic survey sequence.//1.4e-11:249:67//AQ149559
 F-PLACE1006795//Mouse eph-related receptor tyrosine kinase (Mek4) mRNA, complete cds.//1.3e-12:155:80//M68513
 F-PLACE1006800//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-92, complete sequence.//6.7e-05:391:62//AL010272
 F-PLACE1006805//paramecium species 1, 168 nt dna dimer: replication init. region.//9.1e-09:369:62//K00915
 F-PLACE1006815//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 321D2, WORKING DRAFT SEQUENCE.//0.89:465:58//AL031033
 F-PLACE1006819//Homo sapiens clone DJ1163L11, complete sequence.//1.5e-121:618:91//AC005230
 F-PLACE1006829//Brn-3a=class V POU transcription factor [mice, CD/CD, embryo fibroblast cells, Genomic, 2160 nt].//0.011:145:68//S69350
 F-PLACE1006860//Plasmodium falciparum MAL3P7, complete sequence.//2.2e-07:691:58//AL034559
 F-PLACE1006867//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 323M4, WORKING DRAFT SEQUENCE.//1.5e-132:643:98//AL033378
 F-PLACE1006878
 F-PLACE1006883//Mycobacterium tuberculosis H37Rv complete genome: segment 138/162.//1.0:236:62//Z95120
 F-PLACE1006901//Mus musculus t complex testis-specific protein (Tc tex2) gene, t haplotype, promoter sequence.//2.7e-19:171:81//U21672
 F-PLACE1006904
 F-PLACE1006917//H. sapiens CpG island DNA genomic MseI fragment, clone 79g10, forward read cp79g10. flla.//1.3e-21:131:98//Z63175
 F-PLACE1006932//Mus musculus FKBP65 binding protein mRNA, complete cds.//0.99:248:61//L07063
 F-PLACE1006935//Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families.//0.85:161:63//AF029308
 F-PLACE1006956//Hylobates lar involucrin gene, complete cds.//0.077:355:61//M35447
 F-PLACE1006958//Mus musculus osmotic stress protein 94 (Osp94) mRNA, complete cds.//2.9e-89:483:86//U23921
 F-PLACE1006961//Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes.//1.6e-06:651:58//AJ223323
 F-PLACE1006962//H. sapiens irIB mRNA.//7.1e-15:202:71//X63417
 F-PLACE1006966//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y105E8, WORKING DRAFT SEQUENCE.//1.7e-26:451:61//AL022594
 F-PLACE1006989//cSRL-172A4-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-172A4, genomic survey sequence.//1.0:97:67//B03188
 F-PLACE1007014//Rattus norvegicus equilibrative nitrobenzylthioinosine-insensitive nucleoside transporter mRNA, complete cds.//4.2e-07:592:58//AF015305
 F-PLACE1007021//Homo sapiens chromosome 19, cosmid F15403, complete sequence.//5.1e-17:285:70//AC005777
 F-PLACE1007045//Human DNA sequence from PAC 181N1 on chromosome X contains ESTs, STS polymorphic CA repeats.//6.2e-131:775:89//Z82899
 F-PLACE1007053//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.7e-143:675:99//AC004895
 F-PLACE1007068//Homo sapiens chromosome 17, clone hRPK.214_0_1, complete sequence.//1.3e-131:652:97//AC005224
 F-PLACE1007097//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlap with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//8.3e-158:768:97//AL021368
 F-PLACE1007105//Mus musculus muskellin mRNA, complete cds.//4.1e-124:687:91//U72194
 F-PLACE1007111//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 g

【0763】

【表464】

enomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7
e-05:586:56//AC005139
F-PLACE1007112//HS_2234_B2_G10_MF CIT Approved Human Genomic Sperm
Library D Homo sapiens genomic clone Plate=2234 Col=20 Row=N, gen
omic survey sequence.//0.26:200:62//AQ087801
F-PLACE1007132//CIT978SK-A-211C6.TVB CIT978SK Homo sapiens genomic
clone A-211C6, genomic survey sequence.//1.3e-40:255:92//B72112
F-PLACE1007140//QMI orf [Coturnix coturnix, japonica, K2 neuroreti
nal cells, mRNA Partial, 3884 nt].//4.9e-15:386:62//S68151
F-PLACE1007178//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-42
0 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//
0.011:329:61//AC005140
F-PLACE1007226//Human lipocortin (LIP) 2 gene, upstream region.//
0.0036:180:63//M62899
F-PLACE1007238//FMR1 (CGG repeats) [human, Fragile X syndrome pati
ent, Genomic, 429 nt].//2.8e-08:269:63//ST4494
F-PLACE1007239//Homo sapiens mRNA for transcription elongation fac
tor S-II, hS-II-TI, complete cds.//6.3e-57:405:87//D50495
F-PLACE1007242//HS_3006_A1_B11_MR CIT Approved Human Genomic Sperm
Library D Homo sapiens genomic clone Plate=3006 Col=21 Row=C, gen
omic survey sequence.//0.088:191:59//AQ089443
F-PLACE1007243//Human transporter protein (glt7) mRNA, complete cd
s.//7.9e-12:245:66//U49082
F-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//5.2e-144:6
77:98//Y15908
F-PLACE1007274//HS_3003_A1_D08_MF CIT Approved Human Genomic Sperm
Library D Homo sapiens genomic clone Plate=3003 Col=15 Row=G, gen
omic survey sequence.//7.4e-49:345:85//AQ294154
F-PLACE1007276//Fugu rubripes GSS sequence, clone 014010aG11, geno
mic survey sequence.//0.0052:228:62//AL024982
F-PLACE1007282//F. rubripes GSS sequence, clone 019007aB3, genomic
survey sequence.//0.024:289:58//AL011743
F-PLACE1007286//Human Chromosome 16 BAC clone CIT987SK-A-256A9, co
mplete sequence.//0.0048:185:69//AC002492
F-PLACE1007301//Dictyostelium discoideum gene for TRFA, complete c
ds.//0.069:761:57//AB009080
F-PLACE1007317
F-PLACE1007342
F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EB
BP) mRNA, complete cds.//5.4e-120:567:98//AF096870
F-PLACE1007367//Homo sapiens clone RCG22017, WORKING DRAFT SEQUENC
E, 2 unordered pieces.//1.2e-59:613:75//AC005077
F-PLACE1007375//Caenorhabditis elegans cosmid D2092.//1.8e-12:193:
70//U88167
F-PLACE1007386
F-PLACE1007402//HS_2170_A2_D12_MF CIT Approved Human Genomic Sperm
Library D Homo sapiens genomic clone Plate=2170 Col=24 Row=G, gen
omic survey sequence.//5.6e-06:162:67//AQ125590
F-PLACE1007409//Homo sapiens mitoxantone resistance protein 2 mRN
A, complete sequence.//1.6e-25:165:93//AF093772
F-PLACE1007416
F-PLACE1007450//Homo sapiens DNA from chromosome 19, BAC 33152, co
mplete sequence.//4.9e-34:764:62//AC003973
F-PLACE1007452//Mus musculus bet3 (Bet3) mRNA, complete cds.//4.1
e-17:374:64//AF041433
F-PLACE1007454//Homo sapiens (clone s153) mRNA fragment.//8.1e-52:
317:93//L40391
F-PLACE1007460//Human DNA sequence from clone 914P14 on chromosome
Xq23 Contains calpain-like protease gene, DCX (doublecortin) EST
s, CA repeat, GSS, complete sequence.//0.0019:280:64//AL031117
F-PLACE1007478//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-34
SG4 complete genomic sequence, complete sequence.//2.5e-24:362:7
1//AC002302
F-PLACE1007484
F-PLACE1007488//Danio rerio faciogenital dysplasia protein (fgd) m
RNA, complete cds.//3.8e-14:293:63//AF017370
F-PLACE1007507//Human DNA sequence from clone 10SD16 on chromosome
Xp11.3-11.4 Contains pseudogene similar to laminin-binding protei
n, CA repeat, STS, complete sequence.//4.6e-10:152:75//AL031311
F-PLACE1007511//Homo sapiens chromosome 17, clone hRPC.1110_E_20,
complete sequence.//3.6e-139:477:98//AC004231
F-PLACE1007524//Plasmodium falciparum microsatellite 14C sequence.
//0.0055:395:59//AF015461
F-PLACE1007525//Trypanoplasma borelli mitochondrion cytochrome oxi
dase subunit 1 (cox1), cytochrome oxidase subunit 2 (cox2), and ap
ocytochrome b (cytb) genes, complete cds, and complete 9S rRNA gen
e and partial 12S rRNA gene.//0.0013:550:58//U11682
F-PLACE1007537//H. sapiens CpG island DNA genomic MseI fragment, cl
one 198g6, reverse read cpg198g6, rta.//0.98:121:67//Z60280
F-PLACE1007544//Mus musculus chromosome 14 marker um-m24 CA dinucl
eotide DNA sequence.//2.3e-10:141:75//U31508
F-PLACE1007547//Homo sapiens mRNA for KIAA0661 protein, complete c
ds.//3.1e-69:733:71//AB014561
F-PLACE1007557//Drosophila yakuba mitochondrial DNA molecule.//0.0
22:393:61//X03240
F-PLACE1007583//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 545L17, WORKING DRAFT SEQUENCE.//3.6e-114:565:97//AL031
665
F-PLACE1007598//CIT-HSP-2371G14.TF CIT-HSP Homo sapiens genomic cl
one 2371G14, genomic survey sequence.//2.0e-22:304:70//AQ111183
F-PLACE1007618//Homo sapiens chromosome 17, clone hRPC.642_C_21, c
omplete sequence.//1.0:386:59//AC005245
F-PLACE1007621
F-PLACE1007632//Homo sapiens 12p13.3 PAC RPC15-94QJ5 (Roswell Park
Cancer Institute Human PAC Library) complete sequence.//1.0e-88:2
76:96//AC006064
F-PLACE1007645//Bovine elastin mRNA, partial cds.//2.1e-07:110:79/
/M26132
F-PLACE1007649
F-PLACE1007677//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 968D22, WORKING DRAFT SEQUENCE.//1.2e-21:567:64//AL0237
55
F-PLACE1007688//Pseudorabies virus immediate-early gene.//2.2e-05:
287:66//X15120
F-PLACE1007690//Caenorhabditis elegans cosmid R07G3.//0.40:122:70/
/U23452
F-PLACE1007697//Mus musculus LIM/homeobox (Lhx3) gene fragment.//
0.85:117:71//L40483
F-PLACE1007705//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 460J8, WORKING DRAFT SEQUENCE.//0.0035:75:88//AL031662
F-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complet
e cds.//1.3e-147:709:97//AF061243
F-PLACE1007725//Arabidopsis thaliana genomic DNA, chromosome 5. P1
clone: MB818, complete sequence.//1.0:510:58//AB005231
F-PLACE1007729//Human endogenous retrovirus HML6 proviral clone HM
L6p, putative leader region, gag, pro and pol pseudogenes.//4.8e-1
36:516:89//U86698
F-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete c
ds.//7.9e-155:728:98//AB014585
F-PLACE1007737//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUEN
CE, 3 unordered pieces.//5.8e-22:806:60//AC005484
F-PLACE1007743//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383
genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1
e-06:510:56//AC005504
F-PLACE1007746//HS_2268_B1_G10_MF CIT Approved Human Genomic Sperm
Library D Homo sapiens genomic clone Plate=2268 Col=19 Row=N, gen
omic survey sequence.//0.10:171:63//AQ124780
F-PLACE1007791//Plasmodium falciparum DNA *** SEQUENCING IN PROGRE
SS *** from MAL1P6, WORKING DRAFT SEQUENCE.//0.63:241:58//AL031749
F-PLACE1007807//Homo sapiens chromosome 17, clone hRPC.879_D_6, co
mplete sequence.//1.0e-120:743:87//AC005273
F-PLACE1007810//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Hu
man BAC library) complete sequence.//1.0e-113:739:86//AC003658
F-PLACE1007829//CIT-HSP-2383J22.TR CIT-HSP Homo sapiens genomic cl
one 2383J22, genomic survey sequence.//1.0e-47:254:97//AQ196438
F-PLACE1007843//F. rubripes GSS sequence, clone 162K02bC12, genomic
survey sequence.//1.6e-10:148:72//AL006903
F-PLACE1007846//Homo sapiens genomic DNA, chromosome 21q22.2 (Down
Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//3.4e-17
7:844:98//AP000010
F-PLACE1007852//Mouse perlecan mRNA, complete cds.//8.5e-39:243:90
//M77174
F-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete c
ds.//3.9e-189:894:98//AB018309
F-PLACE1007866//CIT-HSP-2353D11.TF.1 CIT-HSP Homo sapiens genomic
clone 2353D11, genomic survey sequence.//0.015:279:61//AQ263271
F-PLACE1007877
F-PLACE1007897
F-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcrip
t KIAA0487.//2.3e-154:755:97//AB007956
F-PLACE1007946//Human chromosome Y cosmid 56B5 genomic sequence, W
ORKING DRAFT SEQUENCE.//1.1e-59:310:81//AC003097
F-PLACE1007954//Homo sapiens BAC clone NH0414C23 from Y, complete
sequence.//2.1e-61:522:79//AC006157
F-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRN
A, complete cds.//2.7e-171:813:98//AF084530
F-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (P
DE8B) mRNA, partial cds.//2.5e-153:730:98//AF079529
F-PLACE1007969//Mus musculus myelin gene expression factor (MEF-2)
mRNA, partial cds.//3.4e-32:383:74//U13262

【0764】

【表465】

F-PLACE1007990//H.sapiens genomic DNA fragment (clone J31A212R).//6.6e-35:198.96//294758
 F-PLACE1008000//Mus musculus vcl 3 mRNA, complete cds.//1.5e-118:708.88//AF087695
 F-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.4e-163:786.98//AC005628
 F-PLACE1008044//Rattus norvegicus nuclear pore complex protein NUP107 mRNA, complete cds.//1.2e-95:625.84//L31840
 F-PLACE1008045//Caenorhabditis elegans cosmid F17C8, complete sequence.//0.016:165.65//Z35719
 F-PLACE1008080//Human DNA sequence from cosmid L118G10, Huntington's Disease Region, chromosome 4p16.3.//4.0e-07:251.64//Z68883
 F-PLACE1008095//RPC111-21F19.TP RPC1-11 Homo sapiens genomic clone RPC1-11-21F19, genomic survey sequence.//1.5e-30:166.99//B85883
 F-PLACE1008111//Aphidius picipes NADH dehydrogenase 1 gene, mitochondrial gene encoding mitochondrial protein, partial cds.//7.5e-06:414.60//AF069163
 F-PLACE1008122//S.cerevisiae chromosome XIV reading frame ORF YOL125w.//0.046:477.59//Z74867
 F-PLACE1008129//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase IIx genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0068:446.57//AC004586
 F-PLACE1008132//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 316D5, WORKING DRAFT SEQUENCE.//3.6e-20:111.93//Z82199
 F-PLACE1008177//Mouse mRNA for meiosis-specific nuclear structural protein 1 (MNS1), complete cds.//2.5e-88:866.73//D14849
 F-PLACE1008181//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 159A1, WORKING DRAFT SEQUENCE.//0.0033:727.56//AL034397
 F-PLACE1008198//HS_3073_A1.C06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3073 Col=11 Row=E, genomic survey sequence.//2.3e-12:94.92//AQ171450
 F-PLACE1008201//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//2.5e-162:791.97//AC005069
 F-PLACE1008209
 F-PLACE1008231//Mouse testis-specific protein mRNA, complete cds.//0.65:174.66//M26332
 F-PLACE1008244//CIT-HSP-2337B4, TR CIT-HSP Homo sapiens genomic clone 2337B4, genomic survey sequence.//5.7e-28:165.95//AQ039317
 F-PLACE1008273//B.primigenius mRNA for coat protein gamma-cop.//2.8e-71:709.71//X92987
 F-PLACE1008275//D.discoideum actin A-13 gene, 5' flank.//0.12:131.64//M29123
 F-PLACE1008280//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome Systems Human BAC Library) complete sequence.//0.011:96.73//AC005913
 F-PLACE1008309//Rattus norvegicus putative four repeat ion channel mRNA, complete cds.//8.2e-86:672.77//AF078779
 F-PLACE1008329//HS_2027_A1.C06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2027 Col=11 Row=E, genomic survey sequence.//8.7e-09:116.81//AQ244432
 F-PLACE1008330//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//2.2e-141:670.98//AC005176
 F-PLACE1008331//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-27:157.78//AC005000
 F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds.//1.1e-137:659.98//AB014579
 F-PLACE1008368//CIT-HSP-2311C9, TR CIT-HSP Homo sapiens genomic clone 2311C9, genomic survey sequence.//7.1e-08:398.60//AQ016352
 F-PLACE1008369//HS_2251_B1.A02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2251 Col=3 Row=B, genomic survey sequence.//2.1e-35:217.93//AQ066512
 F-PLACE1008392//Homo sapiens chromosome 17, clone hRPK.136_H.19, complete sequence.//1.4e-11:403.64//AC005856
 F-PLACE1008398//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 215D11, WORKING DRAFT SEQUENCE.//3.7e-144:681.99//AL034417
 F-PLACE1008401//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0366H07; HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//2.8e-45:257.96//AC004604
 F-PLACE1008402//Homo sapiens mRNA for p115, complete cds.//4.3e-148:711.98//D86326
 F-PLACE1008405//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.089:672.56//AC004688
 F-PLACE1008424
 F-PLACE1008426//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 7/11.//1.0e-88:331.84//AB020864
 F-PLACE1008429//Chromosome 22q13 BAC Clone CIT987SK-38408 complete sequence.//0.55:530.58//M62317
 F-PLACE1008437//CIT-HSP-2376H4, TR CIT-HSP Homo sapiens genomic clone 2376H4, genomic survey sequence.//3.3e-78:349.94//AQ112479
 F-PLACE1008455//HS_2064_B1.E09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2064 Col=17 Row=J, genomic survey sequence.//4.7e-59:471.81//AQ246589
 F-PLACE1008457//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//8.9e-43:307.73//AC004526
 F-PLACE1008465//CIT-HSP-2163F24, TR CIT-HSP Homo sapiens genomic clone 2163F24, genomic survey sequence.//8.9e-41:210.99//B90014
 F-PLACE1008488//Mus musculus mRNA for testis-specific protein kinase 1, complete cds.//0.00013:516.58//AB003494
 F-PLACE1008524//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 34B21, WORKING DRAFT SEQUENCE.//1.3e-161:778.98//AL031778
 F-PLACE1008531//Homo sapiens wbscr1 (WBSR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//1.1e-78:191.100//AF045555
 F-PLACE1008532//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 92N15, WORKING DRAFT SEQUENCE.//3.8e-24:257.70//Z93097
 F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.//1.0e-13:215.71//AC004997
 F-PLACE1008568//Human DNA sequence from PAC 388N15 on chromosome X q21.1.//0.66:263.64//Z99571
 F-PLACE1008584//Homo sapiens cosmid clone U3983 from Xp22.1-22.2, complete sequence.//1.1e-19:315.68//U73023
 F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete cds.//1.2e-173:812.98//AB018334
 F-PLACE1008621//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//3.9e-09:198.71//AC005077
 F-PLACE1008625//Homo sapiens chromosome 5, PAC clone 45L14 (LBML H91), complete sequence.//0.68:568.59//AC005373
 F-PLACE1008626//HS_3221_A2_F03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3221 Col=6 Row=K, genomic survey sequence.//1.7e-13:147.82//AQ180967
 F-PLACE1008627//Cricetulus griseus mRNA for Zn finger factor.//9.7e-98:586.88//Y12836
 F-PLACE1008629//CIT-HSP-2012I4, TR CIT-HSP Homo sapiens genomic clone 2012I4, genomic survey sequence.//0.00085:203.66//B53732
 F-PLACE1008630//Sequence 26 from Patent W09517522.//9.7e-05:97.80//A45356
 F-PLACE1008643//Human mRNA for inter-alpha-trypsin inhibitor family heavy chain-related protein (IHRP), complete cds.//1.4e-23:299.64//D38595
 F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//1.1e-133:622.99//AF044333
 F-PLACE1008693//CIT-HSP-2346F2, TF CIT-HSP Homo sapiens genomic clone 2346F2, genomic survey sequence.//0.24:89.76//AQ060732
 F-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//1.4e-94:420.97//AF038406
 F-PLACE1008715//CIT-HSP-2294K20, TR CIT-HSP Homo sapiens genomic clone 2294K20, genomic survey sequence.//2.1e-70:349.98//AQ007199
 F-PLACE1008748//Arabidopsis thaliana chromosome 1 BAC T14N5 genomic sequence, complete sequence.//0.14:347.59//AC004260
 F-PLACE1008757//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//7.9e-25:244.71//AC003037
 F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, complete cds.//4.5e-120:503.97//AF060543
 F-PLACE1008798//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//0.00026:370.61//AF001549
 F-PLACE1008807//CIT-HSP-2334B19, TF CIT-HSP Homo sapiens genomic clone 2334B19, genomic survey sequence.//3.3e-08:220.65//AQ036643
 F-PLACE1008808//Homo sapiens exonuclease homolog RAD1 (RAD1) mRNA, complete cds.//1.7e-120:470.97//AF030933
 F-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds.//2.8e-87:504.89//AF032668
 F-PLACE1008851//Homo sapiens DNA sequence from PAC 163M9 on chromosome 1p35.1-p36.21. Contains protein synthesis factor (eIF-4C), D1 F1531A pseudogene, ESTs, STS, GSS, complete sequence.//4.0e-21:212.74//AL021920
 F-PLACE1008854
 F-PLACE1008867//Human DNA sequence from clone J42BA131, WORKING DRAFT SEQUENCE.//4.7e-77:477.84//Z82209
 F-PLACE1008887//Homo sapiens BAC clone NH0335J18 from 2, complete sequence.//3.4e-53:699.70//AC005539
 F-PLACE1008902//Mouse G-alpha-13 protein mRNA, complete cds.//2.1e-06:164.68//M63660
 F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds.//6.4e-158:753.98//AB018308
 F-PLACE1008925//Homo sapiens chromosome 16p11.2 BAC clone CIT987S

【0765】

【表466】

K-A-180C2, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00013:40
0:63//AC002042
F-PLACE1008934//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 1104E15, WORKING DRAFT SEQUENCE.//7.4e-05:145:71//AL022
312
F-PLACE1008941//Human zinc finger protein (ZNF141) mRNA, complete
cds.//4.3e-41:282:87//L15309
F-PLACE1008947//Pseudorabies virus with upstream and downstream seq
uences.//5.9e-15:710:60//M34651
F-PLACE1009020//HS_3051_B1_H01_MR CIT Approved Human Genomic Sperm
Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=P, geno
mic survey sequence.//1.9e-21:167:86//AQ253727
F-PLACE1009027//Human DNA sequence from clone 914P14 on chromosome
Xq23 Contains calpain-like protease gene, DCX (doublecortin) EST
s, CA repeat, GSS, complete sequence.//4.1e-152:763:97//AL031117
F-PLACE1009039//HS_2034_A2_F08_T7 CIT Approved Human Genomic Sperm
Library D Homo sapiens genomic clone Plate=2034 Col=16 Row=K, gen
omic survey sequence.//0.17:252:59//AQ230137
F-PLACE1009045//HS_3185_B2_B03_T7 CIT Approved Human Genomic Sperm
Library D Homo sapiens genomic clone Plate=3185 Col=6 Row=D, geno
mic survey sequence.//1.9e-34:260:86//AQ172861
F-PLACE1009048//Pig pituitary glycoprotein hormone alpha subunit g
ene, 5' flank and exon 1.//4.7e-70:463:80//D00766
F-PLACE1009050//Homo sapiens 12q13.1 PAC RPC13-197B17 (Roswell Par
k Cancer Institute Human PAC library) complete sequence.//0.63:28
0:61//AC004241
F-PLACE1009060//Mus musculus mRNA for Alix (ALG-2-interacting prot
ein X), complete CDS.//5.9e-113:725:85//AJ005073
F-PLACE1009090//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 1045J21, WORKING DRAFT SEQUENCE.//9.1e-27:222:84//AL021
919
F-PLACE1009091//Homo sapiens clone DJ0968116, complete sequence.//
0.027:630:58//AC006016
F-PLACE1009094
F-PLACE1009099//Mouse zinc finger protein (mkr4) mRNA, partial cd
s.//2.1e-85:726:76//M36515
F-PLACE1009110
F-PLACE1009111//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 138B7, WORKING DRAFT SEQUENCE.//6.0e-12:362:64//Z98752
F-PLACE1009113//Homo sapiens X-ray repair cross-complementing prot
ein 3 (XRCC3) mRNA, complete cds.//3.4e-138:671:97//AF035586
F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds.//3.6e-
23:718:59//D25215
F-PLACE1009150//Homo sapiens *** SEQUENCING IN PROGRESS ***, WORKI
NG DRAFT SEQUENCE.//6.1e-142:684:98//AJ011929
F-PLACE1009155//Homo sapiens genomic DNA, chromosome 21q11.1, segm
ent 2/28, WORKING DRAFT SEQUENCE.//4.3e-36:227:77//AF000031
F-PLACE1009158//H. sapiens genomic sequence for ERCC2 gene 3' region
involved in DNA excision repair.//1.0:173:60//X52222
F-PLACE1009166
F-PLACE1009172//Human BAC clone TE17 from 12q, complete sequence.//
4.0e-35:257:85//AC002070
F-PLACE1009174//Homo sapiens Xp22 bins 16-17 BAC GSHB-531117 (Geno
me Systems Human BAC Library) complete sequence.//2.9e-19:288:72//
AC004805
F-PLACE1009183//Arabidopsis thaliana genomic DNA, chromosome 5, Pl
clone: MHJ24, complete sequence.//0.053:388:60//AB008266
F-PLACE1009186//Rattus norvegicus fracture callus 1 (FxC1) mRNA, c
omplete cds.//1.8e-50:317:89//AF061242
F-PLACE1009190//RPC111-81N5.TJ RPC111 Homo sapiens genomic clone
R-81N5, genomic survey sequence.//0.91:114:67//AQ281881
F-PLACE1009200//CITB1-E1-2509J16.TF CITB1-E1 Homo sapiens genomic
clone 2509J16, genomic survey sequence.//2.8e-44:175:83//AQ262198
F-PLACE1009230//H.sapiens gene for pregnancy specific beta-1 glyco
protein.//1.1e-106:495:88//X63203
F-PLACE1009246//HS_3058_B1_A06_MF CIT Approved Human Genomic Sperm
Library D Homo sapiens genomic clone Plate=3058 Col=11 Row=B, gen
omic survey sequence.//0.10:175:68//AQ185945
F-PLACE1009298//Mus musculus maternal-embryonic 3 (New3) mRNA, com
plete cds.//1.8e-94:575:89//U47024
F-PLACE1009308//Human clone mcag32 chromosome 7 CTG repeat region.
//0.0017:350:62//U23862
F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD
95) mRNA, complete cds.//3.0e-06:411:59//U83192
F-PLACE1009328//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 191P20, WORKING DRAFT SEQUENCE.//5.7e-138:830:86//AL034
399
F-PLACE1009335//Human (lambda) DNA for immunoglobulin light chain.//
0.071:253:62//D87015
F-PLACE1009338//RPC111-74N24.TV RPC111 Homo sapiens genomic clone
R-74N24, genomic survey sequence.//2.4e-34:180:100//AQ268811
F-PLACE1009368
F-PLACE1009375
F-PLACE1009388//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 1014D13, WORKING DRAFT SEQUENCE.//2.0e-37:288:84//AL022
311
F-PLACE1009398//Human DNA binding protein (HPF2) mRNA, complete cd
s.//4.3e-78:730:74//M27878
F-PLACE1009404//Smd homolog [mice, liver, mRNA Partial, 199 nt.].//
0.16:95:71//S71494
F-PLACE1009410//Homo sapiens chromosome 17, clone hRPK.142_H.19, c
omplete sequence.//1.6e-150:701:99//AC005919
F-PLACE1009434//Mus musculus clone OST431, genomic survey sequenc
e.//2.9e-73:442:88//AF046700
F-PLACE1009443//Mycobacterium tuberculosis H37Rv complete genome:
segment 148/162.//0.012:582:56//AL022022
F-PLACE1009444//Homo sapiens phosphatidylinositol 4-kinase 230 (pi
4K230) mRNA, complete cds.//4.6e-21:146:93//AF012872
F-PLACE1009459//Mus musculus clone OST9217, genomic survey sequenc
e.//2.9e-31:264:81//AF046660
F-PLACE1009468//Sequence 1 from patent US 5580968.//1.9e-83:567:84
//130536
F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67
A1, complete sequence.//1.9e-142:704:97//AC004531
F-PLACE1009477//Human h1p14.3 PAC clone pDJ939m16, complete sequen
ce.//2.2e-09:235:68//AC004601
F-PLACE1009493//Human Chromosome 16 BAC clone CIT987SK-A-363E6, co
mplete sequence.//2.9e-83:171:92//U91321
F-PLACE1009524//Homo sapiens DNA sequence from PAC 63G5 on chromos
ome 22q12.3-13.1. Contains part of a gene for a human SEC7 homolog
B2-1 (cytohesin-2, Arno, ARF exchange factor) LIKE protein, an un
known gene and a gene coding for a Leucine rich protein. Contains
ESTs, STSs and GSSs, complete sequence.//3.8e-69:175:92//Z94160
F-PLACE1009539//Mus musculus synaptotagmin 2 isoform alpha mRNA, co
mplete cds.//7.0e-26:237:78//AF041862
F-PLACE1009542//Human DNA sequence from clone 1039K5 on chromosome
22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding p
rotein, gene similar to monocarboxylate transporter (MCT3), ESTs,
STS, GSS and a CpG island, complete sequence.//3.1e-10:126:79//AL0
31587
F-PLACE1009571//RPC111-60K12.TK RPC111 Homo sapiens genomic clone
R-60K12, genomic survey sequence.//1.4e-05:68:91//AQ195869
F-PLACE1009581
F-PLACE1009595//Homo sapiens chromosome 5, Pl clone 1029A7 (LBNL H
15), complete sequence.//6.6e-19:309:70//AC003959
F-PLACE1009596//Rattus norvegicus platelet-activating factor acety
lhydrolase beta subunit (PAF-AH beta) gene, complete cds.//9.0e-0
9:485:59//AF016049
F-PLACE1009607//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 409J21, WORKING DRAFT SEQUENCE.//4.9e-43:714:66//Z83824
F-PLACE1009613//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 g
enomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.01
7:655:57//AC004157
F-PLACE1009621
F-PLACE1009622//HS-1016-B2-E08-MF.abi CIT Human Genomic Sperm Libr
ary C Homo sapiens genomic clone Plate=CT 791 Col=16 Row=J, genom
ic survey sequence.//2.7e-15:100:98//B33248
F-PLACE1009637//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 g
enomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.6
3:130:67//AC005308
F-PLACE1009639//S.pombe chromosome 11 cosmid c24E9.//0.86:509:58//
AL021816
F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete c
ds.//1.4e-171:816:98//AB011159
F-PLACE1009665//Homo sapiens chromosome 17, clone HC17462L7, compl
ete sequence.//3.4e-67:437:87//AC005177
F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//2.5
e-147:701:98//AF062534
F-PLACE1009708//Homo sapiens clone DJ0935K16, complete sequence.//
1.5e-98:228:100//AC006011
F-PLACE1009721//Human Cosmid g0771a222 from 7q31.3, complete seque
nce.//2.2e-130:736:91//AC000109
F-PLACE1009731//M.musculus mRNA for immunity associated protein 3
8.//1.1e-13:311:64//Y08026
F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds.//4.2
e-125:602:98//AF046024
F-PLACE1009794
F-PLACE1009798//Human DNA sequence from clone 1189B24 on chromosom
e Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit
(EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ), Tubulin Beta and Proto-oncogen

【0766】

【表467】

e Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//1.3e-73:271:84//AL030996

F-PLACE1009845

F-PLACE1009861//B. tauris cathepsin B mRNA, 3' end.//0.00023:147:65//M64620

F-PLACE1009879//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 159A1, WORKING DRAFT SEQUENCE.//4.9e-27:725:63//AL034397

F-PLACE1009886//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167A19, WORKING DRAFT SEQUENCE.//8.2e-12:135:82//AL031427

F-PLACE1009888//F14G3-T7 IGF Arabidopsis thaliana genomic clone F14G3, genomic survey sequence.//0.0044:232:60//AQ251431

F-PLACE1009908//S. pombe chromosome I cosmid c3F10.//1.5e-19:559:59//Z69369

F-PLACE1009921//Homo sapiens cosmid clone HDAB (15149) insert DNA, complete cosmid.//5.9e-48:304:87//M63005

F-PLACE1009924//Homo sapiens chromosome 16p11.2 BAC clone CIT9875 K-201104, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.4e-51:481:78//AC004529

F-PLACE1009925//nxb0027C22r CUGI Rice BAC Library Oryza sativa genomic clone nxb0027C22r, genomic survey sequence.//0.98:220:67//A027066

F-PLACE1009935//Sequence 16 from patent US 5552281.//0.030:152:67//I25655

F-PLACE1009947//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.6e-12:322:67//AC006026

F-PLACE1009971

F-PLACE1009992//HS_3178_B1_F04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3178 Col=7 Row=L, genomic survey sequence.//4.9e-23:142:95//AQ150311

F-PLACE1009995//Caenorhabditis elegans cosmid C01A2, complete sequence.//0.00019:231:64//Z81029

F-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds.//7.9e-87:552:80//U48288

F-PLACE1010023

F-PLACE1010031//Human DNA sequence from clone 30M3 on chromosome 6 p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//6.9e-101:181:98//AL031775

F-PLACE1010053//M. musculus Spnr mRNA for RNA binding protein.//2.3e-136:689:95//X84692

F-PLACE1010069//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 212A2, WORKING DRAFT SEQUENCE.//0.0090:383:60//Z95114

F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//1.8e-166:792:98//AF065482

F-PLACE1010076//Mouse mRNA for TGF-beta type I receptor, complete cds.//7.5e-13:203:77//D25540

F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds.//3.0e-152:727:98//AB007925

F-PLACE1010089//HS_3111_A1_E08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3111 Col=15 Row=L, genomic survey sequence.//4.8e-07:124:78//AQ101268

F-PLACE1010096//R. norvegicus mRNA for 100 kDa protein.//1.2e-108:700:85//X64411

F-PLACE1010102//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.1e-07:476:60//AC005506

F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete cds.//3.8e-25:728:60//AF059569

F-PLACE1010106//Human DNA sequence from PAC 127B14 on chromosome X q22.//6.5e-25:488:63//Z93928

F-PLACE1010134//S. pombe chromosome I cosmid c29B12.//1.9e-13:238:67//Z99164

F-PLACE1010148//Homo sapiens partial human cDNA (660 bp).//4.8e-81:409:98//AJ222636

F-PLACE1010152//CIT-HSP-238IF24.TF CIT-HSP Homo sapiens genomic clone 238IF24, genomic survey sequence.//1.5e-28:163:98//AQ196757

F-PLACE1010181//Homo sapiens PAC clone DJ1139101 from Xq23, complete sequence.//2.4e-15:197:72//AC004973

F-PLACE1010194//Ictalurus punctatus tumor suppressor p53 mRNA, complete cds.//3.0e-14:181:74//AF074967

F-PLACE1010202//Homo sapiens mRNA for MBNL protein.//1.2e-27:509:66//Y13829

F-PLACE1010231//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 287G14, WORKING DRAFT SEQUENCE.//2.3e-101:194:95//AL033

377

F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds.//5.8e-145:693:97//AB007917

F-PLACE1010270//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//2.1e-05:347:60//AC004710

F-PLACE1010274//Caenorhabditis elegans cosmid C01A2, complete sequence.//0.00040:231:64//Z81029

F-PLACE1010293//Homo sapiens chromosome 2 PAC RPC13-417E16 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.5e-25:344:70//AC004464

F-PLACE1010310//Homo sapiens DNA sequence from PAC 329E20 on chromosome 1p34.4-36.13. Contains endothelin-converting-enzyme 1 (ECE-1), EST, STS, CA repeat, complete sequence.//3.5e-10:185:67//AL031005

F-PLACE1010321//Human DNA sequence from clone 299D3 on chromosome 22q13.3, complete sequence.//0.010:524:58//Z84468

F-PLACE1010324//CIT-HSP-2335J21.TR CIT-HSP Homo sapiens genomic clone 2335J21, genomic survey sequence.//9.1e-90:448:97//AQ041837

F-PLACE1010329//Apis mellifera ligustica complete mitochondrial genome.//2.8e-08:384:64//L06178

F-PLACE1010341//HS-1047-A2-C04-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 830 Col=8 Row=E, genomic survey sequence.//4.1e-21:141:92//B38252

F-PLACE1010362//Mycobacterium tuberculosis H37Rv complete genome: segment 155/162.//0.94:398:57//AL022121

F-PLACE1010364//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y102G3, WORKING DRAFT SEQUENCE.//0.11:404:56//A020985

F-PLACE1010383//Homo sapiens chromosome 17, clone hCIT.186.H_2, complete sequence.//0.066:88:76//AC004675

F-PLACE1010401//CIT-HSP-2367K17.TR CIT-HSP Homo sapiens genomic clone 2367K17, genomic survey sequence.//2.4e-71:454:88//AQ076825

F-PLACE1010481//Bos taurus CS-glucuronyl epimerase mRNA, partial cds.//7.5e-134:722:93//AF003927

F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds.//2.2e-150:702:99//AF039081

F-PLACE1010492

F-PLACE1010522//Homo sapiens cosmid LM1937 from Xq28.//0.022:405:60//U82695

F-PLACE1010529//Sequence 1 from patent US 5776717.//2.9e-145:684:98//AR016417

F-PLACE1010547//Human DNA sequence from clone 790B6 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence.//1.0:283:61//AL031677

F-PLACE1010562//RPC111-65116.TX RPC111 Homo sapiens genomic clone R-65116, genomic survey sequence.//0.017:216:67//AQ200831

F-PLACE1010579//Homo sapiens full length insert cDNA Y123D12.//3.9e-19:147:89//AF075014

F-PLACE1010580//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//6.4e-96:559:89//L25125

F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14p (PEX14) mRNA, complete cds.//3.1e-146:707:97//AF045186

F-PLACE1010616//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.045:454:59//AC005308

F-PLACE1010622//Plasmodium falciparum MAL3P2, complete sequence.//9.1e-07:378:60//AL034558

F-PLACE1010624//Streptomyces coelicolor cosmid 5A7.//1.4e-05:518:61//AL031107

F-PLACE1010628//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE, 21 unordered pieces.//5.0e-137:675:97//AC004846

F-PLACE1010629//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-25 SH10, complete sequence.//2.5e-17:187:80//AC004682

F-PLACE1010630//Arabidopsis thaliana genomic DNA, chromosome 5, TA C clone: K21P3, complete sequence.//0.21:159:64//AB016872

F-PLACE1010631//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.2e-144:720:97//AC005069

F-PLACE1010661

F-PLACE1010662//Arabidopsis thaliana DNA chromosome 4, BAC clone F7J7 (ESSA project).//0.90:257:61//AL021960

F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds.//3.3e-73:697:74//U35376

F-PLACE1010714//Human Chromosome 15q11-q13 PAC clone pDJ778a2, complete sequence.//0.010:447:59//AC004583

F-PLACE1010720//Mouse TPA-induced TIS11 mRNA.//2.0e-86:535:88//X14678

F-PLACE1010739//HS_2013_B2_B10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2013 Col=20 Row=D, genomic survey sequence.//5.7e-87:435:97//AQ235864

【0767】

【表468】

F-PLACE1010743//R. norvegicus mRNA for myr5. //1.7e-87:582:85//X77609
 F-PLACE1010761//Homo sapiens chromosome 17, clone hRPK.294_1_22, complete sequence. //4.7e-45:235:99//AC005921
 F-PLACE1010771//M. musculus HCNP mRNA. //1.6e-135:801:88//X68061
 F-PLACE1010785//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-15, complete sequence. //0.35:334:60//AL010221
 F-PLACE1010800//RPC111-79H17.TV RPC111 Homo sapiens genomic clone R-79H17, genomic survey sequence. //5.8e-18:168:82//AQ284252
 F-PLACE1010802//Human Chromosome X clone bWXD531, complete sequence. //1.6e-30:693:63//AC004384
 F-PLACE1010811//RPC111-51NS.TK RPC111 Homo sapiens genomic clone R-51NS, genomic survey sequence. //8.3e-11:142:78//AQ052380
 F-PLACE1010833//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 467K16, WORKING DRAFT SEQUENCE. //7.3e-40:147:88//AL031283
 F-PLACE1010856//M. musculus mRNA for utrophin. //7.3e-17:150:86//Y12229
 F-PLACE1010857//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11. //1.4e-94:422:95//AB020868
 F-PLACE1010870//M. musculus mRNA for ZT3 zinc finger factor. //1.3e-93:530:90//Z67747
 F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds. //1.1e-147:694:98//AB011182
 F-PLACE1010891
 F-PLACE1010896//Mouse BAC mbac20 from 14D1-D2 (T-Cell Receptor Alpha Locus), complete sequence. //3.9e-26:394:68//AC003997
 F-PLACE1010900
 F-PLACE1010916//HS.2242_A1.C04.MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=7 Row=E, genomic survey sequence. //1.0e-78:391:97//AQ146687
 F-PLACE1010917
 F-PLACE1010925//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces. //0.11:629:56//AC004688
 F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds. //9.5e-138:653:98//AB011126
 F-PLACE1010942//Homo sapiens intersectin short form mRNA, complete cds. //5.6e-90:437:98//AF064243
 F-PLACE1010944//Homo sapiens full length insert cDNA clone ZD38E1.2. //1.4e-09:208:68//AF082247
 F-PLACE1010947
 F-PLACE1010954//CIT-HSP-2283D9.TR CIT-HSP Homo sapiens genomic clone 2283D9, genomic survey sequence. //2.1e-29:190:91//B98965
 F-PLACE1010960//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-52, complete sequence. //0.00074:421:60//AL010226
 F-PLACE1010965//CIT-HSP-2386K24.TF.1 CIT-HSP Homo sapiens genomic clone 2386K24, genomic survey sequence. //1.8e-84:412:99//AQ240696
 F-PLACE1011026//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-20, complete sequence. //0.00037:257:64//AL008972
 F-PLACE1011032//Homo sapiens chromosome 5, BAC clone 118L13 (BLN1 H176), complete sequence. //3.8e-06:315:65//AC005348
 F-PLACE1011041//Human Fas-ligand associated factor 3 mRNA, partial cds. //1.5e-56:286:98//U70669
 F-PLACE1011046//Rat phospholipase C-1 mRNA, complete cds. //1.3e-24:278:76//M20636
 F-PLACE1011054//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 981L23, WORKING DRAFT SEQUENCE. //3.8e-27:196:84//AL031685
 F-PLACE1011056//Ovis aries bactinecin 11 (Bac11) gene, exon 4, and complete cds. //5.4e-06:182:67//U77049
 F-PLACE1011057//protein kinase PRK2 [human, D13 B-cell myeloma cell line, mRNA, 3255 nt]. //3.2e-31:169:100//S75548
 F-PLACE1011090//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 998H6, WORKING DRAFT SEQUENCE. //5.1e-80:479:89//AL031687
 F-PLACE1011109//Rattus norvegicus nuclear-encoded mitochondrial elongation factor G mRNA, complete cds. //2.3e-24:192:84//L14684
 F-PLACE1011114//S.cerevisiae chromosome XI reading frame ORF YKR024c. //1.4e-14:346:60//Z28249
 F-PLACE1011133//T7E9-77.1 TAMU Arabidopsis thaliana genomic clone T7E9, genomic survey sequence. //0.010:345:60//B19698
 F-PLACE1011143//CIT-HSP-2375J10.TR CIT-HSP Homo sapiens genomic clone 2375J10, genomic survey sequence. //0.00013:95:76//AQ109305
 F-PLACE1011160//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence. //3.7e-111:692:87//AC004893
 F-PLACE1011165//H. sapiens galactokinase (GK2) mRNA, complete cds. //8.4e-31:194:92//M84443
 F-PLACE1011185//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-24 9810, complete sequence. //3.1e-43:447:72//AC002288
 F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1.4-galactosyltransferase mRNA, complete cds. //3.3e-124:584:99//AF038664
 F-PLACE1011214//HS.2046_A2_B01.MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2046 Col=2 Row=C, genomic survey sequence. //2.0e-39:346:81//AQ305965
 F-PLACE1011219
 F-PLACE1011221//CITBI-E1-2513F18.TR CITBI-E1 Homo sapiens genomic clone 2513F18, genomic survey sequence. //2.4e-20:119:100//AQ279801
 F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cds. //4.4e-146:675:99//AB011101
 F-PLACE1011263//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence. //1.7e-42:212:84//AC005014
 F-PLACE1011273//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y37D8, WORKING DRAFT SEQUENCE. //1.0:214:60//Z92819
 F-PLACE1011291//RPC111-16P9.TP RPC111 Homo sapiens genomic clone RPC111-16P9, genomic survey sequence. //8.0e-08:66:98//B81770
 F-PLACE1011296//Homo sapiens chromosome 16, cosmid clone 443G8 (LA NL), complete sequence. //0.027:135:67//AC004647
 F-PLACE1011310//H. sapiens CpG island DNA genomic MseI fragment, clone 53c10, reverse read cpg53c10.rtlb. //1.4e-05:57:100//Z61496
 F-PLACE1011325//Human immunodeficiency virus type 1 (D9) proviral structural capsid protein (gag) gene, partial cds. //0.077:193:60//L02290
 F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds. //3.1e-150:699:99//AF102265
 F-PLACE1011340//Homo sapiens chromosome 17, clone hRPK.388_F_14, complete sequence. //2.4e-38:186:83//AC005375
 F-PLACE1011371//Mus musculus PK-120 precursor (itih-4) mRNA, complete cds. //6.0e-35:689:63//AF023919
 F-PLACE1011375//Mus musculus Kv3.4 gene, exon 4. //6.0e-88:584:86//AJ010310
 F-PLACE1011399//paramecium species 7, 325 nt dna dimer: replication init. region. //0.00011:255:63//K00919
 F-PLACE1011419//Homo sapiens chromosome 21 PAC LLNLP704G1150Q13. //0.067:337:62//AJ006996
 F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds. //4.6e-157:743:98//AB011102
 F-PLACE1011452//Homo sapiens *** SEQUENCING IN PROGRESS *** WORKING DRAFT SEQUENCE. //1.1e-53:557:73//AJ011929
 F-PLACE1011465//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-24 8FT, complete sequence. //3.5e-71:498:80//AC004605
 F-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds. //4.8e-151:703:99//AB018255
 F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds. //5.2e-145:675:99//AF065482
 F-PLACE1011492//Ray (T. californica) acetylcholine receptor beta-subunit mRNA. //1.0:448:59//J00964
 F-PLACE1011503
 F-PLACE1011520//Homo sapiens clone DJ1119N05, complete sequence. //3.8e-147:692:99//AC004968
 F-PLACE1011563//R. norvegicus mRNA for leucocyte common antigen-related protein (3941 bp). //0.00036:296:61//X83546
 F-PLACE1011567//Homo sapiens PAC clone DJ1164K10 from 7p21-p22, complete sequence. //1.1e-38:315:82//AC004984
 F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds. //1.3e-65:268:86//AF054180
 F-PLACE1011586//Homo sapiens chromosome 17, clone HRPC890E16, complete sequence. //2.0e-82:188:96//AC004477
 F-PLACE1011635//Homo sapiens chromosome 17, clone hRPK.214_0_1, complete sequence. //1.8e-153:752:97//AC005224
 F-PLACE1011641//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence. //4.8e-05:190:67//AE000560
 F-PLACE1011643//Alcaligenes eutrophus phaP gene. //0.16:466:59//X85729
 F-PLACE1011646//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1013A10, WORKING DRAFT SEQUENCE. //9.1e-19:156:76//AL033383
 F-PLACE1011649
 F-PLACE1011650//Homo sapiens retinol dehydrogenase gene, complete cds. //6.4e-09:172:74//AF037062
 F-PLACE1011664//D. melanogaster crn mRNA. //1.1e-52:650:68//X58374
 F-PLACE1011675//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-62 8 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces. //0.11:443:58//AC005507
 F-PLACE1011682//Human DNA sequence from clone 342B11 on chromosome

【0768】

【表469】

22q12.1-12.3. Contains ESTs and a GSS. complete sequence.//0.31:1
27:71//AL008719
F-PLACE1011719//Human BAC clone RG36K23 from 7q31. complete sequence.//4.6e-52:461:77//AC002487
F-PLACE1011725
F-PLACE1011729//Human Chromosome 15q11-q13 clone pDJ276c12 from the Prader-Willi/Angelman syndrome region. WORKING DRAFT SEQUENCE. 3 unordered pieces.//0.011:320:62//AC004737
F-PLACE1011749//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence. WORKING DRAFT SEQUENCE. 9 unordered pieces.//0.0031:544:59//AC004157
F-PLACE1011762//Homo sapiens BAC clone RG437L15 from 8q21. complete sequence.//2.4e-115:682:90//AC004003
F-PLACE1011778//RPC111-22D17.TVB RPC1-11 Homo sapiens genomic clone RPC1-11-22D17. genomic survey sequence.//2.7e-114:611:93//AQ008944
F-PLACE1011783//CIT-HSP-2317N1.TF CIT-HSP Homo sapiens genomic clone 2317N1. genomic survey sequence.//2.3e-17:120:94//AQ042330
F-PLACE1011858//Gallus domesticus filamin mRNA. complete cds.//4.1e-24:565:64//U000147
F-PLACE1011874//Homo Sapiens Chromosome X clone bWXD312. complete sequence.//2.5e-141:678:98//AC004478
F-PLACE1011875//Homo sapiens mRNA for KIA0580 protein. partial cds.//1.6e-108:526:98//AB011152
F-PLACE1011891//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 439F8. WORKING DRAFT SEQUENCE.//0.0014:330:62//AL021392
F-PLACE1011896//Mus musculus Wnt10a mRNA. complete cds.//1.4e-89:678:82//U61969
F-PLACE1011922//Caprine arthritis-encephalitis virus envelope glycoprotein (env) gene. partial cds.//0.069:245:61//U01400
F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA. complete cds.//1.2e-138:664:98//AF059617
F-PLACE1011962//HS_3212_B2_G12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3212 Col=24 Row=N. genomic survey sequence.//2.4e-07:154:74//AQ175369
F-PLACE1011964//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 322P7. WORKING DRAFT SEQUENCE.//3.7e-22:369:69//AL023799
F-PLACE1011982//HS-1041-A1-801-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 823 Col=1 Row=C. genomic survey sequence.//0.44:309:58//B36529
F-PLACE1011995//Homo sapiens Xq28 BAC RPC111-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//8.8e-53:687:71//AC006054
F-PLACE1012031//Homo sapiens mRNA for KIA0713 protein. partial cds.//1.2e-145:690:98//AB018256
F-PLACE2000003//Homo sapiens chromosome 17. clone hRPK.318_A_15. complete sequence.//1.7e-62:293:88//AC005837
F-PLACE2000006//Homo sapiens chromosome 12p13.3 clone RPC11-96H9. WORKING DRAFT SEQUENCE. 66 unordered pieces.//1.4e-116:261:91//AC006057
F-PLACE2000007
F-PLACE2000011//Homo sapiens chromosome 19. cosmid F20887. complete sequence.//5.2e-102:489:99//AC005578
F-PLACE2000014//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1111N9. WORKING DRAFT SEQUENCE.//0.0095:307:62//AL022574
F-PLACE2000015//Homo sapiens clone RG140B11. WORKING DRAFT SEQUENCE. 1 unordered pieces.//2.0e-36:316:81//AC005069
F-PLACE2000017//HS_3042_A1_F08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3042 Col=15 Row=K. genomic survey sequence.//1.0:184:61//AQ098074
F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP-ribose polymerase mRNA. complete cds.//4.6e-84:844:72//AF082556
F-PLACE2000030//Human Chromosome 11 Cosmid cSLR16b6. complete sequence.//2.3e-22:233:77//U73638
F-PLACE2000033//C. capitata mRNA for chorion protein s18.//0.0019:342:62//Y08913
F-PLACE2000034//Rattus norvegicus transmembrane receptor Robo1 mRNA. complete cds.//2.8e-13:335:63//AF041082
F-PLACE2000039//Rattus norvegicus cytoplasmic dynein heavy chain (MAP 1C). mRNA. complete cds.//7.7e-84:489:90//U08505
F-PLACE2000047//Homo sapiens ccr2b (ccr2). ccr2a (ccr2). ccr5 (ccr5) and ccr6 (ccr6) genes. complete cds. and lactoferrin (lactoferrin) gene. partial cds. complete sequence.//5.0e-28:327:76//U95626
F-PLACE2000050//Homo sapiens chromosome 17. clone HRPAC41C23. complete sequence.//1.1e-32:527:68//AC003101
F-PLACE2000061//CIT-HSP-2346L20.TF CIT-HSP Homo sapiens genomic clone 2346L20. genomic survey sequence.//1.1e-05:89:83//AQ059010
F-PLACE2000062//Human membrane-associated lectin type-C mRNA.//9.0

e-113:662:86//W98457
F-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA. complete cds.//2.2e-133:631:98//AF027219
F-PLACE2000097//Homo sapiens chromosome 12p13.3 clone RPC111-189M2 O. WORKING DRAFT SEQUENCE. 39 unordered pieces.//1.6e-16:119:93//AC005910
F-PLACE2000100//HS_3184_A1_D06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=11 Row=G. genomic survey sequence.//1.5e-80:409:97//AQ150004
F-PLACE2000103//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20208. WORKING DRAFT SEQUENCE.//1.0e-172:830:98//AL031848
F-PLACE2000111//Homo sapiens DNA. trinucleotide repeats region.//1.0:200:64//AB018491
F-PLACE2000115
F-PLACE2000124//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67 A1. complete sequence.//6.2e-43:362:80//AC004531
F-PLACE2000132//RPC111-79F15.TV RPC111 Homo sapiens genomic clone R-79F15. genomic survey sequence.//5.4e-35:206:94//AQ284166
F-PLACE2000136//Human BAC clone 7E17 from 12q. complete sequence.//2.7e-12:814:59//AC002070
F-PLACE2000140//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 11703. WORKING DRAFT SEQUENCE.//3.6e-165:799:97//AL020995
F-PLACE2000164//Canine histamine H2 receptor gene. complete cds.//0.10:392:56//M32701
F-PLACE2000170
F-PLACE2000172//Homo sapiens PAC clone DJ0811017 from 7q21-22. complete sequence.//3.9e-91:552:88//AC006005
F-PLACE2000176//Homo sapiens Chromosome 22q11.2 BAC Clone b437g10 In BCRL2-CGT Region. complete sequence.//0.98:201:64//AC004032
F-PLACE2000187
F-PLACE2000216
F-PLACE2000223//RPC111-12L17.TP RPC1-11 Homo sapiens genomic clone RPC1-11-12L17. genomic survey sequence.//0.00039:325:58//B75888
F-PLACE2000235//Human Chromosome 16 BAC clone CIT987SK-254P9. complete sequence.//7.5e-55:237:78//AC003003
F-PLACE2000246//Homo sapiens chromosome 3p clone RPC14-544D10. WORKING DRAFT SEQUENCE. 58 unordered pieces.//2.4e-92:236:94//AC005902
F-PLACE2000264//Human DNA sequence from clone 391022 on chromosome 6p21.2-21.31 Contains pseudogenes similar to ribosomal protein. ESTs. GSSs. complete sequence.//1.4e-32:331:78//AL031577
F-PLACE2000274//Anthracidaris crassispina mRNA for B2HC. partial cds.//8.5e-48:765:66//AB012308
F-PLACE2000302//Kaposi's sarcoma-associated herpes-like virus ORF7 3 homolog gene. complete cds.//8.3e-08:662:58//U52064
F-PLACE2000305//Homo sapiens clone DJ1129L24. WORKING DRAFT SEQUENCE. 5 unordered pieces.//2.4e-08:95:81//AC006021
F-PLACE2000317//HS_3183_B2_F05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3183 Col=10 Row=L. genomic survey sequence.//2.5e-71:346:99//AQ172747
F-PLACE2000335//Homo sapiens clone DJ1032007. WORKING DRAFT SEQUENCE. 3 unordered pieces.//3.7e-14:402:65//AC004952
F-PLACE2000341//Rattus norvegicus sodium-dependent multi-vitamin transporter (SMVT) mRNA. complete cds.//4.5e-77:555:82//AF026554
F-PLACE2000342//Suid herpesvirus 1 UL5 gene. partial cds. UL6 and UL7 genes. complete cds. UL8 gene. partial cds.//1.8e-14:259:71//U66829
F-PLACE2000347//Human DNA from overlapping chromosome 19-specific cosmid R32543. and F15613 containing ZNF gene family member. genomic sequence. complete sequence.//6.0e-34:376:74//AC003006
F-PLACE2000359//RPC111-23J20.TXBR RPC1-11 Homo sapiens genomic clone RPC1-11-23J20. genomic survey sequence.//8.4e-21:288:69//AQ013849
F-PLACE2000366//Human Tigger1 transposable element. complete consensus sequence.//5.0e-114:692:80//U49973
F-PLACE2000371//Homo sapiens 12p13.3 PAC RPC111-29K11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.38:356:58//AC005182
F-PLACE2000373//RPC111-49C18.TJ RPC111.Homo sapiens genomic clone R-49C18. genomic survey sequence.//0.064:132:68//AQ051776
F-PLACE2000379//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Human BAC Library) complete sequence.//1.6e-130:776:88//AC003658
F-PLACE2000394//Homo sapiens chromosome 18 BAC RPC111-128D14 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//5.4e-113:808:83//AC005909
F-PLACE2000398//Mouse hexamer repeat sequence (117) homologous to Drosophila 'period' gene.//0.87:285:63//X06967
F-PLACE2000399

【0769】

【表470】

F-PLACE2000404//Caenorhabditis elegans cosmid R74, complete sequence.//2.9e-59:532:68//Z36238
 F-PLACE2000411//Acanthamoeba castellanii transformation-sensitive protein homolog mRNA, complete cds.//0.44:553:56//U89984
 F-PLACE2000419//Human adenosine deaminase (ADA) gene, complete cds.//1.4e-56:303:86//M13792
 F-PLACE2000425//HS_3047_A1_H05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=9 Row=0, genomic survey sequence.//2.8e-42:224:97//AQ126949
 F-PLACE2000427
 F-PLACE2000433//Homo sapiens chromosome 17, clone hRPK.156_L_14, complete sequence.//1.1e-19:363:67//AC005821
 F-PLACE2000435//HS_3036_B1_F11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=21 Row=L, genomic survey sequence.//3.1e-06:184:66//AQ096999
 F-PLACE2000438//Caenorhabditis elegans cosmid Y45F10D, complete sequence.//4.6e-23:550:62//AL021492
 F-PLACE2000450//Homo sapiens PAC clone DJ1188N21 from 7q11.23-q21.1, complete sequence.//1.0e-78:604:80//AC006025
 F-PLACE2000455//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//8.2e-05:330:63//AC002300
 F-PLACE2000458//Homo sapiens chromosome Sp, BAC clone 50g21 (LBML H154), complete sequence.//5.7e-168:816:97//AC005740
 F-PLACE2000465//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence.//4.3e-33:296:79//AC002037
 F-PLACE2000477//Homo sapiens clone RG052H06, WORKING DRAFT SEQUENCE. 11 unordered pieces.//3.4e-59:598:74//AC005057
 F-PLACE2000004//Human EYA3 homolog (EYA3) mRNA, complete cds.//7.6e-49:361:84//U81602
 F-PLACE2000009//Human placenta (Diff48) mRNA, complete cds.//3.0e-58:713:69//U49187
 F-PLACE2000020//R. norvegicus type III adenylyl cyclase mRNA, complete cds.//6.1e-103:600:89//M55075
 F-PLACE2000029
 F-PLACE2000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//4.4e-115:718:86//Y17267
 F-PLACE2000070//Homo sapiens chromosome 5, BAC clone 194j18 (LBML H158), complete sequence.//1.8e-17:250:74//AC005368
 F-PLACE2000103//Caenorhabditis elegans cosmid C13F10.//4.6e-07:408:61//U97006
 F-PLACE2000119//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0190L06: HTGS phase 1, WORKING DRAFT SEQUENCE, 21 unordered pieces.//1.5e-58:291:86//AC004670
 F-PLACE2000121//Rattus norvegicus rsec15 mRNA, complete cds.//8.1e-81:837:71//AF032668
 F-PLACE2000124//Homo sapiens chromosome 17, clone hRPK.85_B_7, complete sequence.//1.8e-48:330:79//AC005695
 F-PLACE2000136
 F-PLACE2000142//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 349A12, WORKING DRAFT SEQUENCE.//0.011:294:62//AL033520
 F-PLACE2000145//Gallus gallus tensin mRNA, 3' end.//6.9e-52:659:68//L06662
 F-PLACE2000147//Human DNA sequence from clone 267M20 on chromosome Xq22.2-22.3. Contains part of the DIAPH2 gene and a pseudogene, ESTs, STSs and GSSs, complete sequence.//5.1e-37:305:81//AL031053
 F-PLACE2000148//Homo sapiens chromosome Y, clone 47511, complete sequence.//4.7e-32:766:63//AC004474
 F-PLACE2000155//Homo sapiens chromosome 17, clone hRPK.597_M_12, complete sequence.//7.4e-173:822:98//AC005277
 F-PLACE2000156//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//2.2e-81:783:74//AC003682
 F-PLACE2000157
 F-PLACE2000158//, complete sequence.//1.0e-180:845:97//AC005500
 F-PLACE2000160//C1978SK-152K7.TV CIT978SK Homo sapiens genomic clone 152K7, genomic survey sequence.//0.080:259:59//B50878
 F-PLACE2000169//Homo sapiens chromosome 19, BAC CIT-8-191n6, complete sequence.//9.8e-158:749:98//AC006130
 F-PLACE2000194
 F-PLACE2000197//F.rubripes GSS sequence, clone 075W04B87, genomic survey sequence.//1.4e-08:164:68//AL003352
 F-PLACE2000199//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//0.0019:277:58//Z82207
 F-PLACE2000207//Homo sapiens BAC clone GS165L15 from 7p15, complete sequence.//6.6e-21:312:67//AC005013
 F-PLACE2000208//Homo sapiens (clones: CW52-2, CW27-6, CW15-2, CW26-5, 11-67) collagen type VII intergenic region and (COL7A1) gene, complete cds.//1.0:279:61//L23982
 F-PLACE2000218//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//9.3e-43:383:79//AC004086
 F-PLACE3000220//RPC111-54B4.TV RPC111 Homo sapiens genomic clone R-54B4, genomic survey sequence.//2.4e-36:381:76//AQ082056
 F-PLACE3000221//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.2e-135:721:91//AC005231
 F-PLACE3000226
 F-PLACE3000230//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//3.3e-80:498:78//U95626
 F-PLACE3000242//Human DNA sequence from clone 1409 on chromosome X p11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence.//2.6e-54:254:92//Z98046
 F-PLACE3000244//M.musculus mRNA for 200 kD protein.//1.4e-139:850:86//X80169
 F-PLACE3000254//Ateline herpesvirus 3 complete genome.//1.3e-10:399:61//AF083424
 F-PLACE3000271//Human Chromosome 16 BAC clone CIT987SK-A-B15A9, complete sequence.//1.8e-21:350:68//AF001548
 F-PLACE3000276//HS_2026_B1_H11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2026 Col=21 Row=P, genomic survey sequence.//5.7e-45:376:81//AQ231147
 F-PLACE3000304//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//1.6e-138:650:99//AC005328
 F-PLACE3000310
 F-PLACE3000320//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//1.9e-41:379:77//AL034379
 F-PLACE3000322//Homo sapiens chromosome 17, clone hRPK.209_J_20, complete sequence.//3.3e-35:419:68//AC005822
 F-PLACE3000331//CIT-HSP-2347D24, TR CIT-HSP Homo sapiens genomic clone 2347D24, genomic survey sequence.//2.7e-20:119:99//AQ061543
 F-PLACE3000339//Rhodobacter sphaeroides magnesium chelatase subunits Bchl (bchl) and BchD (bchD) genes, complete cds; and BchO (bchO) gene, partial cds.//0.99:310:58//AF017642
 F-PLACE3000341//Homo sapiens 3p22 Contig 7 PAC RP14-672N11 (Roswe 11 Park Cancer Institute Human PAC Library) complete sequence.//7.5e-159:752:98//AC006055
 F-PLACE3000350//Rattus norvegicus serine/threonine protein kinase TA01 mRNA, complete cds.//2.3e-107:592:92//AF084205
 F-PLACE3000352//Human DNA sequence from PAC 293L6 on chromosome 2, complete sequence.//2.1e-37:480:70//Z83732
 F-PLACE3000353
 F-PLACE3000362//Homo sapiens chromosome 17, clone hRPK.215_P_18, complete sequence.//0.00011:373:60//AC005969
 F-PLACE3000363
 F-PLACE3000365//Human DNA sequence from PAC 227P17, between marker s DXS6791 and DXS8038 on chromosome X contains CpG island, EST.//0.074:279:61//Z81007
 F-PLACE3000373//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//2.8e-118:653:92//Z92545
 F-PLACE3000388//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//2.2e-25:288:71//AC005154
 F-PLACE3000399//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 466M1, WORKING DRAFT SEQUENCE.//2.3e-69:303:86//Z97630
 F-PLACE3000400//Caenorhabditis elegans cosmid H03A11, complete sequence.//0.0063:435:58//Z93239
 F-PLACE3000401//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//5.8e-25:292:73//AC006023
 F-PLACE3000402//RPC111-2006.TVB RPC111 Homo sapiens genomic clone RPC111-2006, genomic survey sequence.//1.1e-10:154:74//AQ008761
 F-PLACE3000405//Homo sapiens chromosome 17, clone hRPK.628_E_12, complete sequence.//2.9e-41:515:72//AC005701
 F-PLACE3000406//cSRL-179E11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-179E11, genomic survey sequence.//2.8e-91:540:89//B03443
 F-PLACE3000413
 F-PLACE3000416//F19L8-Sp6 ICF Arabidopsis thaliana genomic clone F19L8, genomic survey sequence.//0.0018:664:55//B11305
 F-PLACE3000425//Human DNA sequence from clone 231L4 on chromosome Xq27.1-27.3 Contains GSS, STS, complete sequence.//1.1e-16:284:70//AL022719
 F-PLACE3000455//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 469D22, WORKING DRAFT SEQUENCE.//3.6e-146:732:96//AL031284
 F-PLACE3000475//HS_2164_A2_H10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2164 Col=20 Row=0, gen

【0770】

【表471】

omic survey sequence.//1.5e-07:159:71//AQ132983
 F-PLACE4000477//Human DNA sequence from PAC 368A4 on chromosome X. Contains ESTs, CELLULAR NUCLEIC ACID BINDING PROTEIN (CNBP) like gene and STSs.//2.9e-11:213:70//Z83843
 F-PLACE4000009//Sequence 93 from patent US 5616500.//9.9e-08:692:60//139845
 F-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds.//1.1e-116:331:100//AB018352
 F-PLACE4000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69 G12, complete sequence.//5.0e-05:244:63//AC004131
 F-PLACE4000049//Homo sapiens Xp22-171-173 BAC GSHB-31214 (Genome Systems Human BAC Library) complete sequence.//1.2e-37:385:74//AC005926
 F-PLACE4000052//M.musculus abcl mRNA.//1.5e-110:671:88//X75926
 F-PLACE4000063
 F-PLACE4000089//M.musculus BOX DNA for regulatory element and promoter region related to EC cell differentiation.//3.7e-12:114:85//X74311
 F-PLACE4000093//CIT-HSP-2380K5.TF CIT-HSP Homo sapiens genomic clone 2380K5, genomic survey sequence.//0.11:245:60//AQ108342
 F-PLACE4000100//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20208, WORKING DRAFT SEQUENCE.//2.9e-19:384:65//AL031848
 F-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cds.//1.2e-145:684:99//AB007931
 F-PLACE4000128//Mus musculus putative transcription factor mRNA, complete cds.//3.7e-62:541:78//AF091234
 F-PLACE4000129
 F-PLACE4000131//HS_3139_B2_F12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3139 Col=24 Row=L, genomic survey sequence.//2.3e-14:221:70//AQ183207
 F-PLACE4000147//Human DNA sequence from clone 740A11 on chromosome Xq22.2-23. Contains part of the COL4A5 gene for Collagen Alpha 5 (IV) Chain Precursor. Contains GSSs, complete sequence.//0.28:412:58//AL031622
 F-PLACE4000156//Human zinc finger protein ZNF136.//7.2e-88:764:76//U09367
 F-PLACE4000192
 F-PLACE4000211
 F-PLACE4000222//344J1.TVB CIT978SKA1 Homo sapiens genomic clone A-344J01, genomic survey sequence.//1.2e-14:177:76//B17158
 F-PLACE4000230//Mus musculus semaphorin VIa mRNA, complete cds.//9.8e-116:662:89//AF030430
 F-PLACE4000233//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//5.2e-54:363:70//AC003973
 F-PLACE4000247
 F-PLACE4000250//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//0.0053:229:65//AC004673
 F-PLACE4000252
 F-PLACE4000259//H.sapiens gene for US snRNP-specific 200kD protein.//2.0e-25:191:87//Z70200
 F-PLACE4000261//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//2.6e-23:314:71//AF084259
 F-PLACE4000269//Rattus norvegicus rexo70 mRNA, complete cds.//5.5e-122:734:88//AF032667
 F-PLACE4000270
 F-PLACE4000300
 F-PLACE4000320//Human FKBP-rapamycin associated protein (FRAP) mRNA, complete cds.//1.4e-21:135:96//L34075
 F-PLACE4000323//HS_2165_B1_B02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2165 Col=3 Row=D, genomic survey sequence.//4.3e-08:170:71//AQ125036
 F-PLACE4000326//Mouse DNA with homology to EBV IR3 repeat, segment 1, clone Mu2.//2.8e-06:311:63//M10296
 F-PLACE4000344//Plasmodium falciparum chromosome 2, section 38 of 73 of the complete sequence.//0.014:252:60//AE001401
 F-PLACE4000367
 F-PLACE4000369
 F-PLACE4000379//CIT-HSP-2350B9.TF CIT-HSP Homo sapiens genomic clone 2350B9, genomic survey sequence.//9.2e-46:282:86//AQ062661
 F-PLACE4000387//CIT-HSP-2382F11.TR CIT-HSP Homo sapiens genomic clone 2382F11, genomic survey sequence.//0.96:102:70//AQ080649
 F-PLACE4000392//Rattus norvegicus polymorphic marker O20U1A1 sequence.//1.2e-05:222:68//AF054088
 F-PLACE4000401//Homo sapiens mRNA for KIAA0540 protein, partial cds.//9.6e-46:605:71//AB014540
 F-PLACE4000411//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 173D1, WORKING DRAFT SEQUENCE.//3.2e-29:179:79//AL031984
 F-PLACE4000431//H.sapiens gene for US snRNP-specific 200kD protein.//4.0e-44:263:92//Z70200
 F-PLACE4000445//HS-1053-B1-002-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 775 Col=3 Row=H, genomic survey sequence.//0.070:47:100//B41346
 F-PLACE4000450
 F-PLACE4000465//Homo sapiens BAC clone RG114B19 from Tq31.1, complete sequence.//2.3e-07:273:65//AC005065
 F-PLACE4000487//Homo sapiens chromosome 17, clone hRPK.156_L14, complete sequence.//4.1e-34:351:70//AC005821
 F-PLACE4000489//HS_3012_B1_G05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3012 Col=9 Row=N, genomic survey sequence.//2.0e-36:220:92//AQ095537
 F-PLACE4000494//Homo sapiens 12p13.3 PAC RPC15-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.3e-57:395:79//AC005865
 F-PLACE4000521//Homo sapiens *** SEQUENCING IN PROGRESS ***, WORKING DRAFT SEQUENCE.//1.6e-163:770:98//AJ011929
 F-PLACE4000522//Feline leukemia virus Notch2 gene, clone FeLV/Notch h2-C, partial cds.//4.0e-124:685:90//U47645
 F-PLACE4000548
 F-PLACE4000558//Bothrops atrox batroxobin gene (EC 3.4.21.29).//0.049:435:59//X12747
 F-PLACE4000581
 F-PLACE4000590//Homo sapiens chromosome Y, clone 47511, complete sequence.//3.6e-20:747:59//AC004474
 F-PLACE4000593//Caenorhabditis elegans cosmid F2507, complete sequence.//5.6e-16:326:65//Z78418
 F-PLACE4000612//Homo sapiens PAC clone DJ0722F20 from Tq31.1-q31.3, complete sequence.//1.7e-163:785:97//AC005281
 F-PLACE4000638//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.7e-74:707:74//AC006039
 F-PLACE4000650
 F-PLACE4000654//Mus musculus mRNA for ubiquitin conjugating enzyme.//1.1e-145:840:89//Y17267
 F-PLACE4000670//Sequence 13 from patent US 5712381.//1.0:311:59//I82816
 F-SKNC1000011//Gallus gallus bone sialoprotein II mRNA, complete cds.//0.014:92:73//U10577
 F-SKNC1000013//Orang-utan involucrin gene, complete cds.//0.021:417:59//M25312
 F-SKNC1000046//Homo sapiens mRNA for KIAA0554 protein, partial cds.//7.6e-147:706:98//AB014554
 F-SKNC1000050//Sequence 5 from patent US 5789181.//1.6e-52:330:90//AR020616
 F-SKNC1000091//Human NK homeobox protein (Nkx6.1) gene, exon 1.//0.0018:375:60//U66797
 F-THYR1000017//Rattus norvegicus pyridoxine 5'-phosphate oxidase mRNA, complete cds.//6.6e-97:542:84//U91561
 F-THYR1000026//Human DNA sequence from clone 83387 on chromosome 22q12.3-13.2 Contains genes for NCF4 (P40PHOX) protein, cytokine receptor common beta chain precursor CSF2RB (partial), ESTs, CA repeat, STS, GSS, complete sequence.//3.5e-46:353:82//AL008637
 F-THYR1000034//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 90L6, WORKING DRAFT SEQUENCE.//0.83:227:61//Z97353
 F-THYR1000035//Human Chromosome X clone hWXD187, complete sequence.//1.2e-39:303:83//AC004383
 F-THYR1000040
 F-THYR1000070//Homo sapiens chromosome 10 clone CIT987SK-1144C6 map 10q25.1, complete sequence.//1.3e-05:613:58//AC005383
 F-THYR1000072//Homo sapiens mRNA for KIAA0657 protein, partial cds.//2.7e-84:722:77//AB014557
 F-THYR1000085
 F-THYR1000092//CIT-HSP-2013L16.TFB CIT-HSP Homo sapiens genomic clone 2013L16, genomic survey sequence.//0.31:186:61//B60606
 F-THYR1000107
 F-THYR1000111//Human genomic DNA sequence from clone 30801 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//6.4e-110:690:87//Z93403
 F-THYR1000121//Rattus norvegicus CTD-binding SR-like protein rAB mRNA, complete cds.//1.4e-127:816:85//U49055
 F-THYR1000124//H.sapiens CpG island DNA genomic MseI fragment, clone 72a7, forward read cpq72a7.tla.//9.5e-26:169:94//Z62724
 F-THYR1000129//Homo sapiens TED protein (TED) mRNA, complete cds.//8.5e-154:732:98//AF087142
 F-THYR1000132//Homo sapiens chromosome 9q34, clone 63G10, complete sequence.//3.7e-39:315:82//AC002096
 F-THYR1000156//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//1.2e-21:335:71//AL023574

【0771】

【表472】

F-THYR01000163//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-A-218C7, complete sequence.//8.4e-52:301:88//AC002331
 F-THYR01000173//Mouse clathrin-associated protein (AP47) mRNA, complete cds.//4.0e-89:821:74//M62419
 F-THYR01000186//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//7.2e-39:293:85//Z82207
 F-THYR01000187//Clostridium tetani gene for tetanus toxin.//0.041:473:57//X06214
 F-THYR01000190//Homo sapiens chromosome 17, clone hRPK.332_H.18, complete sequence.//0.38:184:64//AC005746
 F-THYR01000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//7.5e-174:805:99//AJ005698
 F-THYR01000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//1.2e-86:616:84//AB014552
 F-THYR01000206//HS_3047_A1_A05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=9 Row=A, genomic survey sequence.//0.51:331:63//AQ099134
 F-THYR01000221//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.092:738:56//AC004157
 F-THYR01000241//Callus gallus genome fragment with pentamer tandem repeats.//0.43:191:62//X00186
 F-THYR01000242//Human zinc finger gene HZF7.//2.8e-43:534:64//X60156
 F-THYR01000253//Homo sapiens 3p22 Contig 7 PAC RPC14-672N11 (Rosweil Park Cancer Institute Human PAC Library) complete sequence.//0.95:139:68//AC005055
 F-THYR01000270
 F-THYR01000279//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 531H16, WORKING DRAFT SEQUENCE.//1.4e-174:826:98//AL031664
 F-THYR01000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//3.9e-179:848:98//AB016068
 F-THYR01000320//Mus musculus sphingosine-1-phosphate lyase mRNA, complete cds.//1.0e-44:331:83//AF036894
 F-THYR01000327//Homo sapiens autocrine motility factor receptor (AMFR) mRNA, complete cds.//5.7e-112:641:91//L35233
 F-THYR01000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//2.2e-162:763:98//AB018333
 F-THYR01000358//Human selenium-binding protein (hSBP) mRNA, complete cds.//2.2e-32:177:84//U29091
 F-THYR01000368//Caenorhabditis elegans cosmid W09G3, complete sequence.//0.97:206:60//Z82080
 F-THYR01000381//Arthrobacter sp. gicl gene for beta-1,3-glucanase, complete cds.//0.27:427:62//D23668
 F-THYR01000387//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//9.7e-147:698:98//AC006019
 F-THYR01000394//HS_2061_A2_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2061 Col=8 Row=E, genomic survey sequence.//1.6e-29:202:91//AQ247672
 F-THYR01000395//Drosophila melanogaster ring canal protein and ORF 2 mRNA, complete cds.//4.3e-15:512:59//L08483
 F-THYR01000401
 F-THYR01000408//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//6.3e-130:327:97//AC005740
 F-THYR01000501//H. sapiens Staf50 mRNA.//9.8e-74:615:77//X82200
 F-THYR01000502//Human DNA sequence from PAC 436M11 on chromosome Xp22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RSI gene for retinosis (X-linked, juvenile) 1 (XLRIS1). Contains ESTs, an STS and GSSs, complete sequence.//0.076:380:59//Z94056
 F-THYR01000505
 F-THYR01000558//Human PAC clone 127H14 from 12q, complete sequence.//2.4e-27:412:69//AC002563
 F-THYR01000569//HS_2178_B2_E03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2178 Col=6 Row=J, genomic survey sequence.//1.9e-27:326:74//AQ307499
 F-THYR01000570
 F-THYR01000585//Homo sapiens protein associated with Myc mRNA, complete cds.//7.4e-167:808:97//AF075587
 F-THYR01000596//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence.//0.99:280:61//U91323
 F-THYR01000602//HS_3037_B2_E04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=8 Row=J, genomic survey sequence.//1.2e-05:109:75//AQ097057
 F-THYR01000605//Homo sapiens map 2p11.2: 83cM from CATAS06 repeat region, complete sequence.//1.0:84:70//AF067777
 F-THYR01000625//Homo sapiens chromosome 19, cosmid R29425, complete sequence.//3.4e-174:820:98//AC005546
 F-THYR01000637//Human DNA sequence from clone 91J24 on chromosome 6q24 Contains part of utrophin Gene, part of cytochrome C oxidase gene, EST, CpG island, complete sequence.//3.6e-38:289:84//AL024474
 F-THYR01000641//Plasmodium falciparum MAL3P7, complete sequence.//6.8e-07:540:56//AL034559
 F-THYR01000658//Homo sapiens chromosome 17, clone hRPK.74_E.22, complete sequence.//1.1e-68:468:84//AC005696
 F-THYR01000662//Arabidopsis thaliana genomic DNA, chromosome 5, TA C clone: K23L20, complete sequence.//0.0072:141:70//AB016874
 F-THYR01000666//Mus musculus mRNA for motor domain of KIF9, partial cds.//4.7e-58:367:87//AB001437
 F-THYR01000676//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//1.2e-36:396:71//AC005778
 F-THYR01000684//Fugu rubripes cosmid 165K09 DNA for GRM7, TRIP, Sand, PRGFR3 genes.//5.6e-13:236:69//AJ010317
 F-THYR01000699//RPC111-50D4.TK RPC111 Homo sapiens genomic clone R-50D4, genomic survey sequence.//2.7e-09:135:78//AQ052641
 F-THYR01000712//Homo sapiens BAC clone RG041D11 from Tq21, complete sequence.//5.2e-17:290:67//AC005053
 F-THYR01000715//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds.//8.6e-08:517:60//L14320
 F-THYR01000734//HS_3233_B1_B04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3233 Col=7 Row=D, genomic survey sequence.//6.0e-72:463:89//AQ182143
 F-THYR01000748//Homo sapiens KIAA0411 mRNA, complete cds.//9.7e-34:339:74//AB007871
 F-THYR01000756//M. musculus mRNA for Gal beta1, 3GalNAc alpha2, 3-sialyltransferase.//0.00034:349:60//X73523
 F-THYR01000777//S. griseus strO gene and sts gene cluster.//8.2e-05:625:59//Y08763
 F-THYR01000783//Xenopus laevis tail-specific thyroid hormone up-regulated (gene 5) mRNA, complete cds.//4.0e-70:860:69//U37373
 F-THYR01000787//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 366D1, WORKING DRAFT SEQUENCE.//5.3e-09:221:66//Z97986
 F-THYR01000793
 F-THYR01000796//Cristatella mucedo clone 5.9 microsatellite sequence.//0.34:173:63//AF085422
 F-THYR01000805//Homo sapiens Xp21 PAC RPC11-37A12 containing exons 10 to 16 of the Duchenne Muscular Dystrophy gene, complete sequence.//7.8e-43:677:66//AC004468
 F-THYR01000815//Homo sapiens chromosome 5, BAC clone 189 (LBNL H135), complete sequence.//5.5e-43:405:77//AC005914
 F-THYR01000829//CIT-HSP-2387C10.TF.1 CIT-HSP Homo sapiens genomic clone 2387C10, genomic survey sequence.//2.0e-20:159:88//AQ240053
 F-THYR01000843
 F-THYR01000852//Homo sapiens chromosome 19, cosmid R31855, complete sequence.//1.8e-33:445:72//AC005782
 F-THYR01000855//Mus musculus potassium channel alpha subunit (Kv9.1) mRNA, complete cds.//0.038:208:64//AF008573
 F-THYR01000865//Homo sapiens PAC clone DJ0283M22 from 14, complete sequence.//1.9e-30:286:74//AC005477
 F-THYR01000895//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 385E7, WORKING DRAFT SEQUENCE.//2.8e-18:186:80//AL031720
 F-THYR01000916//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.6e-78:432:93//AC006015
 F-THYR01000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//9.2e-178:839:98//AF079529
 F-THYR01000934//Human pyrroline 5-carboxylate reductase mRNA, complete cds.//3.5e-32:759:63//M77836
 F-THYR01000951//Homo sapiens Chromosome 11q12 pac pJ57114, WORKING DRAFT SEQUENCE, 29 unordered pieces.//4.9e-76:224:93//AC004229
 F-THYR01000952
 F-THYR01000974//HS_3238_B2_F01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=2 Row=L, genomic survey sequence.//2.4e-26:154:96//AQ219846
 F-THYR01000975//Plasmodium falciparum TopoII gene.//0.32:491:58//X79345
 F-THYR01000983//Mwrf9A3 exon amplification products from BACs in M

【0772】

【表473】

vrf region *Mus musculus* genomic, genomic survey sequence.//7.0e-16:112:94//AQ010457
 F-THYR01000984//CIT-HSP-2167017.TR CIT-HSP Homo sapiens genomic clone 2167017, genomic survey sequence.//0.00015:186:66//B91313
 F-THYR01000988//Human Chromosome 11q12.2 PAC clone pD1756b9 containing human ferritin heavy chain mRNA (FTH), WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.024:267:63//AC004588
 F-THYR01001003
 F-THYR01001031//Homo sapiens chromosome 17, clone hRPC.859_0_20, complete sequence.//1.1e-55:543:72//AC003695
 F-THYR01001033//Methanobacterium thermoautotrophicum from bases 48264 to 58328 (section 5 of 148) of the complete genome.//0.94:445:58//AE000799
 F-THYR01001062//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 199H16, WORKING DRAFT SEQUENCE.//4.4e-45:441:75//AL022320
 F-THYR01001093//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence.//4.9e-34:353:76//AC006241
 F-THYR01001100//Human DNA-binding protein mRNA, 3' end.//1.1e-72:742:74//L14787
 F-THYR01001120//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//1.2e-76:521:86//AC005522
 F-THYR01001121//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 671014, WORKING DRAFT SEQUENCE.//0.00078:594:58//AL031595
 F-THYR01001133//Homo sapiens PAC clone DJ1200123 from 7p15, complete sequence.//4.0e-35:349:75//AC004996
 F-THYR01001134//Homo sapiens clone DJ1070G24, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.0:154:66//AC005486
 F-THYR01001142//Human DNA sequence from clone B79B4 on chromosome 22 Contains CA repeat and GSS, complete sequence.//1.4e-44:374:80//Z82178
 F-THYR01001173
 F-THYR01001177//Human pigment epithelium-derived factor gene, complete cds.//1.9e-42:250:86//U29953
 F-THYR01001189//HS_3171_B2_F10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3171 Col=20 Row=L, genomic survey sequence.//1.8e-28:246:83//AQ302330
 F-THYR01001204//Drosophila melanogaster DNA repair protein (mei-41) gene, complete cds, and TH1 gene, partial cds.//4.9e-39:657:64//U34925
 F-THYR01001213//, complete sequence.//1.7e-45:257:84//AC005300
 F-THYR01001262//Homo sapiens genomic DNA, chromosome 21q11.1, segment 1228, WORKING DRAFT SEQUENCE.//1.5e-40:274:87//AP000036
 F-THYR01001271//Streptomyces coelicolor cosmid 1A6.//0.033:364:61//AL023496
 F-THYR01001287//Drosophila melanogaster cosmid clone 86E4.//9.6e-49:586:69//AL021086
 F-THYR01001290//HS_2045_B1_H09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2045 Col=17 Row=P, genomic survey sequence.//4.4e-13:156:78//AQ248237
 F-THYR01001313//S. lavendulae bla gene for beta-lactamase, complete cds.//1.0:229:64//D12693
 F-THYR01001320//Homo sapiens Chromosome 22q11.2 PAC Clone p_n5 in 8CRL2-CGT Region, complete sequence.//1.1e-88:672:82//AC002472
 F-THYR01001321//Human PAC clone DJ527C21 from Xq23, complete sequence.//1.2e-115:740:87//AC000114
 F-THYR01001322//HS_3205_B2_C12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3205 Col=24 Row=F, genomic survey sequence.//0.00031:285:61//AQ304025
 F-THYR01001347//Homo sapiens mRNA for KIAA0745 protein, partial cds.//2.2e-43:638:64//AB018288
 F-THYR01001363//Homo sapiens PAC clone DJ0845121 from 7q11.21-q11.23, complete sequence.//1.0e-09:189:74//AC004905
 F-THYR01001365//Homo sapiens chromosome 10 clone CIT987SK-1163G10 map 10q25, complete sequence.//7.6e-168:821:97//AC005660
 F-THYR01001374//Homo sapiens mRNA for KIAA0707 protein, partial cds.//2.3e-155:740:97//AB014607
 F-THYR01001401//Homo sapiens chromosome 19, cosmid F23149, complete sequence.//3.2e-07:138:73//AC005239
 F-THYR01001403//Homo sapiens chromosome 12p13.3 clone RPC13-454823, WORKING DRAFT SEQUENCE, 48 unordered pieces.//3.6e-70:360:86//AC005845
 F-THYR01001405//Bos taurus mRNA for NDP52, complete cds.//2.6e-14:559:63//AB008852
 F-THYR01001406//Mus musculus putative steroid dehydrogenase (KIK-1) mRNA, complete cds.//1.0e-91:631:82//AF064635
 F-THYR01001411//Homo sapiens chromosome 19, cosmid F18718, complete sequence.//5.5e-42:509:71//AC006126
 F-THYR01001426//*** SEQUENCING IN PROGRESS *** Homo sapiens genomic DNA (PAC 1118i22) from chromosome 11: HTGS phase 1, WORKING DRAFT SEQUENCE.//2.7e-31:172:81//AJ002553
 F-THYR01001434//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.0:98:70//AC000384
 F-THYR01001458//Bos taurus non-muscle myosin heavy chain mRNA, partial cds.//1.9e-58:653:71//U87265
 F-THYR01001480//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//7.5e-42:357:80//AC006001
 F-THYR01001487//H. sapiens DNA sequence.//0.92:160:64//Z22449
 F-THYR01001534//Homo sapiens chromosome 17, clone hCIT.468_F_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.8e-47:266:80//AC004666
 F-THYR01001537//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 998H6, WORKING DRAFT SEQUENCE.//1.3e-79:479:89//AL031687
 F-THYR01001541//Human DNA sequence from clone 399H14 on chromosome Xq26.1-26.3. Contains ESTs, an STS and GSSs, complete sequence.//0.0034:106:77//Z96074
 F-THYR01001559//Rattus norvegicus simple sequence repeat D18Mc6.//1.6e-09:351:63//AF006056
 F-THYR01001570//RPC111-49B23.TJ RPC111 Homo sapiens genomic clone R-49B23, genomic survey sequence.//1.4e-65:384:91//AQ052105
 F-THYR01001573//Homo sapiens clone 24778 unknown mRNA.//8.2e-104:546:95//AF070572
 F-THYR01001584//CIT-HSP-2365J21.TF CIT-HSP Homo sapiens genomic clone 2365J21, genomic survey sequence.//1.3e-24:180:88//AQ080498
 F-THYR01001595//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//8.7e-145:779:93//AL023808
 F-THYR01001602//Homo sapiens chromosome 17, clone hRPK.786_0_4, complete sequence.//2.9e-26:393:68//AC005863
 F-THYR01001605//Dictyostelium discoideum filopodin (tala) gene, complete cds.//0.0012:436:58//U14576
 F-THYR01001617//Homo sapiens full length insert cDNA clone ZD69005.//8.6e-43:342:82//AF086381
 F-THYR01001637//Homo sapiens clone DJ1019E05, WORKING DRAFT SEQUENCE, 10 unordered pieces.//6.2e-15:318:66//AC004950
 F-THYR01001656//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//1.5e-05:147:68//AC004827
 F-THYR01001661
 F-THYR01001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//2.5e-164:780:98//AJ225089
 F-THYR01001673//Homo sapiens clone RG161A02, complete sequence.//4.4e-40:770:64//AC005071
 F-THYR01001703//S. coelicolor plasmid SCP2 transfer region DNA.//0.14:414:59//X72857
 F-THYR01001706//Homo sapiens BAC clone RG281809 from 7q21.1-q31.1, complete sequence.//2.6e-43:308:75//AC004745
 F-THYR01001721//, complete sequence.//9.9e-134:770:91//AC005500
 F-THYR01001738//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 355C18, WORKING DRAFT SEQUENCE.//0.99:163:61//AL022327
 F-THYR01001745
 F-THYR01001746
 F-THYR01001772//HS_3069_B1_C05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3069 Col=9 Row=F, genomic survey sequence.//1.5e-61:360:91//AQ171021
 F-THYR01001793//B. taurus mRNA for beta-subunit of rod photoreceptor CNG-channel.//0.028:446:58//X89626
 F-THYR01001809
 F-THYR01001828//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 110F11, WORKING DRAFT SEQUENCE.//1.3e-175:841:98//AL033526
 F-THYR01001854//Homo sapiens chromosome 17, clone hCITS4K19, complete sequence.//7.9e-07:445:59//AC003664
 F-THYR01001895
 4.4e-13:248:68//AB012576
 F-THYR01001907//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//2.9e-15:144:77//AC005058
 F-YESE1000122//HS_3075_B1_C09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=17 Row=F, genomic survey sequence.//1.1e-16:130:90//AQ143749
 F-Y79AA1000013
 F-Y79AA1000033//Homo sapiens BAC clone GS114109 from 7p14-p15, complete sequence.//2.9e-95:300:94//AC006027
 F-Y79AA1000037//Human prot-oncogene (BML-1) mRNA, complete cds.//2.4e-19:230:66//L13689
 F-Y79AA1000059//Homo sapiens immunophilin homolog ARA9 mRNA, complete cds.//2.2e-38:629:64//U78521
 F-Y79AA1000065//Human DNA sequence from cosmid J256K24, between markers DXS6791 and DXS8038 on chromosome X contains EST.//5.3e-10:1

【0773】

【表474】

17:83//Z72005
 F-Y79AA1000131//Homo sapiens LERK-6 (EPLG6) gene, exon 1.//7.6e-1
 0:381:64//U92893
 F-Y79AA1000181//Human DNA sequence from clone 612B18 on chromosome
 1q24-25.3 Contains exon from gene similar to 40S ribosomal protei
 n, first coding exon of dynamin 2 (DYN11). ESTs, STS, GSS, CpG Isl
 and, complete sequence.//1.4e-165:732:99//AL031864
 F-Y79AA1000202//Drosophila melanogaster DNA sequence (P1 D506882
 (D310)), complete sequence.//9.1e-20:339:65//AC005115
 F-Y79AA1000214//Homo sapiens clone DJ0673B15, WORKING DRAFT SEQUEN
 CE, 33 unordered pieces.//3.7e-72:397:93//AC004854
 F-Y79AA1000230
 F-Y79AA1000231//Mus musculus SIK similar protein mRNA, complete cd
 s.//8.5e-151:833:90//AF053232
 F-Y79AA1000258//Leishmania donovani histidine secretory acid phosph
 atase (SACP-1) gene, complete cds.//0.0099:547:58//U78522
 F-Y79AA1000268//Mus musculus Nip2l mRNA, complete cds.//4.0e-11:42
 4:62//AF035207
 F-Y79AA1000313
 F-Y79AA1000328//CIT-HSP-386A20.TF CIT-HSP Homo sapiens genomic clo
 ne 386A20, genomic survey sequence.//5.9e-07:173:69//B55085
 F-Y79AA1000342//RPC111-57J6.TK.1 RPC111 Homo sapiens genomic clone
 R-57J6, genomic survey sequence.//5.2e-27:151:99//AQ115511
 F-Y79AA1000346//B.primigenius mRNA for coat protein gamma-cop.//5.
 7e-69:694:71//X92987
 F-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//1.8
 e-98:535:92//X84692
 F-Y79AA1000355//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUEN
 CE, 3 unordered pieces.//1.6e-21:129:85//AC005484
 F-Y79AA1000368//H.sapiens CpG island DNA genomic MseI fragment, cl
 one 12f1, reverse read cpg12f1.rttc.//0.00016:53:98//Z56610
 F-Y79AA1000405//Plasmodium falciparum DNA see SEQUENCING IN PROGRE
 SS *** from MAL1P4, WORKING DRAFT SEQUENCE.//0.069:366:59//AL03174
 7
 F-Y79AA1000410//Human DNA sequence from PAC 117P19 on chromosome
 X.//1.0e-25:235:89//Z86061
 F-Y79AA1000420//H.sapiens CpG island DNA genomic MseI fragment, cl
 one 82c3, forward read cpg82c3.ftta.//2.0e-36:194:98//Z63378
 F-Y79AA1000469//Mus musculus ancient ubiquitous 46 kDa protein AUP
 1 precursor (Aup1) mRNA, complete cds.//8.5e-121:696:89//U41736
 F-Y79AA1000480//HS_2175_A2_H11_T7 CIT Approved Human Genomic Sperm
 Library D Homo sapiens genomic clone Plate=2175 Col=22 Row=0, gen
 omic survey sequence.//2.5e-26:178:89//AQ307693
 F-Y79AA1000538//Homo sapiens clone DJ1158B01, WORKING DRAFT SEQUEN
 CE, 23 unordered pieces.//0.67:111:72//AC004980
 F-Y79AA1000539//HS_2237_B2_F10_MF CIT Approved Human Genomic Sperm
 Library D Homo sapiens genomic clone Plate=2237 Col=20 Row=L, gen
 omic survey sequence.//1.2e-14:168:77//AQ153503
 F-Y79AA1000540//Homo sapiens clone DJ0655N24, WORKING DRAFT SEQUEN
 CE, 8 unordered pieces.//0.94:127:67//AC005193
 F-Y79AA1000560//Mouse mRNA for alpha-adaptin (C).//1.7e-114:776:84
 //X14972
 F-Y79AA1000574//M.musculus tex23 mRNA (5' region).//1.8e-23:291:75/
 //X80424
 F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequ
 ence.//8.6e-153:755:97//AF091080
 F-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, co
 mplete cds.//5.2e-135:644:98//AF060503
 F-Y79AA1000705//M.musculus mRNA of enhancer-trap-locus 1.//6.9e-14
 8:902:86//X69942
 F-Y79AA1000734//Homo sapiens PEX11 beta mRNA for peroxisome assemb
 ly factor, complete cds.//4.8e-180:850:98//AB018080
 F-Y79AA1000748//Caenorhabditis elegans cosmid F2585.//0.00019:308:
 60//U23172
 F-Y79AA1000752//Oryctolagus cuniculus mRNA for hnRNP-E1 protein.//
 1.7e-40:513:68//AJ003023
 F-Y79AA1000774
 F-Y79AA1000782
 F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds.
 //3.5e-177:847:97//AF098799
 F-Y79AA1000794//H.sapiens CpG island DNA genomic MseI fragment, cl
 one 45a4, forward read cpg45a4.ftta.//2.5e-13:104:92//Z61120
 F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds.//
 0.98:244:60//AF056085
 F-Y79AA1000802
 F-Y79AA1000805//Human Chromosome 11 Cosmid cSRL30h11, complete seq
 uence.//9.3e-76:528:85//U73642
 F-Y79AA1000824//RPC111-2684.TP RPC111 Homo sapiens genomic clone
 RPC111-2684, genomic survey sequence.//4.4e-14:99:95//B84538
 F-Y79AA1000827//Human DNA sequence *** SEQUENCING IN PROGRESS ***
 from clone 117715, WORKING DRAFT SEQUENCE.//1.5e-08:249:69//AL0223
 15
 F-Y79AA1000833//Macaca fascicularis mRNA for alpha-tubulin.//1.8e-
 103:603:89//X04757
 F-Y79AA1000850
 F-Y79AA1000962//Human DNA sequence from PAC 360E18 on chromosome X
 contains EST, CpG island and polymorphic CA repeat.//0.038:468:59
 //Z82203
 F-Y79AA1000966//Mus musculus COP9 complex subunit 4 (COPS4) mRNA,
 complete cds.//9.7e-150:865:89//AF071314
 F-Y79AA1000968//Rattus norvegicus initiation factor eIF-28 gamma s
 ubunit (eIF-28 gamma) mRNA, complete cds.//6.4e-122:717:88//U38253
 F-Y79AA1000969//Mouse chromosome 6 BAC-284H12 (Research Genetics m
 ouse BAC library) complete sequence.//1.0:155:63//AC002397
 F-Y79AA1000976//Caenorhabditis elegans cosmid F54C1.//4.3e-06:130:
 73//U88165
 F-Y79AA1000985//Mus musculus pericentrin mRNA, complete cds.//2.4
 e-44:428:77//U05823
 F-Y79AA1001023
 F-Y79AA1001041//Human mutY homolog (hMYH) gene, complete cds.//2.3
 e-13:90:100//U63329
 F-Y79AA1001048//Human mRNA for very-long-chain acyl-CoA dehydrogen
 ase (VLCAD), complete cds.//2.6e-28:772:60//D43582
 F-Y79AA1001061//Homo sapiens chromosome 4 clone B331M8 map 4q25, c
 omplete sequence.//9.4e-36:292:82//AC004701
 F-Y79AA1001068//tipAL-AS complex: tipA=TipAL-AS [Streptomyces livi
 dans, Genomic, 1146 nt].//0.17:537:59//S64314
 F-Y79AA1001077//Zea mays mRNA for aldehyde oxidase-2, complete cd
 s.//0.17:231:64//D88452
 F-Y79AA1001078
 F-Y79AA1001105//Zebrafish otx2 mRNA for otx homeoprotein, complete
 cds.//3.1e-63:529:77//D26173
 F-Y79AA1001145//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENC
 E, 7 unordered pieces.//1.3e-23:228:76//AC005015
 F-Y79AA1001167
 F-Y79AA1001177//M.musculus mRNA for Nfix1-protein.//4.0e-10:398:64
 //Y07688
 F-Y79AA1001185//Human DNA sequence *** SEQUENCING IN PROGRESS ***
 from clone 16915, WORKING DRAFT SEQUENCE.//1.1e-113:666:90//Z93015
 F-Y79AA1001211//HS_3124_B2_H08_MR CIT Approved Human Genomic Sperm
 Library D Homo sapiens genomic clone Plate=3124 Col=16 Row=P, gen
 omic survey sequence.//5.5e-12:87:96//AQ187492
 F-Y79AA1001216
 F-Y79AA1001228//Mycobacterium tuberculosis H37Rv complete genome:
 segment 143/162.//0.028:188:67//AL021841
 F-Y79AA1001233//Human placental 17-beta-hydroxysteroid dehydrogena
 se mRNA, complete cds.//3.5e-24:731:60//M35263
 F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete codin
 g sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110113307
 (RZPD Berlin)).//1.2e-133:441:97//AJ005892
 F-Y79AA1001281//HS_2241_B2_F09_MF CIT Approved Human Genomic Sperm
 Library D Homo sapiens genomic clone Plate=2241 Col=18 Row=L, gen
 omic survey sequence.//5.0e-27:169:94//AQ217497
 F-Y79AA1001299//Human Inil mRNA, complete cds.//6.7e-115:323:93//U
 04847
 F-Y79AA1001312
 F-Y79AA1001323
 F-Y79AA1001384
 F-Y79AA1001391//Mus musculus transcription factor HOXA13 (Hoxa13)
 gene, complete cds.//5.8e-42:245:74//U59322
 F-Y79AA1001394//Caenorhabditis elegans cosmid F54B3, complete sequ
 ence.//7.8e-18:636:58//Z48583
 F-Y79AA1001402//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park
 Cancer Institute Human PAC Library) complete sequence.//1.2e-110:7
 38:85//AC005924
 F-Y79AA1001493//H.sapiens DNA sequence.//2.0e-27:254:82//Z22497
 F-Y79AA1001511//Human DNA sequence from clone 931K24 on chromosome
 20p12 Contains ESTs and GSSs, complete sequence.//1.1e-158:804:95
 //AL034430
 F-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor
 (PAF53), complete cds.//1.7e-100:820:78//D14336
 F-Y79AA1001541//HS_3197_A2_G11_MR CIT Approved Human Genomic Sperm
 Library D Homo sapiens genomic clone Plate=3197 Col=22 Row=M, gen
 omic survey sequence.//5.1e-28:218:86//AQ150183
 F-Y79AA1001548//Homo sapiens chromosome 19, cosmid R28738, complet
 e sequence.//5.4e-21:167:86//AC004151
 F-Y79AA1001555//R.norvegicus mRNA for drebrin A.//0.88:463:59//X59
 267
 F-Y79AA1001581//FMR1 (CGG repeats) [human, Fragile X syndrome pati
 ent, Genomic, 429 nt].//0.00051:252:65//S74494

【0774】

【表475】

F-Y79AA1001585//Human hypoxanthine phosphoribosyltransferase (HPR T) gene, complete cds.//7.2e-33:375:76//M26434
 F-Y79AA1001594
 F-Y79AA1001603//Homo sapiens PAC 128M19 derived from chromosome 21 q22.3, containing the HMG-14 and CHD5 genes, complete cds, complete sequence.//4.2e-06:338:66//AF064861
 F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete cds.//0.024:520:57//AB014583
 F-Y79AA1001647//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y53F4, WORKING DRAFT SEQUENCE.//0.014:331:61//Z92860
 F-Y79AA1001665//Human DNA sequence from clone 299D3 on chromosome 22q13.3, complete sequence.//0.99:273:63//Z84468
 F-Y79AA1001679//O. cuniculus lambda-crystallin mRNA, complete cds.//1.2e-97:682:81//M22743
 F-Y79AA1001692//insulin-like growth factor binding protein-2 [human, placenta, Genomic, 1292 nt, segment 1 of 4].//5.6e-05:426:59//S37712
 F-Y79AA1001696//Rice endogenous double-stranded RNA encoding polyp protein (containing putative helicase and putative RNA-dependent RNA polymerase domains), complete cds.//1.0:437:60//D32136
 F-Y79AA1001705//M. musculus fkh-5 gene.//0.18:153:64//X71943
 F-Y79AA1001711//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 32BE19, WORKING DRAFT SEQUENCE.//5.4e-76:191:98//AL022240
 F-Y79AA1001781//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 10/15, WORKING DRAFT SEQUENCE.//0.99:227:63//AP000017
 F-Y79AA1001805//H. sapiens CpG island DNA genomic MseI fragment, clone 13d12, reverse read cpg13d12. rttc.//2.6e-13:88:100//Z64565
 F-Y79AA1001827//Oryctolagus cuniculus PiUS mRNA, complete cds.//3.7e-130:775:88//U74297
 F-Y79AA1001846//CIT-HSP-2300M6.TR CIT-HSP Homo sapiens genomic clone 2300M6, genomic survey sequence.//8.3e-17:218:76//AQ012369
 F-Y79AA1001848//Human mRNA for KIAA0390 gene, complete cds.//4.2e-10:378:62//AB002388
 F-Y79AA1001866//Rattus norvegicus Cys2/His2 zinc finger protein (rKr1) mRNA, complete cds.//6.9e-41:441:71//U41164
 F-Y79AA1001874//Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alternatively spliced isoform of Jagged2, complete cds.//0.00017:412:62//AF029779
 F-Y79AA1001875//CIT-HSP-2317G18.TR CIT-HSP Homo sapiens genomic clone 2317G18, genomic survey sequence.//1.9e-09:271:67//AQ042654
 F-Y79AA1001923//H. sapiens CpG island DNA genomic MseI fragment, clone 193c12, forward read cpg193c12. itla.//0.0031:108:75//Z60186
 F-Y79AA1001963//CITBI-E1-2510J4.TR CITBI-E1 Homo sapiens genomic clone 2510J4, genomic survey sequence.//1.8e-05:56:100//AQ261184
 F-Y79AA1002027//Arabidopsis thaliana ubiquitin-conjugating enzyme 17 (UBC17) mRNA, complete cds.//3.3e-13:451:62//AF028340
 F-Y79AA1002083//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 526114, WORKING DRAFT SEQUENCE.//0.91:134:65//Z82214
 F-Y79AA1002089
 F-Y79AA1002093//Mus musculus transcription factor like protein 4 T CFL4 mRNA, partial cds.//1.2e-112:678:88//U43548
 F-Y79AA1002103//HS_3052_B1_H08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3052 Col=15 Row=P, genomic survey sequence.//6.5e-18:238:72//AQ135014
 F-Y79AA1002115
 F-Y79AA1002125//H. sapiens (DBS135) DNA segment containing GT repeat.//1.5e-14:99:96//X61693
 F-Y79AA1002139//Saccharomyces cerevisiae dnaJ homolog Hlj1p (HLJ1) gene, complete cds.//2.5e-07:208:64//U19358
 F-Y79AA1002204//HS_2235_B2_D12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2235 Col=24 Row=H, genomic survey sequence.//2.9e-13:89:98//AQ154260
 F-Y79AA1002208//CIT-HSP-2006M21.TV CIT-HSP Homo sapiens genomic clone 2006M21, genomic survey sequence.//3.7e-27:154:98//B56397
 F-Y79AA1002209//E.coli tyrS gene coding for tyrosyl-tRNA synthetase.//2.8e-05:143:70//J01719
 F-Y79AA1002210//Homo sapiens chromosome 19, cosmid R28058, complete sequence.//8.3e-22:229:78//AC005615
 F-Y79AA1002211//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//1.0e-06:241:67//AC003043
 F-Y79AA1002220//CIT-HSP-2374P23.TR CIT-HSP Homo sapiens genomic clone 2374P23, genomic survey sequence.//1.3e-68:375:95//AQ109738
 F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds.//0.12:203:63//D42045
 F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//1.3e-174:821:98//AB014592
 F-Y79AA1002246//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.50:470:60//AC005015
 F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds.//5.8e-159:748:98//AB014555
 F-Y79AA1002298//Human density enhanced phosphatase-1 mRNA, complete cds.//0.036:278:62//U10886
 F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds.//6.4e-129:622:97//AB014534
 F-Y79AA1002311//R. norvegicus mRNA for cytosolic resiniferatoxin-binding protein.//2.0e-116:693:82//X67877
 F-Y79AA1002351//S. clavuligerus pah and cas genes.//1.0:369:58//X84101
 F-Y79AA1002361//Rattus norvegicus mRNA for protein phosphatase 1 (GL-subunit).//5.4e-105:762:80//Y18208
 F-Y79AA1002399//Homo sapiens chromosome 17, clone hRPC.700_H_6, complete sequence.//1.0e-159:411:100//AC005920
 F-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence.//1.1e-118:609:84//AC004662
 F-Y79AA1002416//Mus musculus CTP synthetase homolog (CTPsh) mRNA, complete cds.//4.4e-90:529:88//U49385
 F-Y79AA1002431//Chlamydomonas reinhardtii novel protein kinase mRNA A, complete cds.//1.0:166:66//U36196
 F-Y79AA1002433//CIT-HSP-384K8.TF CIT-HSP Homo sapiens genomic clone 384K8, genomic survey sequence.//0.24:85:72//B51917
 F-Y79AA1002472//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//1.9e-13:242:69//AC006116
 F-Y79AA1002482//Homo sapiens full length insert cDNA clone ZC18H06.//1.2e-35:462:71//AF088022
 F-Y79AA1002487//Bovine herpesvirus type 1 genes for UL[27,28,29,30,31].//0.93:215:60//X94677

【0775】

3'末端クローン配列に対するESTとSTSを除いたGenBank相同性検索結果データ
各データは、

クローン配列名、

トップヒットデータのDefinition、

P値:比較配列の長さ (base):相同性(%)、

トップヒットデータのAccession No.の順に//で区切って記載した。

なお、同一クローンで5'末端配列に対応する3'末端配列が決定されていないものは空欄とした。相同性のスコアのP値が1より大であった場合はデータは示さない。

【0776】

【表476】

R-HEMBA1000005//Mouse tumor cell dnaJ-like protein 1 mRNA, complete cds.//3.6e-60:504:78//L16953
 R-HEMBA1000030//F. rubripes GSS sequence, clone 063K10bD3, genomic survey sequence.//0.28:117:68//Z88864
 R-HEMBA1000042//RPC111-77G23.TV RPC111 Homo sapiens genomic clone R-77G23, genomic survey sequence.//1.3e-56:292:97//AQ268240
 R-HEMBA1000046//Homo sapiens chromosome X map Xq28, complete sequence.//9.8e-56:401:82//U82696
 R-HEMBA1000050//Human cosmid insert containing polymorphic marker DXS455.//0.0010:175:68//L31948
 R-HEMBA1000076//Homo sapiens clone DJ1021120, WORKING DRAFT SEQUENCE, 6 unordered pieces.//4.9e-41:364:79//AC005520
 R-HEMBA1000111//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//4.7e-30:229:84//AC003684
 R-HEMBA1000129//Homo sapiens chromosome 17, clone HClT48C15, complete sequence.//2.4e-93:503:93//AC003104
 R-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds.//6.5e-99:514:94//AB018340
 R-HEMBA1000150//Homo sapiens clone RG086D03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.7e-37:289:83//AC005060
 R-HEMBA1000156//Homo sapiens scaffold attachment factor B (SAF-B) mRNA, partial cds.//3.1e-21:417:64//L43631
 R-HEMBA1000158
 R-HEMBA1000168
 R-HEMBA1000180//Plasmodium falciparum encoding Pfz27/25.//0.073:292:56//X84904
 R-HEMBA1000185//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//5.3e-40:286:85//AC006146
 R-HEMBA1000193
 R-HEMBA1000201//Homo sapiens SNF5/INI1 gene, exon 9.//2.0e-24:137:99//Y17126
 R-HEMBA1000213//Caenorhabditis elegans cosmid C44C8.//0.025:192:68//AF100655
 R-HEMBA1000216//Human Chromosome 16 BAC clone CIT987SK-A-815A9, complete sequence.//2.5e-31:269:79//AF001548
 R-HEMBA1000227
 R-HEMBA1000231//Human DNA sequence from PAC 212P9 on chromosome 1p34.1-p35. Contains delta opiate receptor, CpG island, CA repeat.//4.3e-24:400:68//AL009181
 R-HEMBA1000243//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//1.3e-19:319:69//AC004526
 R-HEMBA1000244
 R-HEMBA1000251//Meloidogyne hapla mitochondrial COII gene, 3' end of cds; transfer RNA-His gene; 16S ribosomal RNA gene; ND3 gene, complete cds; cytochrome B (cytb) gene, 5' end of cds.//0.16:338:60//L76262
 R-HEMBA1000264//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 5/15, WORKING DRAFT SEQUENCE.//0.00093:300:66//AP000012
 R-HEMBA1000280//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//3.5e-10:238:70//AC003037
 R-HEMBA1000282//Arabidopsis thaliana BAC 1G002P16.//0.71:344:60//AF007270
 R-HEMBA1000288//Homo sapiens Xp22 PACs RPC11-263P4 and RPC11-164K3 complete sequence.//4.8e-33:267:82//AC003046
 R-HEMBA1000290//Homo sapiens chromosome 17, clone HRPC837J1, complete sequence.//2.2e-15:249:69//AC004223
 R-HEMBA1000302//CIT-HSP-2173N10.TF CIT-HSP Homo sapiens genomic clone 2173N10, genomic survey sequence.//1.0:215:61//B95105
 R-HEMBA1000303//Mus musculus Plenty of SH3s (POSH) mRNA, complete cds.//1.0e-77:551:82//AF030131
 R-HEMBA1000304//Rattus norvegicus Ca2+-dependent activator protein (CAPS) mRNA, complete cds.//2.0e-96:546:90//U16802
 R-HEMBA1000307//Mus musculus mRNA for CDV-1 protein.//3.8e-36:315:68//Y10496
 R-HEMBA1000333//Plasmodium falciparum 307 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.078:379:59//AC005505
 R-HEMBA1000338//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 620E11, WORKING DRAFT SEQUENCE.//2.0e-33:399:72//AL031667
 R-HEMBA1000351//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//1.7e-39:272:87//AJ003147
 R-HEMBA1000355//Human primary A1u transcript.//0.0045:67:85//U67829
 R-HEMBA1000357//Homo sapiens (subclone 9_h8 from PI H16) DNA sequence.//8.7e-93:426:88//L42086
 R-HEMBA1000366//Homo sapiens PAC clone DJ0942116 from 7q11, complete sequence.//1.7e-12:130:83//AC006012
 R-HEMBA1000369//Human DNA sequence from clone 1039K5 on chromosome 22q12.3-13.2 Contains gene similar to PICK1 perinuclear binding protein, gene similar to monocarboxylate transporter (MCT3), ESTs, STS, GSS and a CpG island, complete sequence.//1.9e-69:355:97//AL031587
 R-HEMBA1000376//Homo sapiens chromosome 19, BAC CIT-B-393115 (BC301323), complete sequence.//3.7e-66:410:89//AC006116
 R-HEMBA1000387//Homo sapiens chromosome 17, clone HClT169H9, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.0e-43:363:81//AC002993
 R-HEMBA1000390//Homo sapiens BAC clone RG041D11 from 7q21, complete sequence.//4.6e-23:417:69//AC005053
 R-HEMBA1000392//Human Chromosome 11p14.3 PAC clone pDJ59m18, complete sequence.//6.2e-05:174:68//AC004582
 R-HEMBA1000396//Homo sapiens DNA sequence from PAC 159A15 on chromosome Xp11.21-p11.23. Contains inter-alpha-trypsin inhibitor heavy chain H3 precursor-like protein.//1.4e-62:564:77//AL022575
 R-HEMBA1000411
 R-HEMBA1000418//Liverwort Marchantia polymorpha chloroplast genome DNA.//0.94:210:60//X04465
 R-HEMBA1000422//CIT-HSP-2382A6.TR CIT-HSP Homo sapiens genomic clone 2382A6, genomic survey sequence.//4.4e-12:98:92//AQ078233
 R-HEMBA1000428//Human DNA sequence from clone 393P23 on chromosome Xq21.1-21.33. Contains GSSs, complete sequence.//2.0e-93:526:90//Z95400
 R-HEMBA1000434//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//2.7e-07:452:60//AC004826
 R-HEMBA1000442//E. caballus microsatellite DNA, clone HMB4.//0.39:135:62//Y07733
 R-HEMBA1000456//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-52, complete sequence.//2.6e-05:174:70//AL010226
 R-HEMBA1000459//Arabidopsis thaliana putative transmembrane protein G1p (ATG1), putative nuclear DNA-binding protein G2p (ATG2), Eml protein (ATEM1), putative chlorophyll synthetase (ATG4), putative transmembrane protein G5p (ATG5), putative acyl-coA dehydrogenase (ATG6), and calcium dependent protein kinase genes, complete cds; and unknown genes.//0.013:212:63//AF049236
 R-HEMBA1000460//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//8.6e-114:556:98//AC004839
 R-HEMBA1000464//Caenorhabditis elegans cosmid C34B7, complete sequence.//0.086:334:61//Z83220
 R-HEMBA1000469//Homo sapiens BAC clone RG442F18 from 2, complete sequence.//1.8e-52:472:79//AC005104
 R-HEMBA1000488//, complete sequence.//3.3e-68:200:99//AC005500
 R-HEMBA1000490//Caenorhabditis elegans cosmid Y53C12B, complete sequence.//0.97:233:61//Z99278
 R-HEMBA1000491
 R-HEMBA1000504//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-64, complete sequence.//1.7e-08:440:60//AL009014
 R-HEMBA1000505//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 1/11.//0.37:189:62//AB020858
 R-HEMBA1000508//Human DNA sequence from cosmid V210E9, between markers DXS366 and DXS87 on chromosome X.//1.1e-25:248:80//Z70280
 R-HEMBA1000518//RPC111-6022.TV RPC111 Homo sapiens genomic clone RPC11-6022, genomic survey sequence.//0.0035:293:61//B49544
 R-HEMBA1000519
 R-HEMBA1000520//Arabidopsis thaliana chromosome 11 BAC F10A12 genomic sequence, complete sequence.//0.30:255:63//AC006232
 R-HEMBA1000523//Human cleavage stimulation factor 77kDa subunit mRNA, complete cds.//1.2e-53:203:92//U15782
 R-HEMBA1000531//CIT-HSP-388J17.TR CIT-HSP Homo sapiens genomic clone 388J17, genomic survey sequence.//2.7e-24:137:99//B55638
 R-HEMBA1000540//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 510D11, WORKING DRAFT SEQUENCE.//0.00014:329:60//Z98044
 R-HEMBA1000545//Homo sapiens Xp22 BAC GS-619J3 (Genome Systems Human BAC library) complete sequence.//6.9e-87:552:87//AC004103
 R-HEMBA1000555//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 134019, WORKING DRAFT SEQUENCE.//8.9e-121:584:98//AL034555
 R-HEMBA1000557//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//5.7e-45:307:87//AC004381
 R-HEMBA1000561//Mus musculus clone OST20235, genomic survey sequence.//1.3e-43:279:90//AF046762
 R-HEMBA1000563//Plasmodium falciparum chromosome 2, section 5 of 73 of the complete sequence.//3.8e-05:506:56//AE001368
 R-HEMBA1000568//RPC111-49PB.TK.1 RPC111 Homo sapiens genomic clone R-49PB, genomic survey sequence.//1.7e-101:498:97//AQ116293
 R-HEMBA1000569

【0777】

【表477】

R-HEMBA1000575//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 754E20, WORKING DRAFT SEQUENCE.//1.3e-47:458:75//AL022335

R-HEMBA1000588//Mus musculus FLI-LRR associated protein-1 mRNA, complete cds.//2.9e-62:447:81//AF045573

R-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein.//1.2e-111:591:94//AJ007509

R-HEMBA1000592//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-10, complete sequence.//3.5e-09:421:60//AL010216

R-HEMBA1000594//Homo sapiens clone RG004N09, WORKING DRAFT SEQUENCE. 5 unordered pieces.//1.1e-15:421:66//AC005044

R-HEMBA1000604//HS_2220_A1_G10_WF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2220 Col=19 Row=M, genomic survey sequence.//1.0e-51:306:92//AQ151991

R-HEMBA1000608

R-HEMBA1000622//H. sapiens CpG island DNA genomic MseI fragment, clone 155e4, reverse read cpg155e4.rtlc.//4.5e-16:105:98//Z56962

R-HEMBA1000636//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 1/15, WORKING DRAFT SEQUENCE.//4.8e-62:421:86//AP000008

R-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds.//1.2e-97:443:97//AB014590

R-HEMBA1000655//Homo sapiens chromosome 19, cosmid R26349, complete sequence.//9.8e-61:311:90//AC005953

R-HEMBA1000657

R-HEMBA1000662

R-HEMBA1000673//Human DNA sequence from PAC 448E20 on chromosome X q26.1 contains ESTs and STS.//1.0e-13:351:63//Z97196

R-HEMBA1000682//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE. 4 unordered pieces.//1.2e-50:298:79//AC005377

R-HEMBA1000686//HS_3018_B1_M10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00048:210:62//AQ093513

R-HEMBA1000702//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE. 7 unordered pieces.//9.7e-54:317:88//AC005000

R-HEMBA1000705//Glossonotus univittatus 12S mitochondrial ribosomal RNA, small subunit, mitochondrial gene, partial sequence.//0.080:138:65//U77850

R-HEMBA1000719//Rattus norvegicus mRNA for TESK1, complete cds.//0.96:291:58//D50864

R-HEMBA1000722

R-HEMBA1000726//Homo sapiens PAC clone DJ0701016 from Tq33-q36, complete sequence.//4.4e-26:284:77//AC005531

R-HEMBA1000727//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-89, complete sequence.//9.1e-05:351:60//AL010266

R-HEMBA1000747//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.5e-16:123:93//AL021326

R-HEMBA1000749//Human Chromosome 16 BAC clone CIT987SK-327024, complete sequence.//2.8e-32:298:79//AC003108

R-HEMBA1000752//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STS. Contains polymorphic CA repeat.//2.8e-90:542:90//Z92545

R-HEMBA1000769//Homo sapiens P1 clone GSP13996 from Sq12, complete sequence.//2.7e-36:405:75//AC005031

R-HEMBA1000773//HS_3050_A2_B08_WF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=16 Row=C, genomic survey sequence.//0.00053:268:60//AQ105619

R-HEMBA1000774//Homo sapiens PAC clone DJ0630C24 from Tq31-q32, complete sequence.//4.7e-46:338:85//AC004690

R-HEMBA1000791//***ALU WARNING: Human Alu-Sc subfamily consensus sequence.//5.3e-47:279:91//U14571

R-HEMBA1000817//Sequence 1 from Patent WO 8904839.//0.86:148:67//U09339

R-HEMBA1000822//T. brucei kinetoplast maxicircle variable region DNA.//0.00061:246:61//Z15118

R-HEMBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protein (SRN160) mRNA, complete cds.//6.9e-43:228:98//AF048977

R-HEMBA1000843//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. C contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//1.7e-41:319:84//AL022394

R-HEMBA1000851//Arabidopsis thaliana chromosome I BAC T14N5 genomic sequence, complete sequence.//0.40:168:67//AC004260

R-HEMBA1000852//Homo sapiens Xp22 bins 3-5 PAC RPC14-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//1.5e-112:572:96//AC005295

R-HEMBA1000867//Homo sapiens clone DJ0971C03, WORKING DRAFT SEQUENCE. 18 unordered pieces.//0.11:121:71//AC004938

R-HEMBA1000869//Homo sapiens chromosome 16p11.2 BAC clone CIT9875 K-A-180G2, WORKING DRAFT SEQUENCE. 5 unordered pieces.//3.2e-22:186:76//AC002042

R-HEMBA1000870//Human BAC clone GS542D18 from Tq31-q32, complete sequence.//0.0060:283:63//AC002528

R-HEMBA1000872//Rattus norvegicus polymorphic satellite repetitive elements.//3.8e-05:269:61//M98801

R-HEMBA1000876//Homo sapiens chromosome 12p13.3 clone RPC11-96H9, WORKING DRAFT SEQUENCE. 66 unordered pieces.//6.5e-38:327:77//AC006057

R-HEMBA1000908//CIT-HSP-237314.TR CIT-HSP Homo sapiens genomic clone 237314, genomic survey sequence.//5.0e-34:221:90//AQ108658

R-HEMBA1000910//T. pigmentosa UM1060 macronuclear rDNA telomeric region 3' term.//0.19:280:61//X04205

R-HEMBA1000918//RPC111-68E14.TK RPC111 Homo sapiens genomic clone 68E14, genomic survey sequence.//1.3e-32:172:100//AQ267293

R-HEMBA1000919

R-HEMBA1000934//Homo sapiens DNA sequence from PAC 874C20 on chromosome 6p22.1-22.3. Contains a Zinc Finger Protein ZFP47 LIKE gene, a Zinc Finger Protein pseudogene and a Zinc Finger Protein SRE-ZB P pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.6e-18:284:71//AL021997

R-HEMBA1000942//Homo sapiens clone RG350L10, WORKING DRAFT SEQUENCE. 15 unordered pieces.//1.4e-17:217:76//AC005098

R-HEMBA1000943//Homo sapiens chromosome 17, clone hRPK.640_1_15, complete sequence.//9.0e-113:586:95//AC005324

R-HEMBA1000946//TSN8TFB TAMU Arabidopsis thaliana genomic clone TS N8, genomic survey sequence.//0.030:369:59//B26224

R-HEMBA1000960//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENCE. 10 unordered pieces.//2.5e-52:494:77//AC005096

R-HEMBA1000968//Homo sapiens P1 clone 797a11 containing MHC class II DQ-beta (HLA-DQB) and MHC class II DC-alpha (HLA-DCA) genes, complete cds.//3.5e-77:568:83//U92032

R-HEMBA1000971//RPC111-54D1.TJ RPC111 Homo sapiens genomic clone 54D1, genomic survey sequence.//2.3e-27:153:98//AQ081552

R-HEMBA1000972//Human DNA sequence from clone 111F4 on chromosome Xq23 Contains GSSs, complete sequence.//7.3e-43:375:79//AL023876

R-HEMBA1000974//Homo sapiens clone DA0091H08, complete sequence.//2.8e-104:521:97//AC004817

R-HEMBA1000975//Human DNA sequence from clone 105D16 on chromosome Xp11.3-11.4 Contains pseudogene similar to laminin-binding protein, CA repeat, STS, complete sequence.//8.0e-22:352:68//AL031311

R-HEMBA1000985//Homo sapiens PAC clone DJ0797C05 from Tq31, complete sequence.//8.5e-05:306:63//AC004888

R-HEMBA1000986//Homo sapiens clone RG031N19, WORKING DRAFT SEQUENCE. 1 unordered pieces.//5.7e-37:296:83//AC005632

R-HEMBA1000991//RPC111-22017.TVB RPC111 Homo sapiens genomic clone 22017, genomic survey sequence.//6.5e-44:162:90//AQ008952

R-HEMBA1001007

R-HEMBA1001008//Homo sapiens chromosome 16, P1 clone 79-2A (LANL), complete sequence.//0.082:313:60//AC005365

R-HEMBA1001009//O. sativa osr40g2 gene.//0.99:203:62//Y08987

R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds.//1.0e-113:587:95//AB007937

R-HEMBA1001019//Bos taurus cyclin-dependent kinase 1 (cdk1/cdc2) mRNA, complete cds.//7.4e-24:215:82//L26547

R-HEMBA1001020//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 732E4, WORKING DRAFT SEQUENCE.//2.8e-18:449:64//AL008722

R-HEMBA1001022

R-HEMBA1001024//Homo sapiens BAC clone 393122 from 8q21, complete sequence.//6.6e-48:536:74//AF070717

R-HEMBA1001026//T33H14TF TAMU Arabidopsis thaliana genomic clone T33H14, genomic survey sequence.//0.013:180:66//B97363

R-HEMBA1001043//Caenorhabditis elegans cosmid R10H10, complete sequence.//1.2e-25:438:65//Z70686

R-HEMBA1001051//Homo sapiens 12q24.1 PAC RPC13-521E19 (Roswell Park Cancer Institute Human PAC library) complete sequence.//7.3e-38:188:89//AC004217

R-HEMBA1001052//Rabbit alpha-1-globin gene to theta-1-globin pseudogene region.//2.4e-24:279:74//X04751

R-HEMBA1001060//HS_2056_B1_CD1_MR CIT Approved Human Genomic Sperm

【0778】

【表478】

Library D Homo sapiens genomic clone Plate=2056 Col=1 Row=F, genomic survey sequence.//4.1e-14:137:83//AQ245004
 R-HEMBA1001071//M. musculus COL3A1 gene for collagen alpha-1.//6.9e-38:513:70//X52046
 R-HEMBA1001077//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 150C2, WORKING DRAFT SEQUENCE.//1.9e-22:507:61//AL022318
 R-HEMBA1001080
 R-HEMBA1001085//Human Chromosome 15q26.1 PAC clone pDJ290i21 containing fur, fes, and alpha mannosidase IIX genes, WORKING DRAFT SEQUENCE, 9 unordered pieces.//2.2e-43:317:83//AC004586
 R-HEMBA1001088//Caenorhabditis elegans cosmid C18H7.//0.46:301:60//AF067607
 R-HEMBA1001094//Homo sapiens clone RG491N20, complete sequence.//5.3e-98:501:96//AC005105
 R-HEMBA1001099
 R-HEMBA1001109//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 118J21, WORKING DRAFT SEQUENCE.//3.1e-39:335:80//AL033527
 R-HEMBA1001121//Human cosmid LL12NC01-132B11A, ETV6 gene, intron 2.//9.8e-11:122:81//U81833
 R-HEMBA1001122//Plasmodium falciparum MAL3P6, complete sequence.//0.0024:284:63//Z98551
 R-HEMBA1001123//Human NFE genomic fragment.//3.6e-26:318:72//M98511
 R-HEMBA1001133
 R-HEMBA1001137//Homo sapiens full length insert cDNA clone ZD29F04.//4.2e-88:426:98//AF086241
 R-HEMBA1001140//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.0e-41:304:84//AC005077
 R-HEMBA1001172//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE.//3.7e-36:261:85//Z98304
 R-HEMBA1001174//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//1.0:219:58//AE001398
 R-HEMBA1001197
 R-HEMBA1001208//HS_2233_A1_G10_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2233 Col=19 Row=M, genomic survey sequence.//0.083:174:68//AQ170789
 R-HEMBA1001226//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.1e-59:553:75//AC005377
 R-HEMBA1001235//RPC111-50E6.TJ RPC111 Homo sapiens genomic clone R-50E6, genomic survey sequence.//2.6e-08:97:76//AQ052666
 R-HEMBA1001247//Caenorhabditis elegans cosmid C01F1.//2.4e-05:319:63//U58761
 R-HEMBA1001257//Rattus norvegicus alpha-methylacyl-CoA racemase mRNA, complete cds.//1.5e-24:439:66//U89905
 R-HEMBA1001265//Homo sapiens BAC clone RG139P11 from Tq11-q21, complete sequence.//9.9e-21:537:63//AC004491
 R-HEMBA1001281//Homo sapiens chromosome 17, clone HC1T75G16, complete sequence.//0.022:169:65//AC003042
 R-HEMBA1001286
 R-HEMBA1001289
 R-HEMBA1001294//HS_3219_A2_G01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3219 Col=2 Row=M, genomic survey sequence.//0.24:251:63//AQ189882
 R-HEMBA1001299//Homo sapiens, clone hRPK.12_A_1, complete sequence.//1.3e-38:381:76//AC006222
 R-HEMBA1001302//cDNA encoding a human homologue of a mouse novel polypeptide derived from stromal cell.//4.1e-28:114:92//E12258
 R-HEMBA1001303//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE.//0.00011:382:58//AL031744
 R-HEMBA1001310
 R-HEMBA1001319//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.2e-09:491:58//AC005504
 R-HEMBA1001323//Drosophila yakuba mitochondrial DNA molecule.//8.3e-06:485:60//X03240
 R-HEMBA1001326//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (CAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//2.2e-14:277:69//AL021368
 R-HEMBA1001327//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HNRNP A3 (Heterogeneous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.15:360:61//AL024509
 R-HEMBA1001330//Homo sapiens 12q24 PAC RPC11-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.3e-27:481:67//AC004216
 R-HEMBA1001351//Homo sapiens chromosome 18, clone hRPK.474_N_24, complete sequence.//7.1e-45:252:94//AC006238
 R-HEMBA1001361//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence.//1.4e-113:569:97//AC006241
 R-HEMBA1001375//Homo sapiens full length insert cDNA clone ZEO9H03.//2.8e-89:428:99//AF086542
 R-HEMBA1001377//Homo sapiens PAC clone DJ0728D04, complete sequence.//2.3e-32:324:77//AC004865
 R-HEMBA1001383
 R-HEMBA1001387
 R-HEMBA1001388//Homo sapiens clone RG189J21, WORKING DRAFT SEQUENCE, 15 unordered pieces.//8.9e-06:108:83//AC005073
 R-HEMBA1001391//Yeast mitochondrial aspl gene for ATPase subunit 8.//7.3e-08:500:59//X00960
 R-HEMBA1001398//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//2.3e-48:315:88//AP000050
 R-HEMBA1001405//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.//5.5e-35:464:68//AL034380
 R-HEMBA1001407
 R-HEMBA1001411//Yeast (S. cerevisiae) mitochondria Ser-tRNA-UCN gene and flanks.//0.00029:301:62//K01981
 R-HEMBA1001413
 R-HEMBA1001415//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 41018, WORKING DRAFT SEQUENCE.//5.6e-101:512:96//AL031732
 R-HEMBA1001432//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//6.3e-37:302:81//AC006146
 R-HEMBA1001433//Human DNA sequence from PAC 339A18 on chromosome X p11.2. Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of S. cerevisiae, DNA binding protein similar to URE-B1, ESTs and STS.//1.9e-32:242:79//Z97054
 R-HEMBA1001435//Homo sapiens chromosome 21, Neurofibromatosis 1 (NF1) related locus, complete sequence.//5.7e-59:457:82//AC004527
 R-HEMBA1001442//Human DNA sequence from PAC 507115 on chromosome X q26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//0.051:276:63//Z98950
 R-HEMBA1001446//HS_3207_A1_A08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3207 Col=15 Row=A, genomic survey sequence.//8.9e-06:119:73//AQ175385
 R-HEMBA1001450//Homo sapiens BAC clone RG114B19 from Tq31.1, complete sequence.//0.0043:266:63//AC005065
 R-HEMBA1001454//Homo sapiens PAC clone DJ0673011 from Tq31, complete sequence.//7.1e-25:210:82//AC004855
 R-HEMBA1001455//Homo sapiens chromosome 17, clone hRPK.640_I_15, complete sequence.//2.7e-08:316:62//AC005324
 R-HEMBA1001463//Homo sapiens chromosome 17, clone hRPK.1064_E_11, complete sequence.//0.57:219:60//AC005208
 R-HEMBA1001476//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//9.3e-50:252:80//AC004840
 R-HEMBA1001478
 R-HEMBA1001497
 R-HEMBA1001510//Human HLA class III region containing cAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//3.5e-41:282:86//U89337
 R-HEMBA1001515//Human DNA sequence from PAC 238J17 on chromosome 6 q22. Contains EST and STS.//1.9e-79:529:86//Z98753
 R-HEMBA1001517//Homo sapiens BAC clone RG459N13 from 7p15, complete sequence.//4.3e-18:335:71//AC004549
 R-HEMBA1001522
 R-HEMBA1001526//Human DNA sequence from cosmid 444G9 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs and CpG islands.//5.6e-08:265:67//Z98250
 R-HEMBA1001533//Human DNA sequence from PAC 179M20 on chromosome 2 q012-13.1. Contains adenosine deaminase (ADA), placental protein D iff33, CA repeat, ESTs, STS.//7.8e-16:235:72//Z97053
 R-HEMBA1001557
 R-HEMBA1001566//Human Chromosome X clone bWXD187, complete sequence.//2.2e-44:416:78//AC004383
 R-HEMBA1001569//Sequence 15 from patent US 5693476.//1.8e-59:389:88//177040
 R-HEMBA1001570//Homo sapiens PAC clone DJ0844F09 from 7p12-p13, complete sequence.//1.1e-44:316:87//AC004453
 R-HEMBA1001579//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.0047:437:60//AC005506

【0779】

【表479】

R-HEMBA1001581//P. falciparum complete gene map of plastid-like DNA (IR-B). //2.3e-07:491:58//X95276	t KIAA0500. //2.8e-112:548:98//AB007969
R-HEMBA1001585//Caenorhabditis elegans cosmid C06A6. //0.68:224:62//U41012	R-HEMBA1001809
R-HEMBA1001589	R-HEMBA1001815//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC Library) complete sequence. //2.6e-48:363:84//AC004025
R-HEMBA1001595//CIT-HSP-2349G19. TF CIT-HSP Homo sapiens genomic clone 2349G19, genomic survey sequence. //8.0e-69:337:99//AQ060483	R-HEMBA1001819//Homo sapiens *** SEQUENCING IN PROGRESS *** from P AC 1577, WORKING DRAFT SEQUENCE. //1.1e-15:275:68//AJ009612
R-HEMBA1001608//Homo sapiens chromosome 17, clone HC17462L7, complete sequence. //9.5e-59:514:78//AC005177	R-HEMBA1001820//HS_3022_B1_A09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3022 Col=17 Row=B, genomic survey sequence. //0.00054:335:59//AQ165107
R-HEMBA1001620//S. polyrrhiza mRNA for D-myo-inositol-3-phosphate synthase. //4.5e-12:289:65//Z11693	R-HEMBA1001822//Xenopus laevis intersectin mRNA, complete cds. //1.4e-19:533:63//AF032118
R-HEMBA1001635//HS_2195_A1_E09_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=17 Row=I, genomic survey sequence. //5.8e-09:358:58//AQ292688	R-HEMBA1001824//S. clavuligerus linear plasmid pSCL (complete sequence). //0.62:189:65//X54107
R-HEMBA1001636//Human putative potassium channel subunit (h-erg) mRNA, complete cds. //0.77:225:59//U04270	R-HEMBA1001835//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191J18, WORKING DRAFT SEQUENCE. //1.0:450:60//AL024507
R-HEMBA1001640//Human DNA sequence from PAC 50J22 on chromosome 5p21. Contains ETS related protein TEL like and GS2 like genes. ESTs and an STS. //6.0e-49:404:79//Z84484	R-HEMBA1001844//Human familial Alzheimer's disease (STM2) gene, complete cds. //1.6e-07:170:68//U050871
R-HEMBA1001651	R-HEMBA1001847
R-HEMBA1001655//Homo sapiens chromosome 5, BAC clone 194J18 (LBNL H158), complete sequence. //1.1e-103:532:95//AC005368	R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete cds. //3.3e-108:553:96//AB014517
R-HEMBA1001658//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE. //1.0:197:64//AL023808	R-HEMBA1001864//Homo sapiens genomic DNA, 21q22.1 region, clone: Q 82F5A16, genomic survey sequence. //1.7e-14:245:67//AG002463
R-HEMBA1001661//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence. //1.5e-100:457:93//AC005740	R-HEMBA1001866//HS_2258_B2_D01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2258 Col=2 Row=H, genomic survey sequence. //2.8e-39:397:75//AQ221138
R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MB03 (MBD3) mRNA, complete cds. //1.2e-90:496:91//AF072247	R-HEMBA1001869//Homo sapiens BAC clone RG114819 from 7q31.1, complete sequence. //5.9e-56:303:94//AC005065
R-HEMBA1001675	R-HEMBA1001888//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence. //1.7e-43:281:88//AC006210
R-HEMBA1001678//Homo sapiens voltage dependent anion channel protein mRNA, complete cds. //1.3e-101:534:94//AF038962	R-HEMBA1001896
R-HEMBA1001681//CIT-HSP-2345M7. TF CIT-HSP Homo sapiens genomic clone 2345M7, genomic survey sequence. //0.21:124:68//AQ056593	R-HEMBA1001910
R-HEMBA1001702//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence. //8.3e-06:279:63//AC004801	R-HEMBA1001912//Homo sapiens chromosome 5, P1 clone 1308e5 (LBNL H13), complete sequence. //0.10:307:61//AC004775
R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein, complete cds. //1.9e-96:483:96//AB014598	R-HEMBA1001913
R-HEMBA1001711//Human HepG2 3' region cDNA, clone hmd2b02. //2.3e-31:169:100//D16886	R-HEMBA1001915//HS_2037_A1_E12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037 Col=23 Row=I, genomic survey sequence. //0.071:206:64//AQ233106
R-HEMBA1001712//HS-1015-B1-E01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 790 Col=1 Row=J, genomic survey sequence. //0.0025:200:65//B32577	R-HEMBA1001918//Homo sapiens chromosome 5, P1 clone 1308e5 (LBNL H13), complete sequence. //0.97:449:59//AC004775
R-HEMBA1001714//Rattus norvegicus mitochondrial ATPase inhibitor gene, complete cds. //6.6e-27:316:75//U12250	R-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds. //2.0e-105:534:96//AF000145
R-HEMBA1001718//CIT-HSP-2171J2. TR CIT-HSP Homo sapiens genomic clone 2171J2, genomic survey sequence. //3.1e-41:167:87//B89781	R-HEMBA1001939//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 508115, WORKING DRAFT SEQUENCE. //4.6e-13:120:82//AL021707
R-HEMBA1001723//Rattus norvegicus EH domain binding protein Epsin mRNA, complete cds. //0.53:275:61//AF018261	R-HEMBA1001940//Homo sapiens clone DJ1093116, WORKING DRAFT SEQUENCE. 5 unordered pieces. //2.2e-36:301:81//AC005629
R-HEMBA1001731//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 322P7, WORKING DRAFT SEQUENCE. //2.9e-48:292:84//AL023799	R-HEMBA1001942//Human PAC clone DJ0205E24 from 2q23, complete sequence. //1.9e-10:208:68//AC003013
R-HEMBA1001734//Homo sapiens Chromosome 15q22.3-23 PAC 88m3, WORKING DRAFT SEQUENCE, 2 ordered pieces. //3.2e-33:290:81//AC005959	R-HEMBA1001945//Plasmodium falciparum chromosome 2, section 70 of 73 of the complete sequence. //1.2e-06:393:60//AE001433
R-HEMBA1001744//Human DNA sequence from clone 134E15 on chromosome 6q21 Contains Blimp-1, apoptosis specific protein similar to yeast APC5 ESTs, GSSs and retroviral sequence, complete sequence. //0.98:203:62//AL022067	R-HEMBA1001950//R. prowazekii genomic DNA fragment (clone A437R). //0.33:122:66//Z82646
R-HEMBA1001745//Homo sapiens BAC clone RG298C08 from 7p15-p21, complete sequence. //0.00019:312:59//AC005084	R-HEMBA1001960//Borrelia afzelii V4S61 outer surface protein D (ospD) gene, complete cds. //0.0086:427:59//U05329
R-HEMBA1001746//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces. //0.045:457:61//AC004153	R-HEMBA1001962//Homo sapiens chromosome 4 clone 871M12 map 4q25, complete sequence. //4.5e-07:176:70//AC004069
R-HEMBA1001761//Homo sapiens chromosome X, clone hCIT.200_L_4, complete sequence. //3.8e-39:331:80//AC006121	R-HEMBA1001964//HS_2215_B1_H01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2215 Col=1 Row=P, genomic survey sequence. //7.3e-25:215:74//AQ151931
R-HEMBA1001781//Homo sapiens Xp22 BAC GSHB-590J6 (Genome Systems Human BAC Library) complete sequence. //0.0062:245:60//AC004554	R-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (presumptive isoform of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and GSSs, complete sequence. //1.7e-51:209:95//AL031178
R-HEMBA1001784//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence. //2.1e-22:370:63//AC005740	R-HEMBA1001979//CIT-HSP-2387I12. TF.1 CIT-HSP Homo sapiens genomic clone 2387I12, genomic survey sequence. //4.9e-06:153:71//AQ240461
R-HEMBA1001791//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence. //3.0e-50:408:80//AL023575	R-HEMBA1001987//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence. //3.1e-46:437:77//AL033521
R-HEMBA1001800//CIT-HFP-2049N5. TF CIT-HSP Homo sapiens genomic clone 2049N5, genomic survey sequence. //9.0e-37:335:77//AQ009222	R-HEMBA1001991//Human DNA sequence from PAC 42616 on chromosome 1p34.1-p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat. //1.1e-48:446:78//AL020997
R-HEMBA1001803//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces. //0.86:536:56//AC005506	R-HEMBA1002003//Homo sapiens mRNA for protein phosphatase 2C (beta). //5.1e-90:448:97//AJ005801
R-HEMBA1001804//Mouse interleukin 2 receptor (p55 IL-2R) mRNA, 5' end. //2.9e-93:553:89//M21977	R-HEMBA1002008//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and GTC repeat polymorphisms, complete sequence. //3.2e-42:317:84//Z97181
R-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript	R-HEMBA1002018//HS_3006_B1_D10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3006 Col=19 Row=H, genomic

【0780】

【表480】

omic survey sequence.//1.0:63:74//AQ089717
 R-HEMBA1002022//Homo sapiens chromosome 18, clone hRPK.453_M_1, complete sequence.//0.93:339:59//AC006203
 R-HEMBA1002035//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//1.4e-11:285:67//AC003694
 R-HEMBA1002039
 R-HEMBA1002049//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 117715, WORKING DRAFT SEQUENCE.//5.3e-52:266:84//AL022315
 R-HEMBA1002084//CIT-HSP-2357L11.TR CIT-HSP Homo sapiens genomic clone 2357L11, genomic survey sequence.//0.0013:185:66//AQ063078
 R-HEMBA1002092//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//2.7e-70:479:86//U92703
 R-HEMBA1002100//Homo sapiens thyroid receptor interactor (TRIP7) mRNA, 3' end of cds.//8.5e-32:206:91//L40357
 R-HEMBA1002102//Homo sapiens Chromosome 15q26.1 PAC clone pDJ427d15, complete sequence.//4.3e-42:302:85//AC005800
 R-HEMBA1002113//Human chromosome 12p13 sequence, complete sequence.//1.6e-64:550:80//U47924
 R-HEMBA1002119//Human Chromosome 11 pac pDJ1173a5, complete sequence.//1.2e-92:435:92//AC000378
 R-HEMBA1002125
 R-HEMBA1002139//Human nebulin mRNA, partial cds.//0.056:68:88//U35637
 R-HEMBA1002144//Homo sapiens Chromosome 11p14.3 PAC clone 6-130a9 containing tryptophan hydroxylase gene, complete sequence.//2.0e-26:323:70//AC005728
 R-HEMBA1002150//Human DNA sequence from clone 742C19 on chromosome 22q12.3-13.1. Contains a pseudogene similar to Cytochrome C Oxidase Polypeptide YB and (parts of) up to four novel genes, two with homology to Phorbolins and one a novel Chromobox protein gene. Contains ESTs, an STS, GSSs and putative CpG islands, complete sequence.//1.0:371:61//AL031846
 R-HEMBA1002151
 R-HEMBA1002153//Human BAC 367D17 from chromosome 18, complete sequence.//2.4e-21:322:70//AC003971
 R-HEMBA1002160//Human DNA sequence from PAC 339A18 on chromosome Xp11.2. Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of S.cerevisiae, DNA binding protein similar to URE-B1, ESTs and STS.//2.5e-38:216:84//Z97054
 R-HEMBA1002161//CIT-HSP-2163F10.TF CIT-HSP Homo sapiens genomic clone 2163F10, genomic survey sequence.//3.1e-58:284:80//B89969
 R-HEMBA1002162//Caenorhabditis elegans cosmid F48C11, complete sequence.//0.0079:286:57//Z80789
 R-HEMBA1002166//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//5.9e-53:326:80//AC002980
 R-HEMBA1002177
 R-HEMBA1002185//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 745114, WORKING DRAFT SEQUENCE.//9.5e-37:356:76//AL033532
 R-HEMBA1002189//Homo sapiens Xp22 BAC GSHB-519E5 (Genome Systems Human BAC library) complete sequence.//3.4e-43:244:77//AC003684
 R-HEMBA1002191//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE. 2 unordered pieces.//4.3e-37:323:78//AC005077
 R-HEMBA1002199//Human cosmid g5129g124 from 7q31.3, complete sequence.//1.4e-89:564:87//AC002498
 R-HEMBA1002204//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGLC Region, complete sequence.//1.5e-31:313:71//AC000053
 R-HEMBA1002212//K.lactis mitochondrial COX1 and A8 genes for cytochrome oxidase subunit I and ATPase subunit 8.//0.0023:346:60//X57546
 R-HEMBA1002215//M.musculus mRNA for testin.//4.7e-61:414:84//X78989
 R-HEMBA1002226//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 2705, WORKING DRAFT SEQUENCE.//4.6e-46:375:77//AL033529
 R-HEMBA1002229//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//4.6e-46:238:98//AF089814
 R-HEMBA1002237//Homo sapiens 12q13 PAC RPC11-316M24 (Roswell Park Cancer Institute Human PAC library) complete sequence.//4.3e-25:469:67//AC004242
 R-HEMBA1002253//Homo sapiens BAC clone GS180J15 from 7q31, complete sequence.//5.1e-23:162:82//AC005016
 R-HEMBA1002257
 R-HEMBA1002267//Equus caballus dermatan sulfate proteoglycan II mRNA, complete cds.//4.6e-44:300:88//AF038127
 R-HEMBA1002270//Human BAC clone RG067M09 from 7q21-7q22, complete sequence.//1.9e-19:176:85//AC000057
 R-HEMBA1002321
 R-HEMBA1002326//HS_3061_A1_D06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3061 Col=11 Row=G, gen

omic survey sequence.//1.0:151:65//AQ127617
 R-HEMBA1002337//Saccharomyces cerevisiae RNA polymerase II holoenzyme component (SRB7) gene, complete cds.//3.7e-07:328:63//U23811
 R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds.//2.4e-128:642:96//AB018314
 R-HEMBA1002348//Human DNA sequence from clone 409010 on chromosome 20q12 Contains CA repeat, GSS, STS, complete sequence.//3.7e-07:587:58//AL031256
 R-HEMBA1002349//Leishmania tarentolae maxicircle DNA fragment.//0.018:341:58//X02438
 R-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//1.2e-121:561:93//AF092563
 R-HEMBA1002381//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 11/11.//1.1e-70:559:79//AB020868
 R-HEMBA1002389//HS_3218_B2_E08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=16 Row=J, genomic survey sequence.//0.0011:122:72//AQ213602
 R-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784, complete sequence.//4.2e-81:232:97//AC005954
 R-HEMBA1002419//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence.//0.50:231:64//AC004848
 R-HEMBA1002430//P.falciiparum complete gene map of plastid-like DNA (IR-B).//0.0023:604:56//X95276
 R-HEMBA1002439//Homo sapiens clone GS096J14, WORKING DRAFT SEQUENCE. 3 unordered pieces.//3.4e-23:183:80//AC006026
 R-HEMBA1002458//Human DNA sequence from clone 146H21 on chromosome Xq22 Contains cleavage stimulation factor, 64 KD subunit, gene similar to CYTOCHROME B-245 HEAVY CHAIN, pseudogene similar to hnRNP A1 protein and ESTs, complete sequence.//7.7e-32:161:83//Z83819
 R-HEMBA1002460//Homo sapiens clone DJ1137M13, complete sequence.//2.6e-100:305:100//AC005378
 R-HEMBA1002462//Sequence 43 from patent US 5708157.//2.0e-10:131:77//I80068
 R-HEMBA1002475
 R-HEMBA1002477//Homo sapiens PAC clone DJ0607J23 from 7q21.2-q31.1, complete sequence.//6.6e-33:279:80//AC004841
 R-HEMBA1002486//***ALU WARNING: Human Alu-Sq subfamily consensus sequence.//2.1e-50:290:92//U14573
 R-HEMBA1002495//CITBI-E1-251S110.TR CITBI-E1 Homo sapiens genomic clone 251S110, genomic survey sequence.//1.0:122:68//AQ261762
 R-HEMBA1002498//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE. 15 unordered pieces.//2.8e-22:210:78//AC004963
 R-HEMBA1002503//Homo sapiens chromosome 17, clone HRP1067M6, complete sequence.//2.7e-17:435:58//AC003043
 R-HEMBA1002508//Homo sapiens, clone hRPK.15_A_1, complete sequence.//3.7e-09:408:61//AC006213
 R-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//7.1e-112:456:92//AJ011972
 R-HEMBA1002515
 R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 protein, partial cds.//1.6e-104:564:93//AB007923
 R-HEMBA1002542//HS_3197_B2_B10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3197 Col=20 Row=D, genomic survey sequence.//2.8e-25:186:86//AQ188792
 R-HEMBA1002547//Mus musculus agrin gene, exon 36.//0.0095:93:75//M92658
 R-HEMBA1002552//Homo sapiens clone DJ1137M13, complete sequence.//4.0e-49:308:90//AC005378
 R-HEMBA1002555//Homo sapiens full length insert cDNA clone YR87G10.//8.3e-65:318:99//AF085957
 R-HEMBA1002558//, complete sequence.//2.3e-38:264:89//AC005409
 R-HEMBA1002561//Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence.//7.1e-44:192:80//AL008634
 R-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds.//4.5e-119:587:97//AF075587
 R-HEMBA1002583
 R-HEMBA1002590//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//9.4e-42:248:88//Z95152
 R-HEMBA1002592//Homo sapiens chromosome 19, cosmid R30385, complete sequence.//2.6e-56:302:84//AC004510
 R-HEMBA1002621
 R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds.//6.7e-76:380:97//AB018351
 R-HEMBA1002628//P.falciiparum complete gene map of plastid-like DNA

【0781】

【表481】

(IR-A).//8.8e-05:327:60//X95275
R-HEMBA1002629//Mus musculus clone OST16705, genomic survey sequence.//4.3e-06:205:66//AF046247
R-HEMBA1002645//***ALU WARNING: Human Alu-J subfamily consensus sequence.//7.1e-39:281:84//U14567
R-HEMBA1002651//Homo sapiens PAC clone DJ0593H12 from 7p31, complete sequence.//1.1e-104:500:95//AC004839
R-HEMBA1002659//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//1.2e-61:280:92//AL022323
R-HEMBA1002661//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 225E12, WORKING DRAFT SEQUENCE.//3.2e-41:325:81//AL031772
R-HEMBA1002665//Homo sapiens full length insert cDNA clone YY74A07.//0.00037:79:84//AF088008
R-HEMBA1002678//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1137F22, WORKING DRAFT SEQUENCE.//2.3e-107:561:94//AL034421
R-HEMBA1002679//CIT-HSP-2287E8, TF CIT-HSP Homo sapiens genomic clone 2287E8, genomic survey sequence.//5.4e-17:137:88//B99281
R-HEMBA1002688//Homo sapiens chromosome 5, P1 clone 1354A7 (LBNI H47), complete sequence.//0.033:146:70//AC004503
R-HEMBA1002696
R-HEMBA1002712//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//6.2e-44:302:87//AC003982
R-HEMBA1002716//Mus musculus mRNA for ELM1, complete cds.//1.1e-31:332:76//AB004873
R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds.//1.2e-35:287:81//AB014521
R-HEMBA1002730//D.discoideum actin M6 gene, 5' flank.//0.018:233:66//M29109
R-HEMBA1002742//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1108H3, WORKING DRAFT SEQUENCE.//2.6e-13:419:62//AL033525
R-HEMBA1002746//Mus musculus chromosome 19, clone CIT282B21, complete sequence.//0.019:202:65//AC003694
R-HEMBA1002748//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 404K8, WORKING DRAFT SEQUENCE.//0.046:263:60//AL023883
R-HEMBA1002750//Human DNA sequence from PAC 452H17 on chromosome X contains sodium- and chloride-dependent glycine transporter 1 (GLYT-1) like, ESTs.//0.052:421:58//Z96810
R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds.//1.2e-104:545:95//AB011126
R-HEMBA1002770//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//3.0e-07:523:59//AC005140
R-HEMBA1002777
R-HEMBA1002779//Human HepG2 3' region Mbol cDNA, clone hmdle03m3.//9.4e-25:158:93//D17139
R-HEMBA1002780//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y214H10, WORKING DRAFT SEQUENCE.//1.6e-42:463:75//AL022344
R-HEMBA1002794//Plasmodium falciparum MAL3P8, complete sequence.//2.2e-05:417:59//AL034560
R-HEMBA1002801//Meloidogyne javanica mitochondrial transfer RNA His, 16S ribosomal RNA (16S rRNA) genes, ND3 gene, complete cds, and cytochrome b gene, 5' end of CDS.//0.00055:444:59//L76261
R-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds.//4.4e-115:559:97//AF071185
R-HEMBA1002816//Homo sapiens clone NH0576N21, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.3e-88:329:94//AC005043
R-HEMBA1002826//Homo sapiens genomic DNA, chromosome 21q11.1, segment 12/28, WORKING DRAFT SEQUENCE.//1.9e-22:262:67//AP000041
R-HEMBA1002833//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence.//1.3e-79:396:97//AC004707
R-HEMBA1002850//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.013:393:61//AC005506
R-HEMBA1002863//Homo sapiens chromosome 17, clone hRPC.271_K_11, complete sequence.//4.1e-73:489:85//AC005562
R-HEMBA1002876//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//0.21:549:55//AL034557
R-HEMBA1002886//CIT-HSP-2013C4, TR CIT-HSP Homo sapiens genomic clone 2013C4, genomic survey sequence.//0.30:431:56//B53836
R-HEMBA1002896//Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds.//3.9e-106:541:95//AF037261
R-HEMBA1002921
R-HEMBA1002924//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 7/10.//4.6e-19:139:78//AB020875
R-HEMBA1002934//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE.//7.5e-45:282:89//AL031681
R-HEMBA1002935//CIT-HSP-2282P14, TFB CIT-HSP Homo sapiens genomic clone 2282P14, genomic survey sequence.//1.5e-102:514:97//AQ008584
R-HEMBA1002937//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 745114, WORKING DRAFT SEQUENCE.//3.3e-87:444:97//AL033532
R-HEMBA1002939
R-HEMBA1002944//HS_3107_A1_C05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3107 Col=9 Row=E, genomic survey sequence.//6.3e-21:250:73//AQ103952
R-HEMBA1002951//Xarolycosa miniata mitochondrial 12S rRNA gene.//0.013:228:63//AJ008020
R-HEMBA1002954//HS_3246_A2_G09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3246 Col=18 Row=M, genomic survey sequence.//5.8e-42:258:91//AQ218005
R-HEMBA1002968//Homo sapiens chromosome 17, clone hRPC.112_J_9, complete sequence.//4.2e-38:300:83//AC005553
R-HEMBA1002970//Slime mold (D. discoideum) prestalk D11 gene, complete cds.//5.0e-05:541:57//M11012
R-HEMBA1002971//Homo sapiens mRNA for KIAA0679 protein, partial cds.//7.2e-29:162:99//AB014579
R-HEMBA1002973//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//9.1e-36:520:69//AC006128
R-HEMBA1002997//Homo Sapiens Chromosome X clone bWXD691, complete sequence.//0.00040:504:59//AC004386
R-HEMBA1002999//Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//3.7e-66:556:79//U19614
R-HEMBA1003021//Human Chromosome 11 overlapping pacs pDJ235k10 and pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//1.6e-44:530:70//AC000406
R-HEMBA1003033//Homo sapiens full length insert cDNA clone ZC34B10.//4.6e-78:414:94//AF086194
R-HEMBA1003034//Homo sapiens chromosome 19, cosmid R29351, complete sequence.//9.0e-52:322:75//AC004026
R-HEMBA1003035//HS_2008_A2_G08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2008 Col=16 Row=M, genomic survey sequence.//4.0e-68:343:97//AQ269839
R-HEMBA1003037//347G15, TVB CIT978SKA1 Homo sapiens genomic clone A-347G15, genomic survey sequence.//0.57:188:58//B17694
R-HEMBA1003041//Homo sapiens PAC clone DJ1163J12 from 7q21.2-q31.1, complete sequence.//6.3e-30:350:72//AC004983
R-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds.//4.1e-118:578:97//AF054182
R-HEMBA1003064//Human cosmid LL12NC01-N-136B11, located centromeric to the ETV6 gene, chromosome 12p12-13.//0.0018:271:60//U59962
R-HEMBA1003067//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 633019, WORKING DRAFT SEQUENCE.//5.3e-48:464:76//AL022302
R-HEMBA1003071//CIT-HSP-2370D6, TR CIT-HSP Homo sapiens genomic clone 2370D6, genomic survey sequence.//0.19:48:87//AQ10136
R-HEMBA1003077//Rattus norvegicus Shal-related potassium channel K v4.3 mRNA, complete cds.//4.9e-69:494:84//U42975
R-HEMBA1003078//Human DNA sequence from PAC 339A18 on chromosome X p11.2. Contains KIAA0178 gene, similar to mitosis-specific chromosome segregation protein SMC1 of S. cerevisiae, DNA binding protein similar to URE-B1, ESTs and STS.//1.1e-11:331:64//Z97054
R-HEMBA1003079//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//4.6e-116:576:98//AC004673
R-HEMBA1003083//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone CD442P12: HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.1e-43:280:83//AC005798
R-HEMBA1003086//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.2e-43:281:88//AC006039
R-HEMBA1003096//Human DNA sequence from clone JS06G21, WORKING DRAFT SEQUENCE.//0.00037:421:59//Z82213
R-HEMBA1003098//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0024K08: HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.4e-30:303:78//AC005598
R-HEMBA1003117
R-HEMBA1003129//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 407F11, WORKING DRAFT SEQUENCE.//7.9e-11:109:85//AL022329
R-HEMBA1003133//Homo sapiens chromosome 9, P1 clone 11659, complete sequence.//3.9e-98:484:98//AC004472
R-HEMBA1003136//CIT-HSP-2281L22, TF CIT-HSP Homo sapiens genomic clone 2281L22, genomic survey sequence.//2.0e-10:93:92//B99861
R-HEMBA1003142//Homo sapiens 12q24.2 PAC RPC11-128M12 (Roswell Park Cancer Institute Human PAC library) complete sequence.//9.8e-40:

【0782】

【表482】

270:87//AC004024
R-HEMBA1003148//Homo sapiens mRNA for dachshund protein.//1.1e-11
6:586:96//AJ005670
R-HEMBA1003166//Human DNA sequence from PAC 306D1 on chromosome X
contains ESTs.//6.4e-35:364:70//Z83822
R-HEMBA1003175//Human IFNAR gene for interferon alpha/beta recepto
r.//1.9e-30:282:77//X60459
R-HEMBA1003197
R-HEMBA1003199//HS_2166_A1_E12_MR CIT Approved Human Genomic Sperm
Library D Homo sapiens genomic clone Plate=2166 Col=23 Row=1, gen
omic survey sequence.//0.00026:271:61//AQ164162
R-HEMBA1003202//Homo sapiens clone DJ0592G07, WORKING DRAFT SEQUEN
CE, 3 unordered pieces.//5.4e-44:291:83//AC005480
R-HEMBA1003204//Human BAC clone RG072E11 from 7q21-q22, complete
sequence.//3.1e-10:293:62//AC000118
R-HEMBA1003212//Homo sapiens clone DJ0902E20, WORKING DRAFT SEQUEN
CE, 1 unordered pieces.//1.0:118:69//AC006148
R-HEMBA1003220//HS_3092_B1_F09_MR CIT Approved Human Genomic Sperm
Library D Homo sapiens genomic clone Plate=3092 Col=17 Row=L, gen
omic survey sequence.//0.00014:59:91//AQ128202
R-HEMBA1003222//Caenorhabditis elegans DNA *** SEQUENCING IN PROGR
ESS *** from clone Y43F8, WORKING DRAFT SEQUENCE.//0.84:214:62//Z9
5393
R-HEMBA1003229//RPC111-16F15.TPB RPC111 Homo sapiens genomic clon
e RPC111-16F15, genomic survey sequence.//0.42:167:64//B83610
R-HEMBA1003235//CIT-HSP-2320G19.TF CIT-HSP Homo sapiens genomic cl
one 2320G19, genomic survey sequence.//3.6e-36:195:81//AQ037231
R-HEMBA1003250//HS_2168_A2_C09_MR CIT Approved Human Genomic Sperm
Library D Homo sapiens genomic clone Plate=2168 Col=18 Row=E, gen
omic survey sequence.//1.4e-22:158:89//AQ125356
R-HEMBA1003257//Human PCP4 gene, exon 3 and complete cds.//0.96:26
8:61//U53709
R-HEMBA1003273//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Hu
man BAC library) complete sequence.//1.0e-32:255:84//AC002549
R-HEMBA1003276//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 g
enomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00
44:212:60//AC005308
R-HEMBA1003278//Homo sapiens 12q24.1 PAC RPC111-315L5 (Roswell Park
Cancer Institute Human PAC library) complete sequence.//1.1e-34:2
86:74//AC002395
R-HEMBA1003281//High throughput sequencing of human chromosome 12.
WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.8e-53:428:83//AC0058
40
R-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete c
ds.//3.0e-115:551:99//AB011109
R-HEMBA1003296//CIT-HSP-2196L16.TR CIT-HSP Homo sapiens genomic cl
one 2196L16, genomic survey sequence.//2.9e-20:337:65//AQ003073
R-HEMBA1003304//Sequence 23 from patent US 5552281.//1.8e-31:179:9
7//125662
R-HEMBA1003309//Arabidopsis thaliana genomic DNA, chromosome 5, TA
C clone: K19E20, complete sequence.//0.00019:334:60//AB017061
R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinas
e, complete cds.//2.8e-111:545:97//AB001872
R-HEMBA1003322//Human DNA sequence from clone 23K20 on chromosome
Xq25-26.2 Contains EST, STS, GSS, complete sequence.//0.60:274:61/
AL022153
R-HEMBA1003327//Homo sapiens BAC clone RG351J01 from 7q22-q31, com
plete sequence.//0.00028:172:65//AC005099
R-HEMBA1003328//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENC
E, 18 unordered pieces.//2.2e-44:268:90//AC005081
R-HEMBA1003330//Homo sapiens poly(A) binding protein II (PABP2) ge
ne, complete cds.//7.2e-61:312:97//AF026029
R-HEMBA1003348//***ALU WARNING: Human Alu-J subfamily consensus se
quence.//7.2e-38:186:83//U14567
R-HEMBA1003369//Caenorhabditis elegans cosmid F59C6, complete sequ
ence.//0.00012:465:59//Z79600
R-HEMBA1003370//Homo sapiens chromosome 17, clone hRPC867C24, comp
lete sequence.//3.2e-42:301:87//AC002558
R-HEMBA1003373//Human DNA sequence from clone 109F14 on chromosome
6p21.2-21.3. Contains the alternatively spliced gene for Transcri
ptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A ge
ne, a PUTATIVE ZNF127 LIKE gene, and the PPAR for Peroxisome Prol
iferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear
Hormone Receptor 1, NUC1, NUC1, PPARB). Contains three putative Cp
G islands, ESTs, STSs, GSSs and a ca repeat polymorphism, complete
sequence.//7.4e-34:375:74//AL022721
R-HEMBA1003376//Homo sapiens chromosome 16, cosmid clone RT102 (LA
NL), complete sequence.//1.6e-46:309:88//AC004651
R-HEMBA1003380//HS_3184_B2_E06_MR CIT Approved Human Genomic Sperm
Library D Homo sapiens genomic clone Plate=3184 Col=12 Row=J, gen
omic survey sequence.//1.0e-35:237:88//AQ189144
R-HEMBA1003384//HS_2193_B2_H08_MR CIT Approved Human Genomic Sperm
Library D Homo sapiens genomic clone Plate=2193 Col=16 Row=P, gen
omic survey sequence.//0.00029:96:76//AQ032212
R-HEMBA1003395//Homo sapiens chromosome 17, clone HCIT169H9, WORKI
NG DRAFT SEQUENCE, 6 unordered pieces.//2.6e-21:139:86//AC002993
R-HEMBA1003402//CIT-HSP-2166E19.TR CIT-HSP Homo sapiens genomic cl
one 2166E19, genomic survey sequence.//0.99:144:61//B91549
R-HEMBA1003408
R-HEMBA1003417//Human DNA sequence from clone 496N17 on chromosome
6p11.2-12.3 Contains EST, GSS, complete sequence.//2.5e-112:547:9
8//AL031321
R-HEMBA1003418//Homo sapiens PAC clone DJ0755G17 from 7p21-p22, co
mplete sequence.//0.082:352:59//AC004879
R-HEMBA1003433//Homo sapiens cell cycle regulatory protein p95 (NB
S1) mRNA, complete cds.//9.9e-114:544:98//AF058696
R-HEMBA1003461
R-HEMBA1003463
R-HEMBA1003480//Homo sapiens clone NH0523H20, complete sequence.//
9.1e-106:533:95//AC005041
R-HEMBA1003528
R-HEMBA1003531//Human BAC clone GS552A01 from 7q21-q22, complete s
equence.//3.4e-08:333:64//AC002454
R-HEMBA1003538//Human mRNA for complement component C1r.//1.4e-23:
333:68//X04701
R-HEMBA1003545//Zebrafish mRNA for zfish-2 (insulin gene enhancer
binding protein homolog), complete cds.//0.030:144:68//D38453
R-HEMBA1003548//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 g
enomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00
17:487:57//AC004153
R-HEMBA1003555//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 371H6, WORKING DRAFT SEQUENCE.//2.8e-99:503:96//AL03171
8
R-HEMBA1003556//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome
Systems Human BAC Library) complete sequence.//1.6e-114:574:97//AC
005913
R-HEMBA1003560//Diplolepis rosae microsatellite clone DR04096.//0.
24:116:67//AF034416
R-HEMBA1003568//Homo sapiens clone NH0215P16, WORKING DRAFT SEQUEN
CE, 3 unordered pieces.//3.9e-05:422:63//AC006036
R-HEMBA1003569//Homo sapiens full length insert cDNA clone ZD82D0
6.//8.7e-108:545:95//AF086450
R-HEMBA1003571//Homo sapiens PAC clone DJ0886008 from 7q32-q35, co
mplete sequence.//4.6e-51:570:71//AC004914
R-HEMBA1003579//HS_3237_B2_E05_T7 CIT Approved Human Genomic Sperm
Library D Homo sapiens genomic clone Plate=3237 Col=10 Row=J, gen
omic survey sequence.//8.5e-97:495:95//AQ209302
R-HEMBA1003581//Mouse mRNA for talin.//8.3e-12:128:82//X56123
R-HEMBA1003591//Homo sapiens chromosome 16, BAC clone 2503 (LANL).
complete sequence.//2.9e-87:251:95//AC005774
R-HEMBA1003595//Homo sapiens DNA sequence from BAC 1216H12 on chro
mosome 22q12. Contains a pseudogene with similarity to part of mou
se Ninein and the KIAA0609 gene for a protein similar to C. elegans
XK09C8.4. Contains ESTs, GSSs and a gatt repeat polymorphism, com
plete sequence.//4.5e-52:384:83//AL008715
R-HEMBA1003597//Homo sapiens DNA sequence from PAC 418A9 on chro
some 6q21. Contains the first (5') two exons of a CDK8 (Cell Divis
ion Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogen
e, ESTs and STSs, complete sequence.//4.6e-41:442:74//Z84480
R-HEMBA1003598//Homo sapiens PAC clone DJ0537P09 from 7p11.2-p12,
complete sequence.//1.8e-23:177:88//AC005153
R-HEMBA1003615
R-HEMBA1003617//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 g
enomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.03
9:494:57//AC005139
R-HEMBA1003621//*** SEQUENCING IN PROGRESS *** Homo sapiens chro
some 4, BAC clone CD052122: HTGS phase 1, WORKING DRAFT SEQUENCE,
4 unordered pieces.//2.3e-26:309:75//AC004599
R-HEMBA1003622//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC l
ibrary) complete sequence.//7.1e-56:545:75//AC002980
R-HEMBA1003630//Homo sapiens CC chemokine gene cluster, complete s
equence.//2.8e-32:546:68//AF088219
R-HEMBA1003637//Human BAC clone GS552A01 from 7q21-q22, complete s
equence.//8.0e-25:457:68//AC002454
R-HEMBA1003640//Homo sapiens chromosome X, PAC 671D9, complete seq
uence.//2.8e-40:280:86//AF031078
R-HEMBA1003645//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 32B1, WORKING DRAFT SEQUENCE.//1.7e-33:297:82//AL023693
R-HEMBA1003646//Plasmodium falciparum MAL3P7, complete sequence.//
0.44:319:59//AL034559

【0783】

【表483】

R-HEMBA1003656//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-15 ZES, complete sequence.//6.9e-36:242:80//AC004382

R-HEMBA1003662//Homo sapiens chromosome 17, clone hRPK.332_M_18, complete sequence.//8.6e-117:588:96//AC005746

R-HEMBA1003667//Sequence 8 from patent US 5420245.//1.8e-21:170:88//112222

R-HEMBA1003679//Homo sapiens BAC clone RG114B19 from 7q31.1, complete sequence.//1.6e-22:180:87//AC005065

R-HEMBA1003680//C. elegans cosmid ZK353.//1.1e-06:270:61//L15313

R-HEMBA1003684//Colias alexandra alexandra cytochrome oxidase subunit I (cox1) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.77:171:66//AF044872

R-HEMBA1003690//Homo sapiens 12q13.1 PAC RPC15-1057120 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.6e-104:523:97//AC004466

R-HEMBA1003692//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 508115, WORKING DRAFT SEQUENCE.//1.7e-41:414:77//AL021707

R-HEMBA1003711//Human Chromosome 11 overlapping pacs pJ235k10 and pJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//1.6e-29:304:77//AC000406

R-HEMBA1003714

R-HEMBA1003715//Homo sapiens chromosome 16p11.2 BAC clone CIT987S K-A-68508, WORKING DRAFT SEQUENCE, 16 unordered pieces.//1.4e-63:578:77//AC005136

R-HEMBA1003720//Homo sapiens, WORKING DRAFT SEQUENCE, 135 unordered pieces.//2.4e-36:350:78//AC002353

R-HEMBA1003725//Homo sapiens chromosome 19, cosmid R31973, complete sequence.//6.3e-42:250:75//AC004699

R-HEMBA1003729//RPC111-22D14.TV RPC1-11 Homo sapiens genomic clone RPC1-11-22D14, genomic survey sequence.//1.0:234:62//B86158

R-HEMBA1003733//Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence.//7.7e-80:558:83//AL008634

R-HEMBA1003742//HS_3080_B2_H06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3080 Col=12 Row=P, genomic survey sequence.//3.4e-55:331:91//AQ139179

R-HEMBA1003758//Human DNA sequence from PAC 295C6 on chromosome 1q24. Contains ESTs, CA repeat, STS and CpG island.//4.5e-59:521:75//Z97876

R-HEMBA1003760

R-HEMBA1003773//Mus musculus signal recognition particle receptor beta subunit mRNA, complete cds.//2.6e-72:467:86//U17343

R-HEMBA1003783//Mus musculus bromodomain-containing protein BP75 mRNA, complete cds.//1.0e-77:557:81//AF084259

R-HEMBA1003784

R-HEMBA1003799//Homo sapiens PAC clone DJ1032B10 from 7p15.3-p21, complete sequence.//2.1e-49:390:72//AC004455

R-HEMBA1003803

R-HEMBA1003804//Homo sapiens chromosome 17, clone hCIT.175_E_5, complete sequence.//9.4e-99:359:99//AC004596

R-HEMBA1003805//Human DNA sequence from clone SJ112 on chromosome 6p26-27. Contains the 3' part of the alternatively spliced gene for the human orthologs of mouse KKI-7 and KKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//8.0e-113:567:96//AL031781

R-HEMBA1003807//Bovine dinucleotide microsatellite HJJ1177.//5.4e-18:194:78//W96348

R-HEMBA1003836//Human DNA from overlapping chromosome 19 cosmids R31396, F25451, and R31076 containing COX6B and UPKA, genomic sequence, complete sequence.//3.4e-40:256:85//AC002115

R-HEMBA1003838//CIT-HSP-2380F18.TF CIT-HSP Homo sapiens genomic clone 2380F18, genomic survey sequence.//9.7e-25:150:96//AQ196524

R-HEMBA1003856//Human DNA sequence from clone 272E8 on chromosome Xp22.13-22.31. Contains a pseudogene similar to NDM2-Like P53-binding protein gene. Contains STSs, GSSs and a CA repeat polymorphism, complete sequence.//4.8e-33:486:68//Z93929

R-HEMBA1003864//, complete sequence.//4.4e-100:531:94//AC005300

R-HEMBA1003866//HS_3203_B2_C01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3203 Col=2 Row=F, genomic survey sequence.//2.6e-05:206:64//AQ180298

R-HEMBA1003879//Homo sapiens chromosome 10 clone CIT987SK-1119P3 map 10q25.1, WORKING DRAFT SEQUENCE, 1 ordered pieces.//4.7e-17:170:79//U82207

R-HEMBA1003880//Homo sapiens genomic DNA, chromosome 21q11.1, segment 7/28, WORKING DRAFT SEQUENCE.//7.8e-103:526:96//AP000036

R-HEMBA1003885//Human apolipoprotein apoC-IV (APOC4) gene, complete cds.//3.5e-45:299:87//U32576

R-HEMBA1003893//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1137F22, WORKING DRAFT SEQUENCE.//1.1e-41:386:77//AL034421

R-HEMBA1003902//HS_3031_B2_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3031 Col=14 Row=J, genomic survey sequence.//5.3e-50:293:93//AQ165549

R-HEMBA1003908//CIT-HSP-2367K7.TR CIT-HSP Homo sapiens genomic clone 2367K7, genomic survey sequence.//1.2e-32:220:92//AQ076795

R-HEMBA1003926//Homo sapiens chromosome 5, BAC clone 194j18 (LBNL H158), complete sequence.//3.1e-58:294:85//AC005368

R-HEMBA1003937//Homo sapiens chromosome 3 subtelomeric region.//8.0e-111:590:93//AF109718

R-HEMBA1003939

R-HEMBA1003942//Homo sapiens clone DJ0828F13, complete sequence.//2.2e-08:474:58//AC004904

R-HEMBA1003950//Plasmodium vivax from Brazil cytochrome b (cytb) gene, mitochondrial gene encoding mitochondrial protein, partial cds.//0.034:258:62//AF069619

R-HEMBA1003953//Plasmodium falciparum MAL3P8, complete sequence.//0.095:492:57//AL034560

R-HEMBA1003958//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 64K7, WORKING DRAFT SEQUENCE.//7.3e-40:382:78//AL031668

R-HEMBA1003959//Amaranthus hypochondriacus betaine aldehyde dehydrogenase (ahyd4) gene, complete cds.//0.11:428:60//AF000132

R-HEMBA1003976//Homo sapiens PAC clone DJ0724E13 from 7p11.2-p12, complete sequence.//1.0:222:62//AC004414

R-HEMBA1003978//Sequence 31 from patent US 5708157.//1.9e-14:159:77//180060

R-HEMBA1003985//Homo sapiens 12p13.3 PAC RPC15-927J10 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.6e-14:136:83//AC004804

R-HEMBA1003987//Human chromosome 12p13 sequence, complete sequence.//3.2e-26:268:79//U47924

R-HEMBA1003989//RPC111-52K22.TJ RPC111 Homo sapiens genomic clone R-52K22, genomic survey sequence.//2.2e-86:443:95//AQ052484

R-HEMBA1004000

R-HEMBA1004011

R-HEMBA1004012//Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.//4.7e-38:284:85//AC005670

R-HEMBA1004015//Human DNA sequence from clone 931E15 on chromosome Xq25. Contains STSs, GSSs and genomic marker DXS8098, complete sequence.//0.48:460:58//AL023575

R-HEMBA1004024//Homo sapiens clone RG270D13, WORKING DRAFT SEQUENCE, 18 unordered pieces.//2.5e-21:159:80//AC005081

R-HEMBA1004038//Homo sapiens Xq28 BAC RPC111-382P7 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//7.9e-10:231:66//AC006054

R-HEMBA1004042//Homo sapiens clone DJ0968116, complete sequence.//0.00071:263:68//AC006016

R-HEMBA1004045//Homo sapiens PAC clone DJ0074M20 from X, complete sequence.//8.8e-23:196:69//AC006143

R-HEMBA1004048//CIT-HSP-2288N20.TF CIT-HSP Homo sapiens genomic clone 2288N20, genomic survey sequence.//0.013:162:67//AQ007283

R-HEMBA1004049//Human hsp 70 gene 3' region for 70 kDa heat shock protein.//7.7e-30:176:96//X04677

R-HEMBA1004055//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//8.4e-05:395:63//AC005504

R-HEMBA1004056//Homo sapiens clone DJ0847008, WORKING DRAFT SEQUENCE, 3 unordered pieces.//3.5e-61:551:77//AC005484

R-HEMBA1004074//Homo sapiens clone DJ1032D07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.98:275:63//AC004952

R-HEMBA1004086//Sequence 65 from patent US 5691147.//2.8e-54:313:92//176237

R-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds.//1.1e-11:323:63//AF091234

R-HEMBA1004131//Human mRNA for KIAA0128 gene, partial cds.//9.3e-42:534:69//D50918

R-HEMBA1004132//Homo sapiens chromosome 17, clone hCIT.211_P_7, complete sequence.//6.0e-49:491:76//AC003665

R-HEMBA1004133//HS_3229_B2_E09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3229 Col=18 Row=J, genomic survey sequence.//1.1e-72:374:97//AQ192003

R-HEMBA1004138//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 417W14, WORKING DRAFT SEQUENCE.//3.1e-09:277:66//AL024498

R-HEMBA1004143//Plasmodium falciparum MAL3P4, complete sequence.//0.53:239:61//AL008970

R-HEMBA1004146//Homo sapiens clone DJ0038110, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.0e-35:165:88//AC004820

R-HEMBA1004150//CITBI-E1-251712.TR CITBI-E1 Homo sapiens genomic c

【0784】

【表484】

lone 251712, genomic survey sequence.//0.56:379:59//AQ277616
 R-HEMBA1004164//Human BAC clone GS200K05 from Tq21-q22, complete s
 equence.//4.6e-49:448:77//AC002429
 R-HEMBA1004168//Homo sapiens geminin mRNA, complete cds.//2.4e-11
 0:563:96//AF067855
 R-HEMBA1004199//S.pombe chromosome I cosmid c8A4.//0.73:187:64//Z6
 6569
 R-HEMBA1004200//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems
 Human BAC library) complete sequence.//6.3e-20:293:77//AC004552
 R-HEMBA1004202//rah=ras-related homolog [Mice, HT4 neural cell lin
 e, mRNA, 993 nt].//3.0e-64:517:80//S72304
 R-HEMBA1004203//Homo sapiens clone NH0313P13, WORKING DRAFT SEQUEN
 CE, 15 unordered pieces.//1.0e-97:303:98//AC005488
 R-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA,
 complete cds.//3.6e-116:573:97//U50748
 R-HEMBA1004225//Drosophila melanogaster mitochondrial DNA with 12
 tRNAs and 7 genes.//5.4e-11:493:60//M37275
 R-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, com
 plete cds.//6.1e-76:443:86//AF095927
 R-HEMBA1004238//Homo sapiens chromosome 19, cosmid R28341, complet
 e sequence.//1.1e-42:330:83//AC005763
 R-HEMBA1004241
 R-HEMBA1004246//Homo sapiens genomic DNA, chromosome 21q22.2 (Down
 Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE.//1.1e-45:
 288:85//AF000011
 R-HEMBA1004248//Homo sapiens PAC clone DJ0828B12 from Tq11.23-q21.
 1, complete sequence.//5.2e-09:516:61//AC004903
 R-HEMBA1004264
 R-HEMBA1004267//HS_2255_A2_H12_MR CIT Approved Human Genomic Sperm
 Library D Homo sapiens genomic clone Plate=2255 Col=24 Row=0, gen
 omic survey sequence.//8.6e-59:318:95//AQ068854
 R-HEMBA1004272//Homo sapiens 12p13.3 PAC RPC15-1180D12 (Roswell Pa
 rk Cancer Institute Human PAC Library) complete sequence.//1.1e-11
 3:576:96//AC005831
 R-HEMBA1004275//Homo sapiens clone 617 unknown mRNA, complete sequ
 ence.//4.4e-110:553:96//AF091081
 R-HEMBA1004276
 R-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-
 1 mRNA, complete cds.//1.9e-106:538:97//AF022795
 R-HEMBA1004289//RPC111-74010.TJ RPC111 Homo sapiens genomic clone
 R-74010, genomic survey sequence.//2.3e-37:248:76//AQ266668
 R-HEMBA1004295//Baboon apolipoprotein A-VI mRNA, 3' end.//0.0016:2
 73:64//J13174
 R-HEMBA1004306//HS_3175_B2_F01_T7 CIT Approved Human Genomic Sperm
 Library D Homo sapiens genomic clone Plate=3175 Col=2 Row=L, geno
 mic survey sequence.//1.6e-28:190:77//AQ169206
 R-HEMBA1004312//Human BAC clone RG119P24 from Tq31, complete seque
 nce.//6.3e-36:267:82//AC003088
 R-HEMBA1004321//Homo sapiens *** SEQUENCING IN PROGRESS *** from P
 AC 10155, WORKING DRAFT SEQUENCE.//4.1e-111:576:95//AJ009611
 R-HEMBA1004323//CIT-HSP-2374C8.TR CIT-HSP Homo sapiens genomic clo
 ne 2374C8, genomic survey sequence.//2.7e-42:136:91//AQ114933
 R-HEMBA1004327//CIT-HSP-2303L24.TF CIT-HSP Homo sapiens genomic cl
 one 2303L24, genomic survey sequence.//1.0:78:67//AQ017600
 R-HEMBA1004330//Homo sapiens clone DJ1173120, WORKING DRAFT SEQUEN
 CE, 5 unordered pieces.//2.3e-119:580:98//AC004987
 R-HEMBA1004334//Pimpinella brachycarpa Phyl mRNA, complete cds.//
 3.3e-14:238:69//AF082024
 R-HEMBA1004335//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-11
 6A10, complete sequence.//1.8e-21:291:71//AC004638
 R-HEMBA1004341
 R-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, compl
 ete cds.//4.1e-74:444:90//D89667
 R-HEMBA1004354//Human DNA from overlapping chromosome 19-specific
 cosmids R29515 and R28253, genomic sequence, complete sequence.//
 7.0e-38:287:82//AC003002
 R-HEMBA1004356//Sequence 2 from patent US 5652144.//3.7e-108:588:9
 2//158611
 R-HEMBA1004366//WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-
 14:446:63//AC005949
 R-HEMBA1004372//CIT-HSP-2805C13.TF CIT-HSP Homo sapiens genomic cl
 one 2805C13, genomic survey sequence.//0.010:334:61//B55811
 R-HEMBA1004389//Homo sapiens full length insert cDNA clone ZE09A1
 1.//1.5e-19:170:83//AF086540
 R-HEMBA1004394//Human (D21S198) DNA segment containing (TG)23 repe
 at.//1.0:50:84//X58124
 R-HEMBA1004396//Homo sapiens chromosome 4 clone B24Q9N map 4q25, c
 omplete sequence.//8.2e-34:459:69//AC004057
 R-HEMBA1004405//Homo sapiens BAC clone GS589P19 from 7p13-p14, com
 plete sequence.//2.8e-42:314:84//AC005030
 R-HEMBA1004408
 R-HEMBA1004429//M.musculus of DNA encoding DNA-binding protein.//
 1.6e-66:449:82//Z54200
 R-HEMBA1004433//Homo sapiens chromosome 21q22.3, PAC clones 314N7,
 225L15, BAC clone 7B7, complete sequence bases 1..333303.//7.2e-3
 2:460:68//AJ011930
 R-HEMBA1004460//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUEN
 CE, 21 unordered pieces.//3.9e-113:581:96//AC004846
 R-HEMBA1004461//HS_3244_A2_F12_MR CIT Approved Human Genomic Sperm
 Library D Homo sapiens genomic clone Plate=3244 Col=24 Row=K, gen
 omic survey sequence.//8.0e-83:397:99//AQ220876
 R-HEMBA1004479//Homo sapiens PAC clone DJ0942116 from Tq11, comple
 te sequence.//1.7e-40:485:70//AC006012
 R-HEMBA1004482//Plasmodium falciparum chromosome 2, section 7 of 7
 3 of the complete sequence.//2.2e-11:513:59//AE001370
 R-HEMBA1004502//Homo sapiens chromosome 17, clone hRPK.372_K_20, c
 omplete sequence.//2.0e-08:245:66//AC005951
 R-HEMBA1004506//Human DNA sequence *** SEQUENCING IN PROGRESS ***
 from clone 34606, WORKING DRAFT SEQUENCE.//4.2e-81:582:83//Z84487
 R-HEMBA1004507//Caenorhabditis elegans cosmid C4DC9, complete sequ
 ence.//0.56:235:64//Z70266
 R-HEMBA1004509
 R-HEMBA1004534//Sequence 58 from patent US 5691147.//1.9e-61:430:8
 3//176230
 R-HEMBA1004538//HS_3189_B2_C03_T7 CIT Approved Human Genomic Sperm
 Library D Homo sapiens genomic clone Plate=3189 Col=6 Row=F, geno
 mic survey sequence.//6.1e-21:140:92//AQ170330
 R-HEMBA1004554//CIT-HSP-712K9.TP CIT-HSP Homo sapiens genomic clon
 e 712K9, genomic survey sequence.//1.7e-16:116:93//B73329
 R-HEMBA1004560//Human mRNA for KIAA0281 gene, complete cds.//2.2e-
 14:213:71//D87457
 R-HEMBA1004573
 R-HEMBA1004577//Human DNA sequence from cosmid L247F6, Huntington's
 Disease Region, chromosome 4p16.3 contains protein similar to Mo
 use SH3 binding protein 3BP2, multiple ESTs and a CpG island.//1.
 0:352:60//Z68279
 R-HEMBA1004586
 R-HEMBA1004596//Plasmodium falciparum MAL3P6, complete sequence.//
 0.0012:359:60//Z98551
 R-HEMBA1004610//S.pombe chromosome II cosmid c354.//0.0011:362:62/
 AL022071
 R-HEMBA1004617//Homo sapiens mRNA, chromosome I specific transcrip
 t KIAA0501.//1.4e-50:327:85//ABD07970
 R-HEMBA1004629//Homo sapiens Xp22 bins 16-17 BAC GSHB-531117 (Geno
 me Systems Human BAC Library) complete sequence.//4.4e-13:527:63//
 AC004805
 R-HEMBA1004631//Rattus norvegicus Nclone10 mRNA.//2.9e-24:364:71//
 U31866
 R-HEMBA1004632
 R-HEMBA1004637//Homo sapiens clone DJ0982E09, WORKING DRAFT SEQUEN
 CE, 3 unordered pieces.//7.7e-117:573:98//AC005534
 R-HEMBA1004638//H.sapiens mRNA for DCCR2.//3.8e-19:118:99//X84076
 R-HEMBA1004666//Arabidopsis thaliana chromosome II BAC T4E14 genom
 ic sequence, complete sequence.//0.00013:501:58//AC005171
 R-HEMBA1004669//Human DNA sequence from clone 465N24 on chromosome
 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG island
 s, complete sequence.//1.5e-120:571:98//AL031432
 R-HEMBA1004670//Human DNA sequence *** SEQUENCING IN PROGRESS ***
 from clone 222E13, WORKING DRAFT SEQUENCE.//4.4e-12:110:88//Z93241
 R-HEMBA1004672//Human DNA sequence from PAC 308113 on chromosome 1
 p35-1p36.3.//3.4e-38:324:81//Z99291
 R-HEMBA1004693//Arabidopsis thaliana genomic DNA, chromosome 5, P1
 clone: MP012, complete sequence.//0.86:309:57//AB006702
 R-HEMBA1004697//T33B22TF TAMU Arabidopsis thaliana genomic clone T
 33B22, genomic survey sequence.//0.29:331:61//B97342
 R-HEMBA1004705//Plasmodium falciparum MAL3P7, complete sequence.//
 0.051:424:58//AL034559
 R-HEMBA1004709//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-11
 6A10, complete sequence.//1.7e-49:497:76//AC004638
 R-HEMBA1004711//Homo sapiens chromosome 17, clone hRPK.271_K_11, c
 omplete sequence.//1.6e-38:382:79//AC005562
 R-HEMBA1004725
 R-HEMBA1004730//Homo sapiens Chromosome 17p13 Cosmid Clone cos26,
 complete sequence.//1.1e-58:489:79//AC002085
 R-HEMBA1004733
 R-HEMBA1004734//Human DNA sequence from clone 273N12 on chromosome
 6q16.1-16.3. Contains the gene for the N-Oct5a (N-Oct3, N-Oct5b)
 POU domain proteins and an unknown gene. Contains a putative CpG i
 sland, ESTs, STS, and GSSs, complete sequence.//0.0030:362:61//AL0
 22395

【0785】

【表485】

R-HEMBA1004736//Homo sapiens clone DJ0981007, complete sequence.//1.9e-58:282:87//AC006017

R-HEMBA1004748//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//3.6e-34:287:81//AC004953

R-HEMBA1004751//Human DNA sequence from PAC 507115 on chromosome X q26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gene, ESTs, STSs and a polymorphic CA repeat.//5.3e-40:266:89//Z98950

R-HEMBA1004752//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 495010, WORKING DRAFT SEQUENCE.//3.3e-39:281:85//AL031121

R-HEMBA1004753//Homo sapiens ribosomal protein S20 (RPS20) mRNA, complete cds.//2.6e-65:475:84//L06498

R-HEMBA1004756//Homo sapiens DNA sequence from PAC 86C11 on chromosome 6p21.31-22.1. Contains histone genes H2A1, H2B.1A, H4, H2A.1b, H3 pseudogene, pheromone receptor pseudogene, ESTs, STS and CpG island.//1.8e-08:516:59//AL021807

R-HEMBA1004758//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//5.1e-45:577:72//AC004057

R-HEMBA1004763

R-HEMBA1004768//Human DNA sequence from clone 39SP12 on chromosome 1q24-25. Contains the TXGP1 gene for tax-transcriptionally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Aminotransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//4.1e-60:435:78//AL022310

R-HEMBA1004770//Plasmodium falciparum chromosome 2, section 8 of 73 of the complete sequence.//8.7e-05:476:61//AE001371

R-HEMBA1004771//Homo sapiens Xp22 Cosmid U152D7 (Lawrence Livermore human cosmid library) complete sequence.//5.0e-08:113:80//AC003047

R-HEMBA1004776

R-HEMBA1004778//***ALU WARNING: Human Alu-J subfamily consensus sequence.//1.1e-35:288:84//U14567

R-HEMBA1004795//HIS_3192_B1_F09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3192 Col=17 Row=L, genomic survey sequence.//1.9e-44:233:98//AQ155855

R-HEMBA1004803//Homo sapiens minisatellite ms31 repeat region.//3.0e-67:318:87//AF048728

R-HEMBA1004806

R-HEMBA1004807//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE. 7 unordered pieces.//3.6e-20:333:69//AC005015

R-HEMBA1004816//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//6.3e-13:148:77//Z92545

R-HEMBA1004820//Human arginine-rich nuclear protein mRNA, complete cds.//1.5e-12:141:85//M74002

R-HEMBA1004847//Canine mRNA for 68kDa subunit of signal recognition particle (SRP68).//7.6e-80:297:85//X53744

R-HEMBA1004850

R-HEMBA1004863//Human DNA sequence from PAC 345P10 on chromosome 2 2q12-qter contains ESTs and STS and polymorphic CA repeat D22S927.//2.0e-14:159:79//Z82201

R-HEMBA1004864

R-HEMBA1004865//Homo sapiens Xp22-149 BAC RPC111-46604 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.90:76:76//AC005297

R-HEMBA1004880//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE. 12 unordered pieces.//1.9e-49:551:73//AC004826

R-HEMBA1004889//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 223B1, WORKING DRAFT SEQUENCE.//0.0021:189:65//AL031943

R-HEMBA1004900//Homo sapiens chromosome 17, clone hRPK.180_P.8, complete sequence.//6.6e-11:144:77//AC005972

R-HEMBA1004909//Human DNA sequence from clone 50S813 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//7.6e-46:341:83//Z98052

R-HEMBA1004918//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 994L9, WORKING DRAFT SEQUENCE.//1.6e-54:301:89//AL034554

R-HEMBA1004923//Homo sapiens 47kb DNA fragment from Xq28, proximal to MTM1 gene.//2.0e-07:182:69//Y15994

R-HEMBA1004929

R-HEMBA1004930//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE. 6 unordered pieces.//7.7e-66:547:79//AC005848

R-HEMBA1004933//H. sapiens Humig mRNA.//0.13:233:62//X72755

R-HEMBA1004934//CIT-HSP-2021116.TF CIT-HSP Homo sapiens genomic clone 2021116, genomic survey sequence.//0.66:268:62//B65345

R-HEMBA1004944//CIT-HSP-2281L12.TR CIT-HSP Homo sapiens genomic clone 2281L12, genomic survey sequence.//3.8e-20:104:82//B99849

R-HEMBA1004954//Homo sapiens chromosome 17, clone hRPK.146_P.2, WORKING DRAFT SEQUENCE. 4 unordered pieces.//0.00082:385:60//AC005341

R-HEMBA1004956//CIT-HSP-2305H22.TF CIT-HSP Homo sapiens genomic clone 2305H22, genomic survey sequence.//1.6e-84:411:99//AQ020408

R-HEMBA1004960//Human DNA sequence from PAC 358H7 on chromosome X.//3.3e-22:249:74//Z77249

R-HEMBA1004972//nbxb0003aF01f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0003K01f, genomic survey sequence.//0.52:171:64//AQ049982

R-HEMBA1004973//*** SEQUENCING IN PROGRESS *** EPM1/APEC region of chromosome 21, clones A6B8, B127P21, B173L3, B23W8, C1242C9, C579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in this region has been discontinued by the Stanford Human Genome Center. WORKING DRAFT SEQUENCE. 50 unordered pieces.//0.69:179:64//AC003656

R-HEMBA1004977//Caenorhabditis elegans cosmid F08G2, complete sequence.//7.6e-07:492:58//Z81495

R-HEMBA1004978//Human DNA sequence from clone 522P13 on chromosome 6p21.31-22.3. Contains a 60S Ribosomal Protein L21 pseudogene and an HMRNP A3 (Heterogenous Nuclear Riboprotein A3, FBRNP) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.20:427:60//AL024509

R-HEMBA1004980//CIT-HSP-2379K5.TF CIT-HSP Homo sapiens genomic clone 2379K5, genomic survey sequence.//1.6e-53:331:88//AQ108614

R-HEMBA1004983//Genomic sequence from Human 17, complete sequence.//0.00061:473:58//AC000389

R-HEMBA1004995//Homo sapiens chromosome 16, cosmid clone 306E5 (LA ML), complete sequence.//1.6e-90:527:89//AC004224

R-HEMBA1005008//Human DNA sequence from clone 461P17 on chromosome 20q12-13.2. Contains four novel (pseudo)genes for proteins with Kunitz/Bovine pancreatic trypsin inhibitor and/or WAP-type (Whey Acidic Protein) 'four-disulfide core' domains, COX6C (Cytochrome C oxidase Polypeptide VIC, EC 1.9.3.1) and RPL5 (60S Ribosomal Protein L5) pseudogenes, a pseudogene similar to part of the HSPD1 (HSP60, Mitochondrial Matrix Protein P1 precursor, Heat Shock Protein 60, GROEL protein, HUCHA60) gene, and the Major Epididymis-specific protein E4 precursor (HE4, Epididymis Secretory protein E4, WAP-type (Whey Acidic Protein) 'four-disulfide core' domain) gene. Contains ESTs, an STS, GSSs and a putative CpG island, complete sequence.//5.4e-65:357:83//AL031663

R-HEMBA1005009//Homo sapiens BAF53a (BAF53a) mRNA, complete cds.//5.6e-107:550:96//AF041474

R-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds.//6.3e-104:542:94//AB014548

R-HEMBA1005029//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c), H4FFP (H4/f pseudogene), H2AFC (H2A/c), H3FIK (H3.1/k) and a tRNA A-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSs, GSSs and genomic marker D6S464, complete sequence.//3.1e-67:493:83//AL009179

R-HEMBA1005035//Homo sapiens chromosome 17, clone hCIT.175_E.5, complete sequence.//7.4e-101:537:94//AC004596

R-HEMBA1005039//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE.//9.5e-30:446:68//AL031650

R-HEMBA1005047//Mus musculus mRNA for Rab24 protein.//1.4e-34:229:88//Z22819

R-HEMBA1005050//Human Chromosome X PAC RPC11-290C9 from the Pieter de Jong Human PAC library: complete sequence.//4.0e-43:371:80//AC002404

R-HEMBA1005062//Homo sapiens chromosome 17, clone hCIT.186_H.2, complete sequence.//2.3e-15:269:66//AC004675

R-HEMBA1005066//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE. 1 unordered pieces.//4.0e-30:305:74//AC006030

R-HEMBA1005075

R-HEMBA1005079//Homo sapiens clone HS19.11 Alu-Ya5 sequence.//6.5e-48:245:91//AF015156

R-HEMBA1005083//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE.//1.3e-15:142:83//AL034423

R-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds.//5.3e-110:545:96//AF080561

R-HEMBA1005113//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y53C10, WORKING DRAFT SEQUENCE.//0.026:252:64//Z93340

R-HEMBA1005123//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein

【0786】

【表486】

tein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence. //7.1e-55:306:82//AL022336

R-HEMBA1005131//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE. //6.4e-45:309:87//AL022345

R-HEMBA1005149//Human cosmid LL12NC01-95H4, ETV6 gene, exon 2 and partial cds. //3.2e-31:310:76//U01834

R-HEMBA1005152//Homo sapiens DNA sequence from PAC 13D10 on chromosome 6p22.3-23. Contains CpG island. //1.4e-33:361:79//AL021407

R-HEMBA1005159//Human DNA sequence from clone 163016 on chromosome 1p35.1-36.13 Contains CA repeat, STS, complete sequence. //2.7e-22:440:66//AL031279

R-HEMBA1005185//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y105E8, WORKING DRAFT SEQUENCE. //0.0017:381:58//AL022594

R-HEMBA1005201//P. falciparum complete gene map of plastid-like DNA (IR-B). //8.5e-05:457:57//X95276

R-HEMBA1005202//Human 18S ribosomal RNA. //4.7e-38:236:91//X03205

R-HEMBA1005219

R-HEMBA1005223//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE. 33 unordered pieces. //1.0:209:65//AC004854

R-HEMBA1005232//Homo sapiens chromosome Y, clone 264.M.20, complete sequence. //0.0040:439:58//AC004617

R-HEMBA1005241//Homo sapiens PAC clone DJ0777023 from Tpl4-pl5, complete sequence. //4.2e-111:568:96//AC005154

R-HEMBA1005244//HS_3092_B2_C11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=22 Row=F, genomic survey sequence. //4.9e-12:116:84//AQ127947

R-HEMBA1005251//Homo sapiens PAC clone DJ1182N03 from Tq11.23-q21.1, complete sequence. //3.2e-27:210:84//AC004548

R-HEMBA1005252//Homo sapiens chromosome 17, clone hRPK.318_A_15, complete sequence. //4.6e-105:437:97//AC005837

R-HEMBA1005274//Slime mold mitochondrial DNA, binding region to the membrane system. //0.011:339:59//D08630

R-HEMBA1005275//Homo sapiens PAC clone DJ0886008 from Tq32-q35, complete sequence. //3.4e-17:269:71//AC004914

R-HEMBA1005293//Human DNA sequence from PAC 130N4, BRCA2 gene region on chromosome 13q12-13 contains xst mRNA, ESTs. //6.9e-20:193:73//Z75887

R-HEMBA1005296//HS_3037_B1_D01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=1 Row=H, genomic survey sequence. //0.26:184:64//AQ117120

R-HEMBA1005304//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE. 7 unordered pieces. //1.5e-58:445:78//AC006146

R-HEMBA1005311//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y95E4, WORKING DRAFT SEQUENCE. //9.3e-42:383:78//AL022337

R-HEMBA1005314//Caenorhabditis elegans cosmid F23H11. //0.80:179:65//AF003389

R-HEMBA1005315//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE. 1 unordered pieces. //2.4e-40:409:71//AC006030

R-HEMBA1005318//S. pombe chromosome I cosmid c2E11. //0.97:370:61//AL031181

R-HEMBA1005331//Homo sapiens chromosome 17, clone hRPK.214_C_8, complete sequence. //1.9e-112:577:95//AC005803

R-HEMBA1005353//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 429E7, WORKING DRAFT SEQUENCE. //8.9e-80:406:97//AL031722

R-HEMBA1005359//Homo sapiens chromosome 17, clone hRPK.22_N_12, WORKING DRAFT SEQUENCE. 2 ordered pieces. //3.2e-50:320:84//AC005412

R-HEMBA1005367//RPC111-85E23.TV RPC111 Homo sapiens genomic clone R-85E23, genomic survey sequence. //0.39:148:67//AQ281915

R-HEMBA1005372//Homo sapiens full length insert cDNA YH93B03. //2.6e-108:557:95//AF074997

R-HEMBA1005374//Homo sapiens full length insert cDNA clone ZA95D11. //1.9e-110:531:98//AF086142

R-HEMBA1005389//Human DNA sequence from clone 245G19 on chromosome Xp22.11-22.2 Contains serine-threonine kinase (Tsp3) gene, a pseudogene similar to ALPHA-1 PROTEIN (CONNEXIN 43, CX43, GAP JUNCTION 43 KD HEART PROTEIN), and the 3' end of the RS1 (X-linked juvenile retinoschisis precursor protein) gene. Contains ESTs, STSs and GSSs, complete sequence. //6.0e-41:432:75//Z92542

R-HEMBA1005394//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 681N20, WORKING DRAFT SEQUENCE. //4.9e-107:585:93//AL031670

R-HEMBA1005403//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE. //5.1e-118:586:97//AL034379

R-HEMBA1005408//Bos taurus retina membrane guanylate cyclase ROS-GC2 mRNA, complete cds. //1.6e-06:204:58//U95958

R-HEMBA1005410//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 732E4, WORKING DRAFT SEQUENCE. //1.2e-23:452:66//AL008722

R-HEMBA1005411//RPC111-66N19.TK RPC111 Homo sapiens genomic clone R-66N19, genomic survey sequence. //2.2e-38:222:79//AQ237442

R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds. //5.6e-117:453:99//AF041248

R-HEMBA1005426//Human DNA sequence from PAC 448E20 on chromosome Xq26.1 contains ESTs and STS. //0.86:278:60//Z97196

R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment. //5.4e-46:305:87//L40391

R-HEMBA1005447//Human DNA sequence from clone 48G12 on chromosome Xq27.1-27.3. Contains STSs and GSSs, complete sequence. //3.3e-79:531:86//AL031054

R-HEMBA1005468//Homo sapiens PAC clone DJ0808G16 from Tq11.23-q21, complete sequence. //4.0e-27:469:66//AC004894

R-HEMBA1005469//Homo sapiens chromosome 16, PI clone 96-4B (LANL), complete sequence. //7.2e-40:410:76//AC005212

R-HEMBA1005472//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1090E8, WORKING DRAFT SEQUENCE. //3.1e-40:296:85//AL033524

R-HEMBA1005475//HS_2266_B2_C04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2266 Col=8 Row=F, genomic survey sequence. //0.49:209:61//AQ069377

R-HEMBA1005497

R-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from Tq11.23-q21, complete sequence. //4.5e-116:580:97//AC004957

R-HEMBA1005506//Arabidopsis thaliana BAC T26D22. //0.0050:442:59//AF058826

R-HEMBA1005508//Sigalphus sp. 16S ribosomal RNA gene, partial sequence. //0.020:391:59//AF003509

R-HEMBA1005511//Human DNA sequence from PAC 52D1 on chromosome Xq21.1. Contains CA repeats, STS. //0.44:195:63//Z96811

R-HEMBA1005517//Bovine herpesvirus type 1 early-intermediate transcription control protein (BICP4) gene, complete cds. //0.44:470:57//L14320

R-HEMBA1005518//M. musculus mRNA for paladin gene. //6.2e-29:183:81//X99384

R-HEMBA1005520//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE. 6 unordered pieces. //7.2e-40:281:86//AC004913

R-HEMBA1005526//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 341D10, WORKING DRAFT SEQUENCE. //3.9e-40:482:73//Z97985

R-HEMBA1005528//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11. //3.8e-84:309:99//AB020860

R-HEMBA1005530//Homo sapiens PAC clone 946B23 SCA2 region, SP6 end, genomic sequence, genomic survey sequence. //8.1e-25:154:94//U84091

R-HEMBA1005548//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 970A17, WORKING DRAFT SEQUENCE. //5.3e-105:534:96//AL034431

R-HEMBA1005552//Homo sapiens PAC clone DJ0807C15 from Tq34-q36, complete sequence. //2.8e-69:432:88//AC004743

R-HEMBA1005558

R-HEMBA1005568//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence. //5.9e-33:367:74//AC004087

R-HEMBA1005570//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmalipin, ESTs and GSSs, complete sequence. //2.2e-67:399:91//AL020989

R-HEMBA1005576//Homo sapiens chromosome 16, BAC clone 97H22 (LANL), complete sequence. //1.0:156:63//AC005737

R-HEMBA1005577

R-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds. //9.7e-27:561:64//AB011538

R-HEMBA1005582//Torulopsis glabrata mitochondrial intergenic region ATPase 9-cytochrome oxidase 2 genes. //2.3e-10:404:62//X02171

R-HEMBA1005583//HS_3014_B1_D05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3014 Col=9 Row=H, genomic survey sequence. //3.0e-81:442:94//AQ154499

R-HEMBA1005588//Human DNA sequence from clone 1409 on chromosome Xp11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen IMAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence. //1.8e-54:490:77//Z98046

R-HEMBA1005593//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence. //2.2e-28:262:79//AC005746

R-HEMBA1005595//HS_2224_A2_G03_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2224 Col=6 Row=M, genomic survey sequence. //3.6e-48:263:95//AQ033446

【0787】

【表487】

R-HEMBA1005606//Human PAC clone DJ0093103 from Xq23, complete sequence.//2.5e-08:355:63//AC003983

R-HEMBA1005609//HS_2182_B1_H06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=11 Row=P, genomic survey sequence.//2.2e-82:400:99//AQ023130

R-HEMBA1005616//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 124K22, WORKING DRAFT SEQUENCE.//0.80:308:60//AL031176

R-HEMBA1005621//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 330012, WORKING DRAFT SEQUENCE.//7.4e-76:338:98//AL031731

R-HEMBA1005627//Homo sapiens full length insert cDNA clone ZD5300 2.//4.5e-72:398:93//AF086321

R-HEMBA1005631//Homo sapiens PAC clone DJ1086D14, complete sequence.//3.8e-17:548:60//AC004460

R-HEMBA1005632//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS, CpG island, complete sequence.//1.4e-13:172:75//AL022069

R-HEMBA1005634//RPC111-13015.TVB RPC1-11 Homo sapiens genomic clone RPC1-11-13015, genomic survey sequence.//1.0e-28:153:82//B73293

R-HEMBA1005666//Human DNA sequence from PAC 696H22 on chromosome Xq21.1-21.2. Contains a mouse E25 like gene, a Kinesin like pseudogene and ESTs.//4.5e-51:343:87//AL021786

R-HEMBA1005670//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 11703, WORKING DRAFT SEQUENCE.//2.5e-33:288:78//AL020995

R-HEMBA1005679//Human esterase D mRNA, 3' end.//4.2e-49:322:88//M13450

R-HEMBA1005680//Homo sapiens Chr.14 PAC RPC14-79482 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.0e-36:285:83//AC005924

R-HEMBA1005685//H.sapiens (MARB) chromosome 19 DNA, 343bp.//0.022:65:86//Z35281

R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Ephg8) mRNA, complete cds.//5.4e-46:376:84//U66406

R-HEMBA1005705//RPC111-13014.TP RPC1-11 Homo sapiens genomic clone RPC1-11-13014, genomic survey sequence.//0.071:182:59//B76186

R-HEMBA1005717//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATPSG1, ATPSG2, ATPSG3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//1.0:189:66//Z92545

R-HEMBA1005732//Human Chromosome 11q12 pac pDJ363p2, WORKING DRAFT SEQUENCE, 22 unordered pieces.//2.1e-47:449:75//AC003023

R-HEMBA1005737

R-HEMBA1005746//H.sapiens DNA for repeat unit locus D18S51 (285 bp).//0.11:174:63//X91255

R-HEMBA1005755//Human DNA sequence from clone 396D17 on chromosome 1p33-35.3 Contains EST, STS, GSS, complete sequence.//0.15:160:65//AL008634

R-HEMBA1005765//Human Xq28 cosmids U225B5 and U236A12, complete sequence.//5.2e-39:422:74//U71148

R-HEMBA1005780//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//0.037:261:61//AP000010

R-HEMBA1005813//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//1.7e-26:242:80//AL023808

R-HEMBA1005815//Bufo boreas MVZ 145227 c-mos gene, partial cds.//0.17:199:62//U52805

R-HEMBA1005822//Plasmodium falciparum MAL3P7, complete sequence.//0.26:437:56//AL034559

R-HEMBA1005829//Human Cosmid g1572c035, complete sequence.//3.8e-05:366:61//AC000124

R-HEMBA1005834//Human DNA sequence from clone 51J12 on chromosome 6q26-27. Contains the 3' part of the alternatively spliced exon for the human orthologs of mouse QKI-7 and QKI-7B (KH Domain RNA Binding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Contains ESTs, STSs and GSSs, complete sequence.//8.2e-107:551:96//AL031781

R-HEMBA1005852//F.rubripes GSS sequence, clone 163A22aA4, genomic survey sequence.//2.6e-17:225:72//AL018730

R-HEMBA1005853//Human Chromosome 15 pac pDJ24a8, complete sequence.//1.1e-27:314:75//AC000379

R-HEMBA1005884//Homo sapiens 12p13.3 BAC RPC13-488H23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//2.6e-20:328:67//AC006207

R-HEMBA1005891//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence.//2.0e-102:543:95//AC004945

R-HEMBA1005894

R-HEMBA1005909

R-HEMBA1005911//CIT-HSP-2342E5.TR CIT-HSP Homo sapiens genomic clone 2342E5, genomic survey sequence.//0.0012:315:60//AQ058081

R-HEMBA1005921//P.chrysogenum mitochondrion genes for tRNA-Arg, tRNA-Asn, tRNA-Tyr, small subunit rRNA, and ATPase subunit 6.//0.0090:445:58//Z23072

R-HEMBA1005931//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE.//1.7e-46:351:83//Z98304

R-HEMBA1005934//Homo sapiens chromosome 17, clone hRPK.261_A_13, complete sequence.//0.0052:179:71//AC005138

R-HEMBA1005962//Homo sapiens clone RG012D21, complete sequence.//1.1e-11:149:74//AC005045

R-HEMBA1005963//HS_3055_A1_E08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3055 Col=15 Row=1, genomic survey sequence.//5.4e-79:403:97//AQ147357

R-HEMBA1005990//Homo sapiens 1-1 receptor candidate protein mRNA, complete cds.//6.9e-112:580:95//AF082516

R-HEMBA1005991//Human DNA sequence from clone 58A9 on chromosome 1q24.1-24.3. Contains STSs, GSSs, genomic marker D1S210 and a ca repeat polymorphism, complete sequence.//2.6e-39:299:82//AL031285

R-HEMBA1005999//Homo sapiens clone DJ0691F11, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.1e-29:260:70//AC004859

R-HEMBA1006002//Rattus norvegicus s-nexilin mRNA, complete cds.//6.3e-15:174:78//AF056035

R-HEMBA1006005//Homo sapiens MLL (MLL) gene, exons 1-3, and partial cds.//2.6e-112:574:95//AF036405

R-HEMBA1006031//Homo sapiens mRNA for KIAA0725 protein, partial cds.//7.6e-27:444:67//AB018268

R-HEMBA1006035//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.025:373:60//AC005139

R-HEMBA1006036//Homo sapiens Chromosome 16 BAC clone CIT987SK-625P11, complete sequence.//0.0056:535:59//AC004125

R-HEMBA1006042//HS_2169_A1_B11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2169 Col=21 Row=C, genomic survey sequence.//1.7e-73:390:95//AQ132995

R-HEMBA1006067

R-HEMBA1006081

R-HEMBA1006090//HS_2262_A2_A01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2262 Col=2 Row=A, genomic survey sequence.//2.1e-70:360:97//AQ216324

R-HEMBA1006091

R-HEMBA1006100//Homo sapiens DNA sequence from PAC 212G6 on chromosome Xp11.3-p11.4. Contains synapsin 1, brain protein 4.1, properdin, tyrosine kinase (ELK1) oncogene, ESTs, STS, GSS, complete sequence.//1.6e-36:354:77//AL009172

R-HEMBA1006108

R-HEMBA1006121

R-HEMBA1006124//Human DNA sequence from BAC 175E3 on chromosome 22q11.2-qter. Contains ESTs, STSs and polymorphic CA repeat.//1.3e-12:327:64//Z95113

R-HEMBA1006130//WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.60:326:62//AC005948

R-HEMBA1006138//Homo sapiens chromosome 19, cosmid F16403, complete sequence.//4.3e-52:321:80//AC005777

R-HEMBA1006142//, complete sequence.//1.0e-13:160:78//AC005500

R-HEMBA1006155//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.0013:389:60//AC004688

R-HEMBA1006158//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds.//1.4e-119:574:98//AF048693

R-HEMBA1006173//Mus musculus protein tyrosine phosphatase STEP61 mRNA, complete cds.//4.1e-43:307:85//U28217

R-HEMBA1006182//Homo sapiens BAC clone RG139P11 from 7q11-q21, complete sequence.//1.7e-30:300:71//AC004491

R-HEMBA1006198//**ALU WARNING: Human Alu-J subfamily consensus sequence.//1.3e-36:284:85//U14567

R-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence.//2.1e-110:545:97//AF070557

R-HEMBA1006248//Homo sapiens mRNA for KIAA0667 protein, partial cds.//0.46:365:58//AB014567

R-HEMBA1006252//Human Chromosome 16 BAC clone CIT987SK-A-972D3, complete sequence.//2.8e-41:438:77//U91323

R-HEMBA1006253//Homo sapiens 45kDa splicing factor mRNA, complete cds.//1.8e-28:179:91//AF083384

R-HEMBA1006259//RPC111-44N14.TJ RPC111 Homo sapiens genomic clone R-44N14, genomic survey sequence.//1.5e-48:348:85//AQ203161

R-HEMBA1006268

R-HEMBA1006272//Human DNA sequence from clone 1198H6 on chromosome 1p36.11-36.31. Contains two Melanoma Preferentially Expressed Antigen PRAME LIKE genes. Contains GSSs and ESTs, complete sequence.//

【0788】

【表488】

/2.8e-73:273:87//AL023753
 R-HEMBA1006278//H.sapiens PAP mRNA. //1.6e-54:585:71//X76770
 R-HEMBA1006283//Sequence 7 from patent US 5776683. //9.7e-18:113:98
 //A016240
 R-HEMBA1006284//Homo sapiens chromosome 17, clone hRPC.1028_K_7, c
 omplete sequence. //0.97:447:59//AC004585
 R-HEMBA1006291//Homo sapiens full length insert cDNA clone ZB76B1
 0. //2.9e-94:454:98//AF086161
 R-HEMBA1006293//Sequence 8 from patent US 5721351. //8.1e-10:111:72
 //189415
 R-HEMBA1006309//Homo sapiens chromosome 17, clone hRPK.22_M_12, W
 ORKING DRAFT SEQUENCE, 2 ordered pieces. //8.6e-37:288:84//AC005412
 R-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1
 a (PACS-1) mRNA, complete cds. //6.5e-29:132:81//AF076183
 R-HEMBA1006328//Human DNA sequence *** SEQUENCING IN PROGRESS ***
 from clone 894K16, WORKING DRAFT SEQUENCE. //3.3e-50:340:75//AL0344
 29
 R-HEMBA1006334
 R-HEMBA1006344//Rattus norvegicus nitzin mRNA, partial cds. //8.7e-
 22:259:72//AF087945
 R-HEMBA1006347//Human prostaticin gene, complete cds. //1.8e-78:170:1
 00//U33446
 R-HEMBA1006349//Rat brain calcium channel alpha-1 subunit mRNA, co
 mplete cds. //0.00051:120:73//M57682
 R-HEMBA1006359//CITB1-E1-2516C16.TR CITB1-E1 Homo sapiens genomic
 clone 2516C16, genomic survey sequence. //4.7e-74:576:82//AQ277951
 R-HEMBA1006364//G.gallus gene for transforming growth factor-beta
 2, exons 5-7. //2.5e-21:118:85//X59080
 R-HEMBA1006377//Homo sapiens chromosome 19, cosmid F23149, complet
 e sequence. //5.7e-68:367:85//AC005239
 R-HEMBA1006380//Human BAC clone RC007J15 from Tq31, complete seque
 nce. //6.1e-47:300:83//AC003989
 R-HEMBA1006381//Homo sapiens chromosome 5, BAC clone 189 (LBNL H13
 5), complete sequence. //1.5e-47:336:86//AC005914
 R-HEMBA1006398//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL
 H155), complete sequence. //1.5e-67:501:83//AC005609
 R-HEMBA1006416//Homo sapiens chromosome 17, clone 347_H_5, complet
 e sequence. //4.4e-37:319:76//AC002119
 R-HEMBA1006419//Homo sapiens chromosome 17, clone HCIT542B22, comp
 lete sequence. //2.9e-50:502:75//AC004253
 R-HEMBA1006421//Homo sapiens chromosome 14q24.3 clone BAC270M14 tr
 ansforming growth factor-beta 3 (TGF-beta 3) gene, complete cds; a
 nd unknown genes. //4.1e-116:572:97//AF107885
 R-HEMBA1006424//Human DNA sequence from clone 51J12 on chromosome
 6q26-27. Contains the 3' part of the alternatively spliced gene fo
 r the human orthologs of mouse KKI-7 and KKI-7B (KH Domain RNA Bin
 ding proteins) and zebrafish ZKQ-1 (Quaking protein homolog). Cont
 ains ESTs, STSs and GSSs, complete sequence. //9.4e-117:578:97//AL0
 31781
 R-HEMBA1006425//Human DNA sequence *** SEQUENCING IN PROGRESS ***
 from clone 291J10, WORKING DRAFT SEQUENCE. //2.2e-08:353:63//Z93017
 R-HEMBA1006438//HS_2008_A1_D04_T7 CIT Approved Human Genomic Sperm
 Library D Homo sapiens genomic clone Plate=2008 Col=7 Row=G, geno
 mic survey sequence. //1.2e-29:194:91//AQ245162
 R-HEMBA1006445//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENC
 E, 3 unordered pieces. //0.011:330:60//AC005075
 R-HEMBA1006446//Plasmodium falciparum chromosome 2, section 35 of
 73 of the complete sequence. //0.032:256:61//AE001398
 R-HEMBA1006461//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12,
 U115B9 (Lawrence Livermore human cosmid library) complete sequenc
 e. //5.6e-35:229:77//AC002364
 R-HEMBA1006467//Homo sapiens Chromosome 9p22 Cosmid clone 34a5, co
 mplete sequence. //1.1e-14:354:63//AC002052
 R-HEMBA1006471
 R-HEMBA1006474//p40, p24 [Borna disease virus BDV, WT-1, Halle B1/
 91, horse brain, field isolate, Genomic RNA, 1138 nt, segment 1 of
 3]. //1.1e-14:442:60//S67502
 R-HEMBA1006483//Human chromosome 16p13.1 BAC clone CIT987SK-551C9
 complete sequence. //3.7e-37:290:82//U95742
 R-HEMBA1006485//H.sapiens mRNA for aminopeptidase. //7.6e-91:517:91
 //Y07701
 R-HEMBA1006486//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENC
 E, 5 unordered pieces. //1.1e-33:289:81//AC005089
 R-HEMBA1006489//Human DNA sequence from clone 192P9 on chromosome
 Xp11.23-11.4. Contains a pseudogene similar to rat Plasmolipin, ES
 Ts and GSSs, complete sequence. //6.0e-07:485:60//AL020989
 R-HEMBA1006492//Homo sapiens chromosome 17, clone hRPK.269_G_24, c
 omplete sequence. //4.3e-112:572:95//AC005828
 R-HEMBA1006494//Homo sapiens chromosome 17, clone HRPK987K16, comp
 lete sequence. //2.3e-10:186:67//AC002994

R-HEMBA1006497//RPC111-16L10.TPB RPC1-11 Homo sapiens genomic clon
 e RPC1-11-16L10, genomic survey sequence. //1.5e-10:75:100//B88015
 R-HEMBA1006502//Human DNA sequence from clone 272E8 on chromosome
 Xp22.13-22.31. Contains a pseudogene similar to NDM2-Like P53-bind
 ing protein gene. Contains STSs, GSSs and a CA repeat polymorphis
 m, complete sequence. //3.3e-36:516:70//Z93929
 R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cd
 s. //1.2e-115:570:96//AB014566
 R-HEMBA1006521//Human DNA sequence *** SEQUENCING IN PROGRESS ***
 from clone 54820, WORKING DRAFT SEQUENCE. //2.2e-20:266:71//Z98304
 R-HEMBA1006530//RPC111-52M1.TJ RPC111 Homo sapiens genomic clone
 R-52M1, genomic survey sequence. //0.00015:227:64//AQ052526
 R-HEMBA1006535//HS_2234_B1_B07_MF CIT Approved Human Genomic Sperm
 Library D Homo sapiens genomic clone Plate=2234 Col=13 Row=D, gen
 omic survey sequence. //7.5e-33:191:95//AQ129525
 R-HEMBA1006540//Homo sapiens clone GS051M12, complete sequence. //
 0.026:497:58//AC005007
 R-HEMBA1006546//Homo sapiens chromosome 19, cosmid R33496, complet
 e sequence. //5.2e-41:289:86//AC004603
 R-HEMBA1006559//Mus musculus PRAJA1 (Prajai) mRNA, complete cds. //
 3.4e-64:551:78//U06944
 R-HEMBA1006562//Human Chromosome 11p11.2 PAC clone pJ404m15, comp
 lete sequence. //5.7e-09:266:66//AC002554
 R-HEMBA1006566//HS_2171_B1_B04_MF CIT Approved Human Genomic Sperm
 Library D Homo sapiens genomic clone Plate=2171 Col=7 Row=D, geno
 mic survey sequence. //0.012:306:61//AQ125421
 R-HEMBA1006569//Ovis aries beta actin mRNA, complete cds. //3.8e-7
 0:529:82//J39357
 R-HEMBA1006579//Homo sapiens BAC clone NH0115E20 from Y, complete
 sequence. //1.0:141:65//AC006032
 R-HEMBA1006583//CIT-HSP-2377M16.TR CIT-HSP Homo sapiens genomic cl
 one 2377M16, genomic survey sequence. //1.7e-31:271:76//AQ11875
 R-HEMBA1006595//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122
 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces. //0.0
 93:270:61//AC004709
 R-HEMBA1006597//Homo sapiens P1 clone GSP13996 from 5q12, complete
 sequence. //2.7e-45:371:80//AC005031
 R-HEMBA1006612
 R-HEMBA1006617//Human DNA sequence *** SEQUENCING IN PROGRESS ***
 from clone 8B22, WORKING DRAFT SEQUENCE. //2.1e-20:229:77//AL031737
 R-HEMBA1006624//Human DNA sequence from clone 406A7 on chromosome
 6q23-24. Contains three pseudogenes similar to Elongation Factor
 1-Alpha (EF-1-ALPHA, Statin S1), 60S Acidic Ribosomal Protein P1 a
 nd NADH-Ubiquinone Oxidoreductase 15 kDa subunit, and part of the
 Microtubule Associated Protein E-MAP-115 gene. Contains ESTs, STSs
 and GSSs, complete sequence. //4.8e-40:321:83//AL023284
 R-HEMBA1006631//Human DNA sequence *** SEQUENCING IN PROGRESS ***
 from clone 20208, WORKING DRAFT SEQUENCE. //1.5e-45:477:77//AL03184
 8
 R-HEMBA1006635//***ALU WARNING: Human Alu-Sp subfamily consensus s
 equence. //8.0e-40:245:91//U14572
 R-HEMBA1006639
 R-HEMBA1006643
 R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, co
 mplete cds. //2.5e-106:567:94//U40282
 R-HEMBA1006652//Human BAC clone RG308B22 from Tq22-q31, complete s
 equence. //8.7e-54:334:76//AC002089
 R-HEMBA1006653//Homo sapiens Tq telomere, complete sequence. //5.0
 e-36:207:89//AF027390
 R-HEMBA1006665//HS_3213_B2_D04_T7 CIT Approved Human Genomic Sperm
 Library D Homo sapiens genomic clone Plate=3213 Col=8 Row=H, geno
 mic survey sequence. //1.2e-21:235:67//AQ175625
 R-HEMBA1006674//H.sapiens telomeric DNA sequence, clone 9QTEL023,
 read 9QTEL0023.seq. //2.6e-32:212:83//Z96776
 R-HEMBA1006676//Plasmodium falciparum MAL3P6, complete sequence. //1
 .9e-10:436:60//Z98551
 R-HEMBA1006682//Plasmodium falciparum (strain Dd2) variant-specifi
 c surface protein (var-1) gene, complete cds. //6.1e-06:477:59//L40
 608
 R-HEMBA1006695//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENC
 E, 10 unordered pieces. //1.8e-30:266:80//AC005096
 R-HEMBA1006696
 R-HEMBA1006708
 R-HEMBA1006709//Human DNA sequence *** SEQUENCING IN PROGRESS ***
 from clone 715N11, WORKING DRAFT SEQUENCE. //6.8e-14:139:82//AL0316
 74
 R-HEMBA1006717
 R-HEMBA1006737//Homo sapiens chromosome 17, clone hRPK.269_G_24, c
 omplete sequence. //9.9e-18:365:66//AC005828
 R-HEMBA1006744//Human Chromosome 16 BAC clone CIT987SK-327024, com

【0789】

【表489】

plate sequence.//1.3e-37:380:75//AC003108
 R-HEMBA1006754//Homo sapiens chromosome 5, P1 clone 962c5 (LBNL H8 7), complete sequence.//2.1e-75:338:85//AC003951
 R-HEMBA1006758//Homo sapiens chromosome 5, BAC clone 182a8 (LBNL H 161), complete sequence.//1.2e-112:579:95//AC005752
 R-HEMBA1006761//Plasmodium falciparum MAL3P6, complete sequence.//0.0022:528:58//Z98551
 R-HEMBA1006779//Homo sapiens chromosome 17, clone hRPK.628_E_12, c complete sequence.//2.3e-46:305:87//AC005701
 R-HEMBA1006780//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//7.2e-3 9:305:82//AL022323
 R-HEMBA1006789//Streptomyces coelicolor cosmid 6G4.//0.0085:449:61 //AL031317
 R-HEMBA1006795//Homo sapiens chromosome 17, clone hRPK.346_K_10, c complete sequence.//4.1e-43:355:80//AC006120
 R-HEMBA1006796//HS_3038_B2_H11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3038 Col=22 Row=P, gen omic survey sequence.//0.99:158:63//AQ102483
 R-HEMBA1006807//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUEN CE, 33 unordered pieces.//8.4e-47:481:75//AC004854
 R-HEMBA1006821//Homo sapiens chromosome 17, clone hRPC.62_0_9, com plete sequence.//3.0e-08:84:90//AC004797
 R-HEMBA1006824//Homo sapiens DNA sequence from PAC 958B3 on chromo some Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//3.7e-54:4 96:76//Z93023
 R-HEMBA1006832//Homo sapiens chromosome 17, clone hRPK.243_K_12, c complete sequence.//0.70:206:65//AC005668
 R-HEMBA1006849//Homo sapiens 12q24.1 PAC RPC13-521E19 (Roswell Par k Cancer Institute Human PAC library) complete sequence.//1.2e-46: 281:91//AC004217
 R-HEMBA1006865//Mus musculus clone 101 B1 repeat region sequence./ /0.61:115:70//AF056074
 R-HEMBA1006877//Mus musculus mRNA for oxysterol-binding protein, c complete cds.//3.3e-102:618:87//AB017026
 R-HEMBA1006885
 4.2e-14:379:63//AC006839
 R-HEMBA1006900//CIT-HSP-2006M20, TR CIT-HSP Homo sapiens genomic cl one 2006M20, genomic survey sequence.//2.6e-07:230:66//B56395
 R-HEMBA1006921//Homo sapiens PAC clone DJ0777023 from 7p14-p15, co mplete sequence.//2.1e-68:267:86//AC005154
 R-HEMBA1006926
 R-HEMBA1006929//HS_3244_A2_CD1_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=2 Row=E, geno mic survey sequence.//6.9e-21:191:83//AQ207500
 R-HEMBA1006936
 R-HEMBA1006938//Colias philodice eriphyle large subunit ribosomal RNA gene, partial sequence: tRNA-Val gene, complete sequence; and small subunit ribosomal RNA gene, partial sequence, mitochondrial genes for mitochondrial RNAs.//0.11:309:59//AF044853
 R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like pr otein.//2.0e-75:371:98//AJ010841
 R-HEMBA1006949//Homo sapiens PAC clone DJ0777G09 from 7q34-q36, co mplete sequence.//0.47:240:63//AC005518
 R-HEMBA1006973//HS_2009_A2_A12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2009 Col=24 Row=A, gen omic survey sequence.//9.6e-05:407:60//AQ232302
 R-HEMBA1006976//RPC111-49L11, TJ RPC111 Homo sapiens genomic clone R-49L11, genomic survey sequence.//0.0018:184:63//AQ051701
 R-HEMBA1006993//Human thymopoietin (TMPO) gene, partial exon 5, co mplete exon 7, partial exon 8, and partial cds for thymopoietin be ta.//1.9e-47:394:79//U18271
 R-HEMBA1006996//CIT-HSP-2172D17, TF CIT-HSP Homo sapiens genomic cl one 2172D17, genomic survey sequence.//1.8e-07:365:62//B93406
 R-HEMBA1007002//Plasmodium falciparum MAL3P2, complete sequence.//0.0012:505:56//AL034558
 R-HEMBA1007017//Homo sapiens chromosome 17, clone hRPK.597_M_12, c complete sequence.//5.6e-41:437:71//AC005277
 R-HEMBA1007018//G. gallus mRNA for dynein light chain-A.//8.2e-73:5 56:80//X79088
 R-HEMBA1007045
 R-HEMBA1007051//Human DNA sequence from cosmid N69F4 on chromosome 22q11.2-qter contains EST.//9.9e-27:342:71//Z72006
 R-HEMBA1007052//Homo sapiens FSHD-associated repeat DNA, proximal region.//5.4e-85:558:87//U85056
 R-HEMBA1007062
 R-HEMBA1007066
 R-HEMBA1007073//Homo sapiens chromosome 17, clone hRPK.421_E_14, c complete sequence.//2.0e-66:476:85//AC006141
 R-HEMBA1007078//Homo sapiens chromosome 17, clone hRPK.60_A_24, co mplete sequence.//1.0e-38:179:82//AC005325
 R-HEMBA1007085//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUEN CE, 6 unordered pieces.//3.2e-49:551:73//AC006015
 R-HEMBA1007087//Human Chromosome 11 pac pDJ392a17, complete sequen ce.//1.0:261:61//AC000385
 R-HEMBA1007112//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQ UENCE, 37 unordered pieces.//0.043:295:62//AC004803
 R-HEMBA1007113//Homo sapiens (subclone 6_a8 from P1 H16) DNA sequen ce.//1.4e-52:307:87//L43392
 R-HEMBA1007129//Human DNA sequence from PAC 863K19 on chromosome X. Contains STS.//1.2e-08:131:75//Z92547
 R-HEMBA1007147//H.sapiens CpG island DNA genomic MseI fragment, cl one 65f1, reverse read cpg65f1.rt1a.//0.16:187:64//Z62246
 R-HEMBA1007149//Homo sapiens chromosome 19, cosmid F23149, complet e sequence.//7.6e-108:543:96//AC005239
 R-HEMBA1007151//Homo sapiens PAC clone DJ0745K06 from 7q31, comple te sequence.//0.14:323:58//AC004875
 R-HEMBA1007174//Homo sapiens epsin 2a mRNA, complete cds.//5.1e-10 3:529:94//AF062085
 R-HEMBA1007178//Homo sapiens chromosome 12p13.3 clone RPC111-372B 4, WORKING DRAFT SEQUENCE, 129 ordered pieces.//5.4e-106:537:96//A C005911
 R-HEMBA1007194//Homo sapiens Xp22 bins 87-93 PAC RPC11-122K4 (Rosw ell Park Cancer Institute Human PAC Library) complete sequence.// 4.1e-39:262:80//AC003035
 R-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete c ds.//5.3e-61:332:95//D86987
 R-HEMBA1007206//Homo sapiens DNA sequence from PAC 958B3 on chromo some Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//1.9e-50:4 36:81//Z93023
 R-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cd s.//2.3e-96:471:97//AB018340
 R-HEMBA1007251//Homo sapiens chromosome 5, PAC clone 247f3 (LBNL H 85), complete sequence.//0.011:349:62//AC004777
 R-HEMBA1007256//Homo sapiens PAC clone DJ0676L20 from 7q35-q36, co mplete sequence.//2.8e-10:224:70//AC004856
 R-HEMBA1007267//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//3.4e-53:36 2:86//AC005924
 R-HEMBA1007273
 R-HEMBA1007279//Rickettsia prowazekii strain Madrid E, complete ge nome: segment 4/4.//0.042:454:57//AJ235273
 R-HEMBA1007281//Rickettsia prowazekii strain Madrid E, complete ge nome: segment 3/4.//0.99:288:60//AJ235272
 R-HEMBA1007288//Human DNA sequence from clone 422G23 on chromosome 6q24 Contains EST, STS, GSS, CpG island, complete sequence.//7.4 e-107:554:95//AL031003
 R-HEMBA1007300//Caenorhabditis elegans cosmid C48C5.//0.22:474:59// U39994
 R-HEMBA1007301
 R-HEMBA1007319//Campylobacter jejuni repetitive DNA, clone pINT.// 4.9e-08:524:58//Y14425
 R-HEMBA1007320//Homo sapiens genomic DNA, chromosome 21q11.1, segm ent 14/28, WORKING DRAFT SEQUENCE.//3.4e-16:244:71//AP000043
 R-HEMBA1007322//Homo sapiens BAC clone RG324D18 from 7p15-p21, com plete sequence.//3.9e-83:383:85//AC005251
 R-HEMBA1007327//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 7706, WORKING DRAFT SEQUENCE.//1.6e-38:533:71//Z96804
 R-HEMBA1007341//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 268D13, WORKING DRAFT SEQUENCE.//3.6e-21:394:66//AL0235 13
 R-HEMBA1007342//Human BAC clone GS368F15 from 7q31, complete sequen ce.//1.7e-15:190:73//AC003080
 R-HEMBA1007347//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone N38G6, WORKING DRAFT SEQUENCE.//2.2e-47:455:77//Z96802
 R-HEMBA1000005//Homo sapiens 3p21.1-9 PAC RPC14-793P23 (Roswell Pa rk Cancer Institute Human PAC Library) complete sequence.//1.1e-6 2:539:79//AC006208
 R-HEMBA1000008//Homo sapiens chromosome 17, clone hCIT.211_P_7, co mplete sequence.//1.2e-36:285:83//AC003665
 R-HEMBA1000018//Homo sapiens clone DJ0038110, WORKING DRAFT SEQUEN CE, 5 unordered pieces.//1.2e-51:416:79//AC004820
 R-HEMBA1000024//Human DNA sequence from BAC 175E3 on chromosome 22 q11.2-qter. Contains ESTs, STSs and polymorphic CA repeat.//3.9e-1 8:211:79//Z95113
 R-HEMBA1000025//HS_3064_B2_807_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=14 Row=D, gen omic survey sequence.//5.9e-40:254:90//AQ132765
 R-HEMBA1000030//Human DNA sequence from clone 108K11 on chromosome 6p21 Contains SRP20 (SR protein family member), Ndr protein kinas

【0790】

【表490】

e gene similar to yeast suppressor protein SRP40. EST and GSS, complete sequence.//1.5e-32:452:70//Z85986

R-HEM8B100036//CIT-HSP-2024L15. TF CIT-HSP Homo sapiens genomic clone 2024L15, genomic survey sequence.//9.3e-63:541:77//B66264

R-HEM8B100037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//7.6e-91:467:97//AF084928

R-HEM8B100039//Homo sapiens chromosome 17, clone hRPK.401_0_9, complete sequence.//2.4e-44:456:68//AC005291

R-HEM8B100044//Human BAC clone RGD16J04 from 7q21, complete sequence.//1.4e-54:307:80//AC002064

R-HEM8B100048//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279810, complete sequence.//3.8e-09:330:63//AC002300

R-HEM8B100050//Human DNA sequence from PAC 436M11 on chromosome X p22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the R51 gene for retinoblastoma (X-linked, juvenile) 1 (XLR51). Contains ESTs, an STS and GSSs, complete sequence.//6.7e-12:225:65//Z94056

R-HEM8B100054//Human DNA sequence from clone 444C7 on chromosome 6p22.3-23. Contains an EST, an STS and GSSs, complete sequence.//8.9e-76:557:82//AL033521

R-HEM8B100055//Human housekeeping (Q1Z TF5) gene, exons 2 through 7, complete cds.//1.6e-88:350:86//M81806

R-HEM8B100059//Homo sapiens clone DJ0850101, WORKING DRAFT SEQUENCE, 1 unordered pieces.//4.9e-12:356:65//AC006009

R-HEM8B100083//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//3.7e-41:311:82//AC004840

R-HEM8B100089//Homo sapiens clone DJ1021120, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.6e-34:314:78//AC005520

R-HEM8B100099//Homo sapiens DNA sequence from BAC 1216H12 on chromosome 22q12. Contains a pseudogene with similarity to part of mouse Ninoin and the KIAA0609 gene for a protein similar to C. elegans K09C8.4. Contains ESTs, GSSs and a ggtt repeat polymorphism, complete sequence.//8.8e-32:434:71//AL008715

R-HEM8B100103//Human DNA sequence from BAC 445C9 on chromosome 22q12.1. Contains CRYBB1, beta B1 crystallin, CRYBA4, beta A4 crystallin, high mobility group-1 protein (HMG-1), ESTs.//2.5e-16:207:74//Z95115

R-HEM8B100113//HS_3013_A1_B08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3013 Col=15 Row=C, genomic survey sequence.//0.94:211:63//AQ118730

R-HEM8B100119//Homo sapiens ASMTL gene.//1.9e-106:531:96//Y15521

R-HEM8B100136//Human Chromosome X, complete sequence.//0.00073:359:59//AC002407

R-HEM8B100141//Homo sapiens chromosome 21q22.3 PAC 39C17, complete sequence.//6.8e-41:280:74//AF043945

R-HEM8B100144//Homo sapiens chromosome 17, clone hCIT.507_E_2, complete sequence.//0.00083:206:66//AC004134

R-HEM8B100173//Homo sapiens, WORKING DRAFT SEQUENCE, 97 unordered pieces.//2.5e-82:401:90//AC004085

R-HEM8B100175

R-HEM8B100198//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//0.91:428:56//AL021368

R-HEM8B100215//Homo sapiens DNA sequence from PAC 69E11 on chromosome 1q23-24. Contains a NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, CI-MLRQ) LIKE pseudogene, a 60S Ribosomal protein L34 LIKE pseudogene, an unknown gene similar to yeast YPR037W and worm C02C2.6 predicted genes, a predicted CpG island, ESTs and an STS, complete sequence.//4.4e-54:298:91//AL021397

R-HEM8B100217

R-HEM8B100218//Homo sapiens 12q24 PAC RPC11-66E7 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.8e-32:517:70//AC004216

R-HEM8B100226//Human DNA sequence from cosmid COS12 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3. Contains ESTs, Flanking sequences of 3' alpha globin HVR and CpG island.//2.5e-77:450:92//Z69706

R-HEM8B100240//Homo sapiens chromosome 9 duplication of the T cell receptor beta locus and trypsinogen gene families.//4.1e-05:310:62//AF029308

R-HEM8B100244//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1112F19, WORKING DRAFT SEQUENCE.//1.3e-43:278:85//AL034420

R-HEM8B100250//Human DNA sequence from clone 34B20 on chromosome 6p21.31-22.2. Contains seventeen Histone (pseudo)genes and a 40S Ribosomal protein-370 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//3.8e-16:484:64//AL031777

R-HEM8B100258//Human hereditary haemochromatosis region, histone 2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Ro Ret gene, and sodium phosphate transporter (NPT3) gene, complete cds.//4.3e-11:286:67//U91328

R-HEM8B100264//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//1.2e-42:406:79//AF079765

R-HEM8B100266//RPC111-76C20, TV RPC111 Homo sapiens genomic clone 76C20, genomic survey sequence.//1.0:232:59//AQ265533

R-HEM8B100272//HS_3032_B1_H06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=11 Row=P, genomic survey sequence.//0.0082:209:62//AQ096702

R-HEM8B100274//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGLC Region, complete sequence.//1.6e-45:277:72//AC000053

R-HEM8B100284//Homo sapiens full length insert cDNA clone Y88A05.//6.9e-112:572:96//AF088018

R-HEM8B100307//Homo sapiens chromosome 17, clone hRPK.471_L_13, complete sequence.//5.7e-96:523:93//AC005244

R-HEM8B100312//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 32B1, WORKING DRAFT SEQUENCE.//7.5e-21:218:67//AL023693

R-HEM8B100317//Toxoplasma gondii chloroplast, complete genome.//0.062:354:58//U87145

R-HEM8B100318//Human DNA sequence from PAC 292H14 on chromosome X p21. Contains STS and CA repeat polymorphism.//4.5e-52:302:81//AL008710

R-HEM8B100335//Homo sapiens chromosome 5, P1 clone 1041F10 (LBNL H88), complete sequence.//1.9e-16:139:84//AC005179

R-HEM8B100336//Homo sapiens complete genomic sequence between D16S3070 and D16S3275, containing Familial Mediterranean Fever gene disease.//0.0062:231:64//AJ003147

R-HEM8B100337//CIT-HSP-2329010. TF CIT-HSP Homo sapiens genomic clone 2329010, genomic survey sequence.//1.2e-31:192:92//AQ035976

R-HEM8B100338//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-24B7, complete sequence.//1.9e-39:477:71//AC004605

R-HEM8B100339//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 862K6, WORKING DRAFT SEQUENCE.//4.1e-54:357:76//AL031681

R-HEM8B100341//Homo sapiens 12q24 PAC RPC13-424M6 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.8e-19:501:63//AC002350

R-HEM8B100343//Homo sapiens chromosome 16, cosmid clone 367E12 (L AML), complete sequence.//3.6e-41:457:72//AC004644

R-HEM8B100354//Human DNA sequence from PAC 560B9 on chromosome 1q24-1q25. Contains profilin-like pseudogene, 60S ribosomal protein L4 pseudogene RNA binding protein, ESTs, GSS.//7.2e-36:325:74//Z98751

R-HEM8B100369//Homo sapiens chromosome 4 clone 8366024 map 4q25, complete sequence.//9.0e-25:179:79//AC004067

R-HEM8B100374//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 75N14, WORKING DRAFT SEQUENCE.//8.4e-58:332:79//Z97199

R-HEM8B100376//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.1e-47:309:88//D87675

R-HEM8B100391//Homo sapiens clone RG269P13, WORKING DRAFT SEQUENCE, 6 unordered pieces.//5.7e-46:302:85//AC005080

R-HEM8B100399//Homo sapiens Rad17-like protein (RAD17) mRNA, complete cds.//1.0e-107:531:97//AF076838

R-HEM8B100402//Human DNA sequence from clone 505B13 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//1.1e-25:441:67//Z98052

R-HEM8B100404//HS_2246_A2_D01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2246 Col=2 Row=G, genomic survey sequence.//0.0025:196:63//AQ084251

R-HEM8B100420//Homo sapiens Chromosome 22q11.2 Cosmid Clone 817g In IGLC Region, complete sequence.//1.2e-29:358:72//AC000053

R-HEM8B100434//Homo sapiens chromosome 4 clone 871M12 map 4q25, complete sequence.//2.8e-51:299:89//AC004069

R-HEM8B100438//HS_2239_B2_E08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2239 Col=16 Row=J, genomic survey sequence.//1.3e-10:76:100//AQ067700

R-HEM8B100441//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//4.4e-60:281:90//Z82207

R-HEM8B100449//Homo sapiens clone DJ0898018, WORKING DRAFT SEQUENCE, 8 unordered pieces.//4.8e-11:228:68//AC004920

R-HEM8B100455//Homo sapiens clone GS051M12, complete sequence.//3.1e-14:388:65//AC005007

R-HEM8B100472//Homo sapiens chromosome 17, clone HCIT48C15, complete sequence.//4.9e-34:320:79//AC003104

R-HEM8B100480//Human DNA sequence from Fosmid 65B7 on chromosome 22q11.2-qtter. Contains exons 6-12 of the SLC5A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (Hi

【0791】

【表491】

gh Affinity Sodium-Glucose Cotransporter), complete sequence.//3.4e-36:285:82//Z83849
 R-HEMBB1000487
 R-HEMBB1000490//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE.//1.5e-34:281:81//AL034423
 R-HEMBB1000491//Homo sapiens DNA sequence from PAC 95883 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//8.5e-37:483:72//Z93023
 R-HEMBB1000493//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPAR for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUC1, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a ca repeat polymorphism, complete sequence.//7.6e-14:217:71//AL022721
 R-HEMBB1000510//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27K12, WORKING DRAFT SEQUENCE.//7.1e-44:221:80//AL033397
 R-HEMBB1000518//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//3.5e-51:280:90//AC002477
 R-HEMBB1000523//Homo sapiens PAC clone DJ0167F23 from 7p15, complete sequence.//1.7e-53:304:82//AC004079
 R-HEMBB1000530//Homo sapiens chromosome 17, clone hCIT.162_E_12, complete sequence.//4.2e-74:428:92//AC006236
 R-HEMBB1000550//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//5.6e-13:112:80//U91321
 R-HEMBB1000554//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 409J21, WORKING DRAFT SEQUENCE.//5.1e-14:239:63//Z83824
 R-HEMBB1000556//Homo sapiens enolpyruvate kinase (EYPL) mRNA, complete cds.//0.031:275:60//U53786
 R-HEMBB1000564//Homo sapiens chromosome 5, BAC clone 189 (LBML H135), complete sequence.//3.1e-17:227:76//AC005914
 R-HEMBB1000573//Borrelia afzelii (strain NT28) DNA, internal transcribed spacer.//0.078:161:63//D84405
 R-HEMBB1000575//Homo sapiens chromosome 17, clone hRPC.859_O_20, complete sequence.//7.2e-52:260:80//AC003695
 R-HEMBB1000586//Human DNA sequence from cosmid Y210E9, between markers DXS366 and DXS87 on chromosome X.//2.0e-33:305:79//Z70280
 R-HEMBB1000589//Homo sapiens chromosome 17, clone hRPC.1064_E_11, complete sequence.//1.3e-14:409:65//AC005208
 R-HEMBB1000591//Homo sapiens Xp22 bins 45-47 BAC GSHB-665W22 (Genome Systems Human BAC Library) complete sequence.//6.2e-39:493:71//AC005184
 R-HEMBB1000592//Homo sapiens 12p13.3 PAC RPC15-1180D12 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.6e-08:254:64//AC005831
 R-HEMBB1000598//Homo sapiens chromosome 11 pac pDJ159a1, complete sequence.//3.3e-38:407:76//AC000381
 R-HEMBB1000623//CIT-HSP-2374P17, TR CIT-HSP Homo sapiens genomic clone 2374P17, genomic survey sequence.//1.3e-41:212:100//AQ109717
 R-HEMBB1000630//Human DNA sequence from clone 413H6 on chromosome 6p22.3-24.3. Contains a hamster Androgen-dependent Expressed Protein like protein gene, ESTs and GSSs, complete sequence.//5.2e-31:319:78//AL022724
 R-HEMBB1000631//Sequence 28 from patent US 5708157.//6.8e-20:208:80//I80058
 R-HEMBB1000632//Homo sapiens Cosmid C4, WORKING DRAFT SEQUENCE, 1 ordered pieces.//7.4e-47:457:75//AC004176
 R-HEMBB1000637//Human BAC clone RG094H21 from 7q21-q22, complete sequence.//2.9e-45:263:87//AC003085
 R-HEMBB1000638//Genomic sequence from Human 6, complete sequence.//9.1e-34:375:73//AC002112
 R-HEMBB1000643//HS_2242_A2_B07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-2242 Col=14 Row=C, genomic survey sequence.//0.010:239:60//AQ065993
 R-HEMBB1000649//Homo sapiens RBP56/HTAF1168 gene, exon 7.//8.3e-63:306:100//AB010061
 R-HEMBB1000652//Human DNA sequence from PAC 467D16 on chromosome 6p22.3-24.1. Contains the 3' part of the SCA1 (ataxin-1) gene with a poly-glutamine (CAG repeat) polymorphism, the 3' part of the GMP reductase, Guanosine 5'-monophosphate oxidoreductase) gene, ESTs and an STS with a polymorphic CA repeat.//3.3e-14:450:64//AL009031
 R-HEMBB1000665//Arabidopsis thaliana genomic DNA, chromosome 5, PI clone: MXA21, complete sequence.//0.98:251:63//AB005247
 R-HEMBB1000671//Human DNA sequence from PAC 106C24, between markers DXS294 and DXS730 on chromosome X.//6.8e-58:296:85//Z83313
 R-HEMBB1000673//CITB1-E1-2506F20, TR CITB1-E1 Homo sapiens genomic clone 2506F20, genomic survey sequence.//0.98:71:76//AQ264731
 R-HEMBB1000684//Human DNA sequence from clone 1158E12 on chromosome Xp11.23-11.4 Contains EST, STS, GSS, CpG island, complete sequence.//2.6e-11:153:77//AL031584
 R-HEMBB1000688//Homo sapiens neuroan mRNA, complete cds.//2.0e-50:287:93//AF040723
 R-HEMBB1000705//Homo sapiens chromosome 19, cosmid R30538, complete sequence.//3.4e-18:340:65//AC005943
 R-HEMBB1000706//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 462C17, WORKING DRAFT SEQUENCE.//4.7e-10:358:64//AL033380
 R-HEMBB1000709//RPC111-79A8.TV RPC111 Homo sapiens genomic clone R-79A8, genomic survey sequence.//1.4e-40:262:89//AQ282374
 R-HEMBB1000725//Arabidopsis thaliana genomic DNA, chromosome 5, PI clone: MGN6, complete sequence.//0.00018:386:60//AB017066
 R-HEMBB1000726//Homo sapiens PAC clone DJ1185I07 from 7q11.23-q21, complete sequence.//1.5e-48:316:88//AC004990
 R-HEMBB1000738//Homo sapiens PAC clone DJ0745K06 from 7q31, complete sequence.//7.1e-53:382:85//AC004875
 R-HEMBB1000749//Homo sapiens clone RG140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.5e-51:438:80//AC005069
 R-HEMBB1000763//Plasmid Col 1b-P9 (from E.coli K12) colicin 1b promoter region and 5' coding region.//1.0:115:63//K02071
 R-HEMBB1000770//Human Rhesus blood group antigen (RHCE) gene, intron 6, partial sequence.//5.6e-24:183:86//U83205
 R-HEMBB1000781//Homo sapiens Xp22 PACs RPC11-263P4 and RPC11-164K3 complete sequence.//0.00054:154:67//AC003046
 R-HEMBB1000789//RPC111-2114.TVB RPC11-11 Homo sapiens genomic clone RPC11-2114, genomic survey sequence.//3.0e-09:299:64//B63628
 R-HEMBB1000790//Human Chromosome 16 BAC clone CIT987SK-A-362G6, complete sequence.//4.5e-46:185:85//U95740
 R-HEMBB1000794//HS_3253_A1_G06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3253 Col=11 Row=M, genomic survey sequence.//5.7e-13:172:65//AQ216291
 R-HEMBB1000807
 R-HEMBB1000810//Human BAC clone RG114A06 from 7q31, complete sequence.//1.3e-24:385:71//AC002542
 R-HEMBB1000821
 R-HEMBB1000822//CITB1-E1-2517E13.TF CITB1-E1 Homo sapiens genomic clone 2517E13, genomic survey sequence.//4.5e-08:278:64//AQ279944
 R-HEMBB1000826//Homo sapiens genomic DNA, chromosome 21q11.1, segment 14/28, WORKING DRAFT SEQUENCE.//1.2e-44:521:72//AP000043
 R-HEMBB1000827//Homo sapiens clone DJ0981007, complete sequence.//6.8e-43:319:84//AC006017
 R-HEMBB1000831//HS_3247_B2_A09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3247 Col=18 Row=B, genomic survey sequence.//5.5e-74:381:96//AQ223850
 R-HEMBB1000835//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//4.2e-17:167:80//AL021368
 R-HEMBB1000840//Homo sapiens clone DJ1039L24, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.9e-26:220:73//AC005283
 R-HEMBB1000848//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered pieces.//7.8e-39:356:79//AC004086
 R-HEMBB1000852//HS_3075_A2_B07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3075 Col=14 Row=C, genomic survey sequence.//3.4e-11:151:75//AQ138816
 R-HEMBB1000870//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 72E17, WORKING DRAFT SEQUENCE.//1.8e-44:454:75//AL033523
 R-HEMBB1000876//Human DNA sequence from clone 91J24 on chromosome 6q24 Contains part of utrophin Gene, part of cytochrome C oxidase gene, EST, CpG island, complete sequence.//0.0016:227:65//AL024474
 R-HEMBB1000883//Homo sapiens chromosome 19, cosmid F19678, complete sequence.//0.62:238:62//AC005621
 R-HEMBB1000887//Synthetic human/adenovirus type 5 recombination junction.//9.9e-24:275:76//M34061
 R-HEMBB1000888//CIT-HSP-2282A13, TR CIT-HSP Homo sapiens genomic clone 2282A13, genomic survey sequence.//2.4e-05:310:60//AQ00826
 R-HEMBB1000890//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.//6.5e-44:305:84//AC005995
 R-HEMBB1000893//Homo sapiens BAC clone RG363E19 from 7q31.1, complete sequence.//3.7e-30:265:80//AC004492
 R-HEMBB1000908//RPC111-13P12.TV RPC11-11 Homo sapiens genomic clone RPC11-11-13P12, genomic survey sequence.//0.98:183:61//B76199
 R-HEMBB1000910//Homo sapiens Chromosome 22q11.2 Cosmid Clone 50d10

【0792】

【表492】

In IGLC Region, complete sequence.//1.7e-28:302:76//AC000024
 R-HEMBB1000913//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//4.1e-34:314:76//AC003037
 R-HEMBB1000915//Human chromosome 16p11.2-p12 BAC clone CIT987SK-22 406 complete sequence.//6.3e-09:536:59//U95739
 R-HEMBB1000917//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 16915, WORKING DRAFT SEQUENCE.//1.6e-47:234:86//Z93015
 R-HEMBB1000927
 R-HEMBB1000947//CIT-HSP-2287M13.TF CIT-HSP Homo sapiens genomic clone 2287M13, genomic survey sequence.//0.090:115:69//B99228
 R-HEMBB1000959//Homo sapiens chromosome 17, clone HRPC905N1, complete sequence.//5.7e-89:544:90//AC003098
 R-HEMBB1000973//Arabidopsis thaliana chromosome 11 BAC F219 genomic sequence, complete sequence.//0.038:377:58//AC005580
 R-HEMBB1000975//Arabidopsis thaliana chromosome 11 BAC FSH14 genomic sequence, complete sequence.//1.0e-05:342:62//AC006234
 R-HEMBB1000981//CIT-HSP-2386J13.TF.1 CIT-HSP Homo sapiens genomic clone 2386J13, genomic survey sequence.//1.1e-18:231:74//AQ239443
 R-HEMBB1000985//HS_3184_A1_012_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3184 Col=23 Row=G, genomic survey sequence.//6.3e-52:286:95//AQ150008
 R-HEMBB1000991
 R-HEMBB1000996//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1, 2, and 3, complete sequence.//1.4e-42:343:81//AC002368
 R-HEMBB1001004
 R-HEMBB1001008//CITBI-E1-2504L23.TF CITBI-E1 Homo sapiens genomic clone 2504L23, genomic survey sequence.//3.1e-57:317:94//AQ262056
 R-HEMBB1001011//HS_3017_B1_C03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3017 Col=5 Row=N, genomic survey sequence.//7.3e-34:237:86//AQ101944
 R-HEMBB1001014//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460J8, WORKING DRAFT SEQUENCE.//2.4e-49:417:80//AL031662
 R-HEMBB1001020//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete sequence.//7.6e-41:303:76//AC002549
 R-HEMBB1001024//Homo sapiens (subclone 2_g5 from P1 H16) DNA sequence.//7.4e-48:341:85//L48475
 R-HEMBB1001037//Homo sapiens 22q11 BAC Clone 489d1 in MDR Region, complete sequence.//2.0e-50:416:82//AC005527
 R-HEMBB1001047//Homo sapiens chromosome 19, cosmid R31973, complete sequence.//8.4e-22:288:71//AC004699
 R-HEMBB1001051//H. sapiens mRNA for FAM protein.//7.1e-18:114:98//X96586
 R-HEMBB1001056//Homo sapiens clone DJ0953A04, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.1e-94:520:93//AC006014
 R-HEMBB1001058//Homo sapiens clone UMGCC.y17c131 from 6p21, complete sequence.//1.1e-56:242:82//AC004187
 R-HEMBB1001060//Human Tigger1 transposable element, complete consensus sequence.//4.2e-66:323:81//U49973
 R-HEMBB1001063//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 523G1, WORKING DRAFT SEQUENCE.//4.0e-114:556:98//AL034375
 R-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.8e-105:512:97//AF034803
 R-HEMBB1001096//Human DNA sequence from PAC 24608, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//2.4e-13:225:69//Z76735
 R-HEMBB1001102//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SM1/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily A, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.4e-35:295:80//AL022577
 R-HEMBB1001105//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 462023, WORKING DRAFT SEQUENCE.//7.9e-46:380:80//AL031431
 R-HEMBB1001114//Homo sapiens DNA sequence from PAC 118E23 on chromosome Xq25-q27.1. Contains glypican-3 precursor (intestinal protein OCI-5) (GTR2-2). 5' UTR. ESTs, STS.//1.1e-38:306:84//Z99570
 R-HEMBB1001117//RPC111-3518.TK RPC111 Homo sapiens genomic clone RPC111-3518, genomic survey sequence.//1.5e-08:67:100//AQ047113
 R-HEMBB1001119//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//9.0e-26:481:67//AC003071
 R-HEMBB1001126//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//0.045:127:69//Z99495
 R-HEMBB1001133//Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subunit mRNA, complete cds.//5.0e-23:285:73//W25077
 R-HEMBB1001137//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-09, complete sequence.//2.5e-07:334:62//AL010222
 R-HEMBB1001142//Human BAC clone RG164L14 from 7q21-q22, complete sequence.//2.5e-46:412:79//AC002564
 R-HEMBB1001151//Mus musculus IFN alpha-treated embryonic fibroblast mRNA.//1.8e-11:148:77//U51904
 R-HEMBB1001153//RPC111-10L7.TP RPC111 Homo sapiens genomic clone RPC111-10L7, genomic survey sequence.//2.3e-34:213:82//B71766
 R-HEMBB1001169//Homo sapiens chromosome 17, clone HCIT39G8, complete sequence.//0.040:465:56//AC003070
 R-HEMBB1001175//Sequence 1 from patent US 5618695.//2.8e-15:176:80//I40055
 R-HEMBB1001177
 R-HEMBB1001182//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-52, complete sequence.//1.9e-05:174:70//AL010226
 R-HEMBB1001199
 R-HEMBB1001208
 R-HEMBB1001209//RPC111-41E13.TP RPC111 Homo sapiens genomic clone RPC111-41E13, genomic survey sequence.//1.1e-95:473:97//AQ029098
 R-HEMBB1001210//Homo sapiens chromosome 15, cosmid clone 330D11 (LAML), complete sequence.//6.2e-08:412:61//AC005199
 R-HEMBB1001218//RPC111-13L8.TV RPC111 Homo sapiens genomic clone RPC111-13L8, genomic survey sequence.//1.0e-46:498:74//B75158
 R-HEMBB1001221//RPC111-62024.TJ RPC111 Homo sapiens genomic clone R-62024, genomic survey sequence.//3.2e-09:215:68//AQ200950
 R-HEMBB1001234
 R-HEMBB1001242
 R-HEMBB1001249//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.4e-33:361:72//AC005377
 R-HEMBB1001253//Homo sapiens chromosome 3, olfactory receptor pseudogene cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseudogene, partial sequence.//3.8e-105:517:98//AF042089
 R-HEMBB1001254//Methanococcus jannaschii section 3 of 150 of the complete genome.//0.96:203:61//U67461
 R-HEMBB1001267//Human DNA sequence from clone 1409 on chromosome X p11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain L1EKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE-LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032, complete sequence.//2.8e-39:320:80//Z98046
 R-HEMBB1001271//Homo sapiens chromosome 17, clone hRPC.349_A_8, complete sequence.//3.9e-47:494:75//AC005544
 R-HEMBB1001282//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 184J9, WORKING DRAFT SEQUENCE.//0.0011:97:79//AL031428
 R-HEMBB1001288
 R-HEMBB1001289//Homo sapiens chromosome 5, BAC clone 343g16 (LBNL H180), complete sequence.//2.0e-31:301:78//AC005601
 R-HEMBB1001294//Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.//0.053:283:60//AC003083
 R-HEMBB1001302
 R-HEMBB1001304//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27K12, WORKING DRAFT SEQUENCE.//6.3e-15:396:64//AL033397
 R-HEMBB1001314//Homo sapiens genomic DNA, 21q region, clone: f30F8 SpN6, genomic survey sequence.//3.4e-42:293:86//AC013777
 R-HEMBB1001315//Human NFE genomic fragment.//7.5e-30:243:78//W95511
 R-HEMBB1001317//Homo sapiens chromosome 17, clone hRPC.1028_K_7, complete sequence.//2.3e-39:301:82//AC004585
 R-HEMBB1001326//HS_3054_A1_F12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=23 Row=K, genomic survey sequence.//0.90:117:63//AQ106096
 R-HEMBB1001331//Mus musculus mRNA for hepatoma-derived growth factor, complete cds, strain: BALB/c.//0.037:103:77//D63850
 R-HEMBB1001335//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//9.1e-19:229:77//AC003037
 R-HEMBB1001337
 R-HEMBB1001339//Homo sapiens FSHD-associated repeat DNA, proximal region.//2.9e-45:551:72//U85056
 R-HEMBB1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//2.7e-59:292:99//AF097441
 R-HEMBB1001348//Homo sapiens clone DJ0691F11, WORKING DRAFT SEQUENCE, 11 unordered pieces.//9.1e-41:326:82//AC004859
 R-HEMBB1001356//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//1.8e-11:213:67//Z82207
 R-HEMBB1001364//HS_3050_A2_F05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=10 Row=K, genomic survey sequence.//1.8e-21:158:91//AQ13940
 R-HEMBB1001366//Homo sapiens chromosome 10 clone CIT987SK-118815

【0793】

【表493】

ap 10p11.2-10p12.1, complete sequence.//4.1e-37:419:73//AC005876
 R-HEM8B1001367//Human Chromosome 16 BAC clone CIT987SK-A-234F9, complete sequence.//9.5e-15:201:75//U91326
 R-HEM8B1001369//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 477J10, WORKING DRAFT SEQUENCE.//1.8e-28:224:83//AL021686
 R-HEM8B1001380//HS_2267_B1_F11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2267 Col=21 Row=L, genomic survey sequence.//4.0e-14:100:95//AQ084896
 R-HEM8B1001384//Mus musculus COP9 complex subunit 4 (COP54) mRNA, complete cds.//9.6e-55:312:81//AF071314
 R-HEM8B1001387//Homo sapiens chromosome 9, P1 clone 8660 (LBML H105), complete sequence.//1.0:166:63//AC003953
 R-HEM8B1001394//Homo sapiens chromosome 17, clone hRPK.215_E_13, complete sequence.//1.4e-55:494:76//AC005549
 R-HEM8B1001410//Homo sapiens PAC clone DJ1102B04 from Tq11.23-Tq21, complete sequence.//0.011:208:63//AC006204
 R-HEM8B1001424//Homo sapiens, WORKING DRAFT SEQUENCE, 76 unordered pieces.//1.5e-22:325:69//AC002370
 R-HEM8B1001426//Homo sapiens 12q24 PAC RPC13-424M6 (Roswell Park Cancer Institute Human PAC library) complete sequence.//1.3e-46:328:84//AC002350
 R-HEM8B1001429//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0481P14: HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces.//6.6e-105:550:95//AC006160
 R-HEM8B1001436
 R-HEM8B1001443//HS_2228_A1_B05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=9 Row=C, genomic survey sequence.//0.37:173:62//AQ066934
 R-HEM8B1001449//Homo sapiens clone DJ1129E22, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.7e-23:339:69//AC005522
 R-HEM8B1001454//Homo sapiens chromosome 5, P1 clone 1307e8 (LBML H60), complete sequence.//1.1e-39:299:84//AC005355
 R-HEM8B1001458//Plasmodium falciparum chromosome 2, section 67 of 73 of the complete sequence.//6.0e-05:486:59//AE001430
 R-HEM8B1001463//Homo sapiens PAC clone DJ0777023 from Tpl4-p15, complete sequence.//1.2e-50:317:89//AC005154
 R-HEM8B1001464//CIT-HSP-2370C10.TF CIT-HSP Homo sapiens genomic clone 2370C10, genomic survey sequence.//0.20:95:71//AQ107941
 R-HEM8B1001482//Mus musculus clone OST20235, genomic survey sequence.//4.3e-09:192:70//AF046762
 R-HEM8B1001500//Human DNA sequence from PAC 465G10 on chromosome X contains Menkes Disease (ATPA) putative Cutt-transporting P-type ATPase exons 2 to 21, PGAM-B, ESTs.//1.9e-21:253:70//Z94801
 R-HEM8B1001521//Mus musculus clone OST1209, genomic survey sequence.//7.5e-30:332:75//AF046642
 R-HEM8B1001527//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENCE, 7 unordered pieces.//9.5e-55:483:76//AC005090
 R-HEM8B1001531//Human BAC clone 7E17 from 12q, complete sequence.//1.3e-08:159:71//AC002070
 R-HEM8B1001535//Human DNA sequence from cosmid E127C11 on chromosome 22q11.2-oter contains STS.//4.0e-30:285:79//Z74581
 R-HEM8B1001536//Homo sapiens cosmid clone LUCA16 from 3p21.3, complete sequence.//1.6e-39:342:80//U73169
 R-HEM8B1001537//Genomic sequence from Human 9q34, complete sequence.//3.7e-41:361:77//AC000394
 R-HEM8B1001555//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-48SG10, complete sequence.//0.34:212:61//AC003049
 R-HEM8B1001562//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-32BA3, complete sequence.//8.0e-40:267:88//AC002301
 R-HEM8B1001564//Homo sapiens clone DJ0414A15, WORKING DRAFT SEQUENCE, 9 unordered pieces.//5.1e-30:286:76//AC005225
 R-HEM8B1001565//Homo sapiens clone DJ0607J02, WORKING DRAFT SEQUENCE, 12 unordered pieces.//2.5e-15:194:75//AC004840
 R-HEM8B1001585//Human DNA sequence from clone 79086 on chromosome 20p11.22-12.2. Contains STSs and GSSs, complete sequence.//2.6e-33:234:79//AL031677
 R-HEM8B1001586//Homo sapiens clone NHD479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//2.7e-30:371:74//AC005236
 R-HEM8B1001588//Homo sapiens Xp22 GS-52411 (Genome Systems Human BAC library), complete sequence.//8.0e-32:323:73//AC003106
 R-HEM8B1001603//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-59, complete sequence.//0.034:302:59//AL010235
 R-HEM8B1001618//Homo sapiens DNA sequence from PAC 95883 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//7.1e-31:503:68//Z93023
 R-HEM8B1001619//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//3.7e-50:539:72//AC002368
 R-HEM8B1001630//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs, polymorphic CA repeat, CpG island, CpG island genomic fragments.//1.3e-27:228:82//Z86062
 R-HEM8B1001635//Homo Sapiens Chromosome X clone bWXD90, complete sequence.//1.5e-23:407:69//AC004075
 R-HEM8B1001637//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1,2, and 3, complete sequence.//3.9e-54:519:74//AC002368
 R-HEM8B1001641//Human DNA sequence from clone 133H11 on chromosome 6p24. Contains STSs, GSSs and genomic marker D6S410, complete sequence.//1.9e-08:464:60//AL024506
 R-HEM8B1001653//Homo sapiens chromosome 17, clone HC1T3L16, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.8e-39:318:82//AC002344
 R-HEM8B1001665//***ALU WARNING: Human Alu-Sp subfamily consensus sequence.//3.8e-47:283:90//U14572
 R-HEM8B1001668
 R-HEM8B1001673//Homo sapiens mRNA for KIAA0645 protein, complete cds.//1.8e-115:573:97//AB014546
 R-HEM8B1001684//Sequence 1 from patent US 5700927.//1.9e-40:343:77//186429
 R-HEM8B1001685//Homo sapiens chromosome 17, clone hRPK.721_K_1, complete sequence.//2.6e-43:311:83//AC005411
 R-HEM8B1001695
 R-HEM8B1001704//CIT-HSP-2324C15.TR CIT-HSP Homo sapiens genomic clone 2324C15, genomic survey sequence.//0.0074:259:58//AQ028704
 R-HEM8B1001706//Homo sapiens clone DJ0665P05, WORKING DRAFT SEQUENCE, 5 unordered pieces.//9.1e-34:296:80//AC004851
 R-HEM8B1001707//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-319E8, complete sequence.//7.7e-32:241:76//AC004020
 R-HEM8B1001717//CIT-HSP-2378C19.TF CIT-HSP Homo sapiens genomic clone 2378C19, genomic survey sequence.//4.8e-35:228:89//AQ108992
 R-HEM8B1001735//Homo sapiens chromosome 5, BAC clone 114k9 (LBML H94), complete sequence.//1.8e-10:80:90//AC005613
 R-HEM8B1001736//CIT-HSP-2369K6.TF CIT-HSP Homo sapiens genomic clone 2369K6, genomic survey sequence.//9.9e-38:242:90//AQ075221
 R-HEM8B1001747//Homo sapiens cosmid Qc14E2, Qc12H12, Qc11F9, Qc10G9, LA173 and Qc17B8 from Xq28, complete sequence.//3.3e-60:366:80//U82671
 R-HEM8B1001749//Homo sapiens chromosome 17, clone hRPK.259_G_18, complete sequence.//1.4e-60:242:92//AC005829
 R-HEM8B1001753//RPC111-59J22.TK RPC111 Homo sapiens genomic clone R-59J22, genomic survey sequence.//6.2e-08:281:64//AQ000446
 R-HEM8B1001756//Homo sapiens BAC clone RG293F17 from Tpl5-p21, complete sequence.//3.1e-18:395:67//AC004130
 R-HEM8B1001760//Homo sapiens genomic DNA, chromosome 21q11.1, segment 21/28, WORKING DRAFT SEQUENCE.//9.9e-18:416:64//AP000050
 R-HEM8B1001762//Mus musculus major histocompatibility locus class II region: major histocompatibility protein class II alpha chain (IAalpha) and major histocompatibility protein class II beta chain (IEbeta) genes, complete cds; butyrophilin-like (NG9), butyrophilin-like (NG10), hypothetical protein (NG8), and butyrophilin-like (NG11) genes, partial cds; NG12 pseudogene, partial sequence; and hypothetical butyrophilin-like protein (NG13) gene, partial cds.//0.21:521:57//AF050157
 R-HEM8B1001785//Torulopsis glabrata mitochondrial intergenic region ATPase 6-ATPase 9 genes.//0.00073:189:65//X02170
 R-HEM8B1001797//Plasmodium falciparum 307 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.0049:322:62//AC005140
 R-HEM8B1001802//Human desmin gene, complete cds.//8.1e-95:510:93//M63391
 R-HEM8B1001812//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 356B8, WORKING DRAFT SEQUENCE.//1.3e-71:368:96//Z98882
 R-HEM8B1001816//Homo sapiens chromosome 21 PAC LLNLP704G1150Q13.//8.4e-21:164:76//AJ006996
 R-HEM8B1001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds.//1.7e-104:498:98//AF056209
 R-HEM8B1001836//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//9.2e-44:388:71//AC005328
 R-HEM8B1001839
 R-HEM8B1001850//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MOP10, complete sequence.//0.00093:488:60//AB005241
 R-HEM8B1001863//Human poly(ADP-ribose) polymerase gene, 5' end.//1.2e-16:458:65//M60436
 R-HEM8B1001867//Human DNA sequence from cosmid U25D11, between markers DXS366 and DXS87 on chromosome X.//5.0e-31:399:74//Z68327
 R-HEM8B1001868//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MYN8, complete sequence.//0.26:303:59//AB020754
 R-HEM8B1001869//Homo sapiens chromosome 17, clone hC1T529110, comp

【0794】

【表494】

lete sequence.//7.0e-37:285:85//AC002553
R-HEMBB1001872//Caenorhabditis elegans DNA *** SEQUENCING IN PROGR
ESS *** from clone Y44F5, WORKING DRAFT SEQUENCE.//0.093:367:58//A
L009027
R-HEMBB1001874
R-HEMBB1001875//Lactococcus lactis DPC3147 plasmid pMRC01, complet
e plasmid sequence.//0.037:406:60//AE001272
R-HEMBB1001880//Homo sapiens chromosome 17, clone hRPK.235_1_10, c
omplete sequence.//1.3e-49:461:77//AC005922
R-HEMBB1001899//Caenorhabditis elegans DNA *** SEQUENCING IN PROGR
ESS *** from clone Y116A8, WORKING DRAFT SEQUENCE.//0.56:295:60//Z
98858
R-HEMBB1001905//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone Y738F9, WORKING DRAFT SEQUENCE.//1.9e-28:181:75//AL0223
45
R-HEMBB1001906
R-HEMBB1001908//Genomic sequence from Human 17, complete sequence.
//2.9e-36:274:76//AC001231
R-HEMBB1001910//Homo sapiens chromosome 17, clone HCIT39G8, comple
te sequence.//3.5e-41:408:76//AC003070
R-HEMBB1001911//Homo sapiens *** SEQUENCING IN PROGRESS *** WORKI
NG DRAFT SEQUENCE.//6.1e-64:310:89//AJ011929
R-HEMBB1001915//Mouse mRNA for arylhydrocarbon receptor, complete
cds.//2.0e-20:220:78//D38417
R-HEMBB1001921//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 1141E15, WORKING DRAFT SEQUENCE.//1.9e-47:410:80//AL034
422
R-HEMBB1001922//Homo sapiens chromosome 17, clone HCIT421K24, comple
te sequence.//6.2e-32:378:74//AC004099
R-HEMBB1001925//Human Chromosome 11 overlapping pacs pDJ235k10 and
pDJ239b22, WORKING DRAFT SEQUENCE, 17 unordered pieces.//8.2e-41:
304:84//AC000406
R-HEMBB1001930//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncoge
ne of hepatocellular colorectal and non-small cell lung cancer, s
egment 10/11.//8.3e-12:202:69//AB020867
R-HEMBB1001944//P. falciparum gene for beta subunit RNA polymerase.
//0.00090:264:62//X75544
R-HEMBB1001945//Swietenia humilis DNA for simple tandem repeat (24
bp).//0.056:224:62//AJ000408
R-HEMBB1001947//RPC111-60L13.TJ RPC111 Homo sapiens genomic clone
R-60L13, genomic survey sequence.//7.4e-23:146:94//AQ202335
R-HEMBB1001950//Human DNA sequence from clone 415G2 on chromosome
22 Contains synapsin IIIa exon 1, EST and GSS, complete sequence.//
0.57:115:68//Z83846
R-HEMBB1001952//Homo Sapiens Chromosome X clone bWID171, WORKING D
RAFT SEQUENCE, 1 ordered pieces.//5.6e-36:283:84//AC004676
R-HEMBB1001953//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUEN
CE, 7 unordered pieces.//8.9e-60:334:82//AC005037
R-HEMBB1001957//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENC
E, 2 unordered pieces.//1.9e-56:518:77//AC005077
R-HEMBB1001962//Homo sapiens chromosome 16, BAC clone 462G18 (LAM
L), complete sequence.//3.2e-19:157:86//AC005736
R-HEMBB1001967//Homo sapiens DNA for amyloid precursor protein, co
mplete cds.//5.7e-68:314:89//D87675
R-HEMBB1001973//Homo sapiens *** SEQUENCING IN PROGRESS *** from P
AC E7.1 / cosmid 40M1, WORKING DRAFT SEQUENCE.//1.4e-37:484:70//AJ
009617
R-HEMBB1001983//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 215D11, WORKING DRAFT SEQUENCE.//2.1e-28:286:75//AL0344
17
R-HEMBB1001988//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 1112F19, WORKING DRAFT SEQUENCE.//6.9e-29:203:88//AL034
420
R-HEMBB1001990//Homo sapiens full length insert cDNA clone ZC33G0
3.//7.8e-95:456:99//AF006192
R-HEMBB1001996
R-HEMBB1001997//Homo sapiens clone RC05Q15, WORKING DRAFT SEQUENC
E, 26 unordered pieces.//6.4e-26:162:83//AC005055
R-HEMBB1002002//Human DNA sequence from PAC 2A2 on chromosome X co
ntains ESTs.//8.2e-83:362:93//Z84816
R-HEMBB1002005//Homo sapiens chromosome 3p clone RPC15-1034C16, WO
RKING DRAFT SEQUENCE, 45 unordered pieces.//8.5e-36:291:83//AC0059
03
R-HEMBB1002009//Homo sapiens clone DJ0828F13, complete sequence.//
5.6e-08:307:65//AC004904
R-HEMBB1002015//HS-1039-A1-C10-MF.abi CIT Human Genomic Sperm Lib
rary C Homo sapiens genomic clone Plate-CT 821 Col=19 Row=E, genom
ic survey sequence.//1.9e-05:375:62//B36336
R-HEMBB1002042//CIT-HSP-2313E13.TF CIT-HSP Homo sapiens genomic cl
one 2313E13, genomic survey sequence.//0.34:241:62//AQ028389
R-HEMBB1002043//Homo sapiens chromosome 21, PI clone LBL98 (LBNL H
8), complete sequence.//7.4e-35:297:82//AC005612
R-HEMBB1002044//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL
H154), complete sequence.//5.8e-96:582:90//AC005740
R-HEMBB1002045//Homo sapiens chromosome 19, cosmid F22676, complet
e sequence.//4.7e-63:575:77//AC005778
R-HEMBB1002049//Human Chromosome X clone bWID187, complete sequenc
e.//1.9e-21:384:64//AC004383
R-HEMBB1002050//Homo sapiens chromosome 17, clone hRPK.112_J_9, co
mplete sequence.//2.5e-37:368:76//AC005553
R-HEMBB1002058//Homo sapiens chromosome 5, BAC clone 205e20 (LBNL
H170), complete sequence.//0.30:167:65//AC004782
R-HEMBB1002069//Homo sapiens chromosome 19, cosmid R33516, complet
e sequence.//2.3e-73:449:84//AC004799
R-HEMBB1002092//Homo sapiens chromosome 17, clone hRPK.269_G_24, c
omplete sequence.//3.8e-45:307:87//AC005828
R-HEMBB1002094//Homo sapiens chromosome 19, cosmid R30538, complet
e sequence.//3.1e-47:457:76//AC005943
R-HEMBB1002115//HS_2223_B1_G10_MF CIT Approved Human Genomic Sperm
Library D Homo sapiens genomic clone Plate=2223 Col=19 Row=N, gen
omic survey sequence.//3.0e-58:295:98//AQ152279
R-HEMBB1002139//ALU WARNING: Human Alu-Sq subfamily consensus s
equence.//6.6e-49:283:93//U14573
R-HEMBB1002142//Homo sapiens clone DJ0813F11, WORKING DRAFT SEQUEN
CE, 5 unordered pieces.//1.1e-45:451:76//AC006006
R-HEMBB1002152//Homo sapiens chromosome 10 clone CIT987SK-1079E16
map 10q25, complete sequence.//1.3e-57:359:81//AC005881
R-HEMBB1002189//Human Chromosome 11 pac pDJ392a17, complete sequen
ce.//4.5e-43:420:77//AC000385
R-HEMBB1002190//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUEN
CE, 6 unordered pieces.//8.2e-33:340:64//AC004913
R-HEMBB1002193//Sequence 5 from patent US 5709858.//3.2e-23:154:92
//180846
R-HEMBB1002217//Homo sapiens clone HS19.2 Alu-Ya5 sequence.//2.6e-
52:415:81//AF015148
R-HEMBB1002218//, complete sequence.//3.4e-17:178:82//AC005300
R-HEMBB1002232//*** SEQUENCING IN PROGRESS *** Homo sapiens chromo
some 4, BAC clone C0052122; HTGS phase 1, WORKING DRAFT SEQUENCE,
4 unordered pieces.//1.6e-55:292:88//AC004599
R-HEMBB1002247//Homo sapiens chromosome 17, clone hRPK.259_G_18, c
omplete sequence.//2.9e-13:227:70//AC005829
R-HEMBB1002249//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 455J7, WORKING DRAFT SEQUENCE.//1.1e-06:284:64//AL03173
3
R-HEMBB1002254//Human Chromosome X, WORKING DRAFT SEQUENCE, 6 unor
dered pieces.//6.3e-104:593:91//AC002415
R-HEMBB1002255//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 292E10, WORKING DRAFT SEQUENCE.//2.1e-40:284:85//Z93930
R-HEMBB1002266//Plasmodium falciparum DNA *** SEQUENCING IN PROGRE
SS *** from contig 4-10, complete sequence.//1.3e-09:371:63//AL010
216
R-HEMBB1002280//Homo sapiens PAC clone DJ0545C24 from 7q21-q22, co
mplete sequence.//1.3e-39:247:86//AC004534
R-HEMBB1002300//Human Chromosome 11 Cosmid cSRL30h11, complete seq
uence.//4.1e-84:549:86//U73642
R-HEMBB1002306//Homo sapiens BAC clone RG136N17 from 7p15-p21, com
plete sequence.//2.5e-10:164:71//AC004129
R-HEMBB1002327//Homo sapiens BAC clone GS539F22 from 7p12-p14, com
plete sequence.//0.39:365:59//AC005028
R-HEMBB1002329//HS-1049-B1-D05-MR.abi CIT Human Genomic Sperm Lib
rary C Homo sapiens genomic clone Plate=CT 771 Col=9 Row=H, genom
ic survey sequence.//0.96:180:58//B39313
R-HEMBB1002340//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, co
mplete sequence.//7.9e-17:258:73//AC004849
R-HEMBB1002342//Homo sapiens mRNA for putative thioredoxin-like pr
otein.//6.9e-96:479:97//AJ010841
R-HEMBB1002358//Human Xp22 BAC CT-285115 (from CalTech/Research Ge
netics), PAC RPC11-27C22 (from Roswell Park Cancer Center), and C
osmid U35B5 (from Lawrence Livermore), complete sequence.//2.3e-5
3:309:83//AC002366
R-HEMBB1002359//Homo sapiens clone NH0486122, WORKING DRAFT SEQUEN
CE, 5 unordered pieces.//4.9e-27:350:74//AC005038
R-HEMBB1002364//Homo sapiens Xp22 PAC RPC11-108M6 (Roswell Park Ca
ncer Center PAC library) complete sequence.//8.6e-53:302:79//AC003
036
R-HEMBB1002371//Human gene for catalase (EC 1.11.1.6) exon 11 mapp
ing to chromosome 11, band p13.//3.2e-38:199:100//X04094
R-HEMBB1002381//Homo sapiens (JH8) mRNA, partial cds.//3.2e-07:12
0:78//AF072467
R-HEMBB1002383//Human DNA sequence from cosmid U19H10 on chromosom

【0795】

【表495】

e X. Contains ESTs and CA repeat. //0.98:351:58//AL021182
 R-HEM8B1002387//HS-1052-82-G10-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 774 Col=20 Row=N, genomic survey sequence. //2.0e-07:276:67//B41091
 R-HEM8B1002415//Homo sapiens chromosome 17, clone hRPK.209_0_14, complete sequence. //1.4e-25:202:79//AC005730
 R-HEM8B1002425//Homo sapiens chromosome 19, cosmid R33516, complete sequence. //3.6e-60:401:87//AC004799
 R-HEM8B1002442//Homo sapiens clone UGCC:r9a from 6p21, complete sequence. //3.1e-51:358:81//AC006046
 R-HEM8B1002453//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 86D1, WORKING DRAFT SEQUENCE. //1.4e-115:557:98//AL034349
 R-HEM8B1002457//Human DNA sequence from clone 364122 on chromosome Xq21.31-22.3. Contains an STS and GSSs, complete sequence. //6.3e-37:338:80//AL031012
 R-HEM8B1002458//Homo sapiens T-cell receptor alpha delta locus from bases 250472 to 501670 (section 2 of 5) of the Complete Nucleotide Sequence. //9.7e-09:314:64//AE000659
 R-HEM8B1002477//Arabidopsis thaliana DNA chromosome 4, BAC clone T12H17 (ESSA11 project). //0.42:110:74//AL021635
 R-HEM8B1002489//Salvelinus fontinalis microsatellite sequence SF0-12. //6.6e-06:167:71//U50302
 R-HEM8B1002492//RPC111-74F21.TK RPC111 Homo sapiens genomic clone R-74F21, genomic survey sequence. //3.1e-14:410:63//AQ238960
 R-HEM8B1002495//HS_3220_A2_F07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220 Col=14 Row=K, genomic survey sequence. //1.3e-24:137:100//AQ180762
 R-HEM8B1002502//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence. //9.6e-81:538:86//AC005120
 R-HEM8B1002509//Human DNA sequence from clone 581F12 on chromosome Xq21. Contains Eukaryotic Translation Initiation Factor EIF3 P35 Subunit and 60S Ribosomal protein L22 pseudogenes. Contains ESTs, complete sequence. //0.0061:482:57//AL031313
 R-HEM8B1002510//HS_2179_A1_F03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2179 Col=5 Row=K, genomic survey sequence. //6.9e-35:423:72//AQ298309
 R-HEM8B1002520//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27X12, WORKING DRAFT SEQUENCE. //2.0e-62:201:85//AL033397
 R-HEM8B1002522//Homo sapiens chromosome 5, Pac clone 61c2 (LBNL H139), complete sequence. //0.99:323:58//AC004225
 R-HEM8B1002531
 R-HEM8B1002534//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 2/15, WORKING DRAFT SEQUENCE. //1.0e-61:380:79//AP000009
 R-HEM8B1002545//RPC111-2F3.TVB RPC111 Homo sapiens genomic clone RPC111-2F3, genomic survey sequence. //3.5e-12:414:63//B63283
 R-HEM8B1002550
 R-HEM8B1002556//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0481P14: HTGS phase 1, WORKING DRAFT SEQUENCE, 7 unordered pieces. //2.6e-62:299:85//AC006160
 R-HEM8B1002579//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1141E15, WORKING DRAFT SEQUENCE. //1.7e-42:286:88//AL034422
 R-HEM8B1002582//Homo sapiens clone DJ1119N05, complete sequence. //3.0e-14:426:60//AC004968
 R-HEM8B1002590//Homo sapiens clone RG132J19, complete sequence. //1.1e-30:392:74//AC005163
 R-HEM8B1002596//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50B115, WORKING DRAFT SEQUENCE. //8.5e-44:335:83//AL02107
 R-HEM8B1002600//Homo sapiens 12p13.3 PAC RPC15-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence. //2.0e-105:470:96//AC005865
 R-HEM8B1002601//Homo sapiens chromosome 17, clone HRPK837J1, complete sequence. //1.3e-44:445:77//AC004223
 R-HEM8B1002603//Homo sapiens clone UGCC:y23c049 from 6p21, complete sequence. //7.0e-40:321:82//AC006162
 R-HEM8B1002607//CIT-HSP-2347D7.TF CIT-HSP Homo sapiens genomic clone 2347D7, genomic survey sequence. //1.1e-44:234:98//AQ060197
 R-HEM8B1002610//Human Chromosome 16 BAC clone CIT987SK-A-36366, complete sequence. //7.0e-22:455:65//U91321
 R-HEM8B1002613//Homo sapiens 12p13.3 BAC RPC111-476M19 (Roswell Park Cancer Institute Human BAC Library) complete sequence. //3.3e-72:302:85//AC005908
 R-HEM8B1002614//Homo sapiens 12q13.1 PAC RPC111-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence. //3.8e-10:512:60//AC004801
 R-HEM8B1002617//Homo sapiens clone DJ1021120, WORKING DRAFT SEQUENCE, 6 unordered pieces. //6.8e-24:486:63//AC005520
 R-HEM8B1002623//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence. //2.4e-41:326:83//AC004953
 R-HEM8B1002635//Homo sapiens chromosome 12p13.3 clone RPC111-189M20, WORKING DRAFT SEQUENCE, 39 unordered pieces. //2.6e-42:360:80//AC005910
 R-HEM8B1002664//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence. //9.1e-51:335:87//AF042090
 R-HEM8B1002677//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), 01 (o1), 03 (o3), 02 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds. //0.0011:399:59//AF030694
 R-HEM8B1002683//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence. //4.1e-55:515:76//AF042090
 R-HEM8B1002684//Human BAC clone RG066D11 from 7q22, complete sequence. //1.7e-18:504:62//AC002430
 R-HEM8B1002686//Homo sapiens full length insert cDNA clone ZC65D06. //7.0e-85:413:99//AF086217
 R-HEM8B1002692//Homo sapiens 12p13.3 BAC RPC111-319E16 (Roswell Park Cancer Institute Human BAC Library) complete sequence. //9.8e-69:505:82//AC006206
 R-HEM8B1002697//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces. //0.26:390:58//AC004153
 R-HEM8B1002699//Human NFE genomic fragment. //8.0e-32:226:79//M98511
 R-HEM8B1002702//CIT-HSP-344K23.TVC CIT-HSP Homo sapiens genomic clone 344K23, genomic survey sequence. //8.6e-43:351:80//B59764
 R-HEM8B1002705//Plasmodium yoelii rhoptry protein, complete cds. //0.0064:454:59//L27838
 R-HEM8B1002712//Human DNA sequence from clone 50S813 on chromosome 1p36.2-36.3 Contains CA repeat and GSSs, complete sequence. //9.6e-09:187:67//Z98052
 R-MAMMA1000009//Homo sapiens clone NH0469M07, WORKING DRAFT SEQUENCE, 7 unordered pieces. //4.1e-21:201:80//AC005037
 R-MAMMA1000019//Homo sapiens chromosome 21q22.2 PAC clone P169K17, complete sequence. //4.2e-48:306:82//AF015720
 R-MAMMA1000020//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, VTA protein pseudogene, EST, GSS, complete sequence. //1.4e-41:306:86//AL022163
 R-MAMMA1000025//Human DNA sequence from clone 512B11 on chromosome 6p24-25. Contains the Desmoplakin 1 (DP1) gene, ESTs, STSs and GSSs, complete sequence. //6.1e-36:281:83//AL031058
 R-MAMMA1000043//Homo sapiens Chromosome 22q11.2 Cosmid Clone 8c in DCCR Region, complete sequence. //1.3e-67:321:88//AC000090
 R-MAMMA1000045//Homo sapiens chromosome 4 clone 8220G8 map 4q21, complete sequence. //6.7e-86:559:86//AC004054
 R-MAMMA1000055//Branta canadensis CA dinucleotide repeat locus Bca micro1. //0.79:63:77//AF025889
 R-MAMMA1000057//Homo sapiens DNA sequence from cosmid ICK0721Q on chromosome 6. Contains a 60S Ribosomal Protein L35A LIKE pseudogene, a gene coding for a 60S Ribosomal Protein L12 LIKE protein in a n intron of the HSET gene coding for a Kinesin related protein, the PHE1 (PHF2) gene coding for alternative splice products PHD finger proteins 1 and 2, the gene coding for five different alternatively spliced mRNAs coding for a protein similar to CYTA (CYCY) and identical to a polypeptide coded for by a known patented cDNA, and the first two exons of the gene coding for the human homolog of the rat synaptic ras GTPase-activating protein p135 SynGAP. Contains three predicted CpG islands, ESTs and an STS, complete sequence. //1.6e-53:397:83//AL021366
 R-MAMMA1000069//Homo sapiens clone RG052M06, WORKING DRAFT SEQUENCE, 11 unordered pieces. //2.0e-37:295:83//AC005057
 R-MAMMA1000084//Homo sapiens chromosome Xp22-135-136 clone GSHB-56711, WORKING DRAFT SEQUENCE, 35 unordered pieces. //7.1e-45:296:88//AC005867
 R-MAMMA1000085
 R-MAMMA1000092//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 774G10, WORKING DRAFT SEQUENCE. //8.2e-34:539:69//AL034410
 R-MAMMA1000103//Homo sapiens chromosome 17, clone hCIT.91_J_4, complete sequence. //3.4e-39:297:85//AC003976
 R-MAMMA1000117//Homo sapiens p47-phox (MCF1) pseudogene, clone P38, exon 5. //2.6e-07:162:67//U69641
 R-MAMMA1000129//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE, 6 unordered pieces. //6.1e-13:141:80//AC004882
 R-MAMMA1000133
 R-MAMMA1000134//Homo sapiens chromosome 19, cosmid R26660, complete

【0796】

【表496】

e sequence.//9.7e-18:171:80//AC005328	73 of the complete sequence.//0.97:293:64//AE001388
R-MAMMA1000139//Homo sapiens clone DJ241P17, WORKING DRAFT SEQUENC	R-MAMMA1000348//Homo sapiens BAC129, complete sequence.//4.4e-27:3
E, 7 unordered pieces.//1.2e-49:366:75//AC005000	65:72//U85195
R-MAMMA1000143//Homo sapiens *** SEQUENCING IN PROGRESS *** from P	R-MAMMA1000356//Drosophila melanogaster DNA sequence (P1 DS02252
AC 09.2, WORKING DRAFT SEQUENCE.//3.9e-56:318:89//AJ009615	(D97)), complete sequence.//0.73:332:61//AC002493
R-MAMMA1000155//Human DNA sequence from clone 323M22 on chromosome	R-MAMMA1000360//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, co
22q13.1-13.2. Contains the 5' part of the human ortholog of chick	mplete sequence.//4.6e-80:279:89//AC005189
on P52 and mouse H74, and a novel gene coding for a protein simila	R-MAMMA1000361//Human DNA sequence *** SEQUENCING IN PROGRESS ***
r to KIAA0173 and worm Tubulin Tyrosine Ligase. Contains ESTs, STS	from clone 753D4, WORKING DRAFT SEQUENCE.//7.8e-18:346:63//AL03167
s, GSSs, genomic marker D22S418 and putative CpG islands, complete	6
sequence.//2.1e-68:562:78//AL022476	R-MAMMA1000372//Human DNA sequence *** SEQUENCING IN PROGRESS ***
R-MAMMA1000163//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENC	from clone Y214H10, WORKING DRAFT SEQUENCE.//5.3e-40:299:83//AL022
E, 5 unordered pieces.//5.3e-06:408:58//AC005089	344
R-MAMMA1000171//CIT-HSP-2335L20, TR CIT-HSP Homo sapiens genomic cl	R-MAMMA1000385//Human DNA sequence *** SEQUENCING IN PROGRESS ***
one 2335L20, genomic survey sequence.//1.5e-42:173:89//AQ037381	from clone 310013, WORKING DRAFT SEQUENCE.//1.0e-28:225:84//AL0316
R-MAMMA1000173	58
R-MAMMA1000175//H. sapiens CpG island DNA genomic MseI fragment, cl	R-MAMMA1000388//CIT-HSP-232103, TR CIT-HSP Homo sapiens genomic clo
one 186C5, reverse read cpg186C5, rtlib.//0.072:90:72//Z57594	ne 232103, genomic survey sequence.//4.7e-60:298:99//AQ038102
R-MAMMA1000183//Homo sapiens Xp22 BAC GSHB-184P14 (Genome Systems	R-MAMMA1000395
Human BAC library) complete sequence.//1.5e-44:445:75//AC004552	R-MAMMA1000402//Homo sapiens PAC clone DJ1107K12 from 7p12-p14, co
R-MAMMA1000198//Homo sapiens clone c102D0968, complete sequence.//	mplete sequence.//1.4e-84:276:88//AC004692
1.9e-23:135:85//AF038667	R-MAMMA1000410//Human Chromosome 16 BAC clone CIT987SK-A-211C6, co
R-MAMMA1000221//HS_3242_B2_H02_T7 CIT Approved Human Genomic Sperm	mplete sequence.//6.7e-35:360:76//AC002394
Library D Homo sapiens genomic clone Plate=3242 Col=4 Row=P, geno	R-MAMMA1000413//Homo sapiens chromosome 17, clone hRPC.842_A_23, c
mic survey sequence.//0.031:167:67//AQ220385	mplete sequence.//3.1e-69:327:79//AC004662
R-MAMMA1000227//Human DNA sequence *** SEQUENCING IN PROGRESS ***	R-MAMMA1000414//Homo sapiens DNA sequence from PAC 164L12 on chrom
from clone 1071N3, WORKING DRAFT SEQUENCE.//4.5e-36:487:71//AL0317	osome Xq13.1-Xq21.2. Contains GSS (BAC end sequence), STS.//3.6e-4
28	1:180:87//AL009028
R-MAMMA1000241//Homo sapiens DNA sequence from PAC 93L7 on chromos	R-MAMMA1000416//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUEN
ome Xq21. Contains part of the CHM (TCD, REPI) gene coding for RAB	CE, 4 unordered pieces.//3.1e-59:478:77//AC005377
Escort protein 1 (REP-1, RAB proteins geranylgeranyltransferase c	R-MAMMA1000421//Human coxVib gene, last exon and flanking sequenc
omponent A 1, Choroideremia protein, Tapetochooidal Dystrophy (T	e.//5.3e-53:294:82//X58139
CD) protein). Contains ESTs and an STS, complete sequence.//6.2e-0	R-MAMMA1000422//Human DNA sequence *** SEQUENCING IN PROGRESS ***
7:445:59//AL022401	from clone 8822, WORKING DRAFT SEQUENCE.//1.0:252:59//AL031737
R-MAMMA1000251//Homo sapiens chromosome 19, cosmid F23465, complet	R-MAMMA1000423//Homo sapiens clone DA0065G23, complete sequence.//
e sequence.//1.6e-25:390:69//AC005266	2.0e-50:491:76//AC004816
R-MAMMA1000254//Homo sapiens DNA sequence from BAC 1216H12 on chro	R-MAMMA1000424//Human DNA sequence from PAC 507115 on chromosome X
mosome 22q12. Contains a pseudogene with similarity to part of mou	q26.3-27.3. Contains 60S ribosomal protein L44 (L41, L36) like gen
se Ninein and the KIAA0509 gene for a protein similar to C. elegans	e, ESTs, STSs and a polymorphic CA repeat.//3.5e-40:340:80//Z98950
s K09C8.4. Contains ESTs, GSSs and a gatt repeat polymorphism, com	R-MAMMA1000429//Mus musculus SDP8 mRNA, complete cds.//0.0019:87:7
plete sequence.//1.1e-37:327:80//AL008715	9//AF062484
R-MAMMA1000257//Human DNA sequence *** SEQUENCING IN PROGRESS ***	R-MAMMA1000431//Homo sapiens clone DJ0098022, WORKING DRAFT SEQUEN
from clone 1125A11, WORKING DRAFT SEQUENCE.//1.3e-22:281:74//AL034	CE, 5 unordered pieces.//2.0e-58:564:77//AC004821
549	R-MAMMA1000444//Human BAC clone RG126M09 from 7q21-q22, complete s
R-MAMMA1000264//*** SEQUENCING IN PROGRESS *** EPM1/APECD region	equency.//3.0e-43:328:83//AC002067
of chromosome 21, clones AB8E8, B127P21, B173L3, B23N8, C1242C9, C	R-MAMMA1000446//Human chromosome X clone Qc15B1, complete sequenc
579E2, A70B6, B159G9, B175D10, B52C10, C124G1 Note: Sequencing in	e.//0.95:209:65//U82672
this region has been discontinued by the Stanford Human Genome Cen	R-MAMMA1000458//Arabidopsis thaliana genomic DNA, chromosome 5, Pl
ter, WORKING DRAFT SEQUENCE, 50 unordered pieces.//1.7e-29:337:67/	clone: MIX3, complete sequence.//0.99:182:61//AB019236
/AC003656	R-MAMMA1000468
R-MAMMA1000266//Human DNA sequence *** SEQUENCING IN PROGRESS ***	R-MAMMA1000472//Homo sapiens genomic DNA, 21q region, clone: 655M9
from clone 681N20, WORKING DRAFT SEQUENCE.//7.7e-37:339:80//AL0316	N34, genomic survey sequence.//1.0e-38:142:88//AC010148
70	R-MAMMA1000478//Human DNA sequence *** SEQUENCING IN PROGRESS ***
R-MAMMA1000270//Human Chromosome 16 BAC clone CIT987SK-A-270G1, co	from clone 16915, WORKING DRAFT SEQUENCE.//1.3e-37:286:83//Z93015
mplete sequence.//1.2e-40:283:86//AF001549	R-MAMMA1000483//CIT-HSP-384B14, TR CIT-HSP Homo sapiens genomic clo
R-MAMMA1000277//CIT-HSP-516K6, TP CIT-HSP Homo sapiens genomic clone	ne 384B14, genomic survey sequence.//4.3e-34:158:86//B54637
e 516K6, genomic survey sequence.//3.0e-29:265:80//B49900	R-MAMMA1000490//Homo sapiens chromosome 19, BAC CIT-B-191n6, compl
R-MAMMA1000278//Sequence 25 from patent US 5708157.//2.6e-39:282:8	ete sequence.//4.2e-98:569:90//AC006130
2//180056	R-MAMMA1000500//Human BRCA1, Rho7 and vatl genes, complete cds, an
R-MAMMA1000279//Homo sapiens chromosome 16, cosmid clone 390H2 (LA	d ipf35 gene, partial cds.//1.2e-41:334:79//L78833
NL), complete sequence.//1.6e-52:295:84//AC004494	R-MAMMA1000501//Human DNA sequence *** SEQUENCING IN PROGRESS ***
R-MAMMA1000284//CITBI-E1-2522B20, TF CITBI-E1 Homo sapiens genomic	from clone 153C14, WORKING DRAFT SEQUENCE.//1.4e-38:250:84//AL0311
clone 2522B20, genomic survey sequence.//1.8e-11:288:61//AQ280722	18
R-MAMMA1000287	R-MAMMA1000516//Human DNA sequence *** SEQUENCING IN PROGRESS ***
R-MAMMA1000302//Homo sapiens chromosome 17, clone hRPK.112_J_9, co	from clone 424J12, WORKING DRAFT SEQUENCE.//1.3e-43:318:83//Z82207
mplete sequence.//4.1e-16:169:77//AC005553	R-MAMMA1000522//Human DNA sequence from clone 739H11 on chromosome
R-MAMMA1000307//RPC111-89L1, TV RPC111 Homo sapiens genomic clone	1p33-34.2 Contains KIAA0237 gene, EST, STS, GSS, complete sequenc
R-89L1, genomic survey sequence.//1.3e-86:429:97//AQ284795	e.//4.4e-13:202:73//AL031289
R-MAMMA1000309//Homo sapiens hJAG2.del-E6 (JAG2) mRNA, alternative	R-MAMMA1000559//Human DNA sequence *** SEQUENCING IN PROGRESS ***
ly spliced isoform of Jagged2, complete cds.//0.00020:384:60//AF02	from clone 16915, WORKING DRAFT SEQUENCE.//2.2e-30:245:83//Z93015
9779	R-MAMMA1000565//Homo sapiens chromosome 10 clone LA10NC01_183_B_7
R-MAMMA1000312//Ichneutes sp. 16S ribosomal RNA gene, partial sequ	map 10q24, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.6e-39:281:
ence.//0.0026:310:60//AF003518	80//U82205
R-MAMMA1000313//Human cosmid Xq28_1A649, complete sequence.//1.5e-	R-MAMMA1000567//Rattus norvegicus nonmuscle caldesmon mRNA, comple
26:317:67//U82694	te cds.//9.2e-19:216:76//U18419
R-MAMMA1000331//Homo sapiens clone DJ1007F24, WORKING DRAFT SEQUEN	R-MAMMA1000576
CE, 5 unordered pieces.//3.1e-39:277:86//AC004947	R-MAMMA1000583//Homo sapiens chromosome 17, clone hRPK.112_H_10, c
R-MAMMA1000339//Homo sapiens clone HS19.1 Alu-Ya5 sequence.//3.2e-	mplete sequence.//5.4e-53:297:85//AC005666
44:180:89//AF015147	R-MAMMA1000585//Homo sapiens clone DJ1015P16, WORKING DRAFT SEQUEN
R-MAMMA1000340//Plasmodium falciparum chromosome 2, section 25 of	CE, 4 unordered pieces.//1.2e-35:450:71//AC006018

【0797】

【表497】

R-MAMMA1000594//Homo sapiens *** SEQUENCING IN PROGRESS *** from c
osmid 5LS. WORKING DRAFT SEQUENCE. //4.3e-26:293:75//AJ009613
R-MAMMA1000597//CIT-HSP-2341F4.TF CIT-HSP Homo sapiens genomic clo
ne 2341F4, genomic survey sequence. //0.83:110:70//AQ057131
R-MAMMA1000605//Homo sapiens clone DJ1090E20, WORKING DRAFT SEQUEN
CE, 4 unordered pieces. //2.6e-50:290:86//AC004956
R-MAMMA1000612//CIT-HSP-2334J18.TF CIT-HSP Homo sapiens genomic cl
one 2334J18, genomic survey sequence. //0.76:132:65//AQ038364
R-MAMMA1000616//Ibalia leucospoides mitochondrion 16S rRNA gene, p
artial sequence. //6.8e-06:431:59//U06970
R-MAMMA1000621//Human NBR2 mRNA, complete cds. //5.3e-27:258:80//U0
8573
R-MAMMA1000623
R-MAMMA1000625//Homo sapiens chromosome 19, cosmid R31665, complet
e sequence. //3.3e-07:325:63//AC005498
R-MAMMA1000643//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 39B17, WORKING DRAFT SEQUENCE. //1.4e-06:236:68//AL02365
6
R-MAMMA1000664//*** SEQUENCING IN PROGRESS *** Homo sapiens chromo
some 4, BAC clone C0326F06: HTGS phase 1, WORKING DRAFT SEQUENCE,
16 unordered pieces. //1.4e-40:338:81//AC004555
R-MAMMA1000669//Human DNA sequence from clone 453C12 on chromosome
20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) pr
edicts a gene like the mouse transcription factor RBP-L, MATN4 (m
atrilin-4) STS, GSS, CpG island, complete sequence. //1.2e-46:327:8
6//AL021578
R-MAMMA1000670
R-MAMMA1000672//Human DNA sequence from clone 478D8 on chromosome
6p24. Contains STSs and GSSs, complete sequence. //2.2e-29:328:76//
AL031785
R-MAMMA1000684//Mus musculus frizzled-1 mRNA, complete cds. //0.21:
247:63//AF054623
R-MAMMA1000696//Human Chromosome X clone bWDX173, WORKING DRAFT SE
QUENCE, 2 ordered pieces. //2.7e-46:464:71//AC004387
R-MAMMA1000707//Homo sapiens clone RG219E16, WORKING DRAFT SEQUENC
E, 3 unordered pieces. //3.4e-09:244:66//AC005075
R-MAMMA1000713//Homo sapiens clone DJ0425102, WORKING DRAFT SEQUEN
CE, 5 unordered pieces. //3.7e-51:439:74//AC005478
R-MAMMA1000714//Homo sapiens BAC clone RG152H24 from 7p15-p21, com
plete sequence. //2.8e-29:288:75//AC004694
R-MAMMA1000718//Human Xp22 BAC CT-285115 (from CalTech/Research Ge
netics), PAC RPC11-27C22 (from Roswell Park Cancer Center), and C
osmid U35B5 (from Lawrence Livermore), complete sequence. //3.0e-3
7:231:91//AC002366
R-MAMMA1000720//Homo sapiens chromosome 19, cosmid R33632, complet
e sequence. //1.4e-35:299:81//AC005781
R-MAMMA1000723//Human DNA sequence from clone 551E13 on chromosome
Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogen
e, VT4 protein pseudogene, EST, GSS, complete sequence. //3.9e-59:4
09:79//AL022163
R-MAMMA1000731//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENC
E, 2 unordered pieces. //9.4e-29:560:66//AC005077
R-MAMMA1000732//Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUEN
CE, 10 unordered pieces. //2.4e-14:309:68//AC004832
R-MAMMA1000733//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 732E4, WORKING DRAFT SEQUENCE. //4.1e-29:377:71//AL00872
2
R-MAMMA1000734//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 191J18, WORKING DRAFT SEQUENCE. //2.0e-108:420:99//AL024
507
R-MAMMA1000738//Human V beta T-cell receptor (TCRBV) gene locus. //
6.6e-41:347:82//U03115
R-MAMMA1000744//T2708-T7 TAMU Arabidopsis thaliana genomic clone T
2708, genomic survey sequence. //0.095:367:60//B20150
R-MAMMA1000746//*** SEQUENCING IN PROGRESS *** Homo sapiens chromo
some 4, BAC clone C0135005: HTGS phase 1, WORKING DRAFT SEQUENCE,
23 unordered pieces. //7.4e-95:569:87//AC004661
R-MAMMA1000752//Homo sapiens BAC clone BK085E05 from 22q12.1-qter,
complete sequence. //1.3e-48:295:84//AC003071
R-MAMMA1000760//Human DNA sequence from clone B79B4 on chromosome
22 Contains CA repeat and GSS, complete sequence. //5.7e-45:347:82/
Z82178
R-MAMMA1000761//Homo sapiens cosmid clone LUCA16 from 3p21.3, comp
lete sequence. //1.1e-32:292:80//U73169
R-MAMMA1000775//Homo sapiens chromosome 17, clone hRPK.22_M.12, W
ORKING DRAFT SEQUENCE, 2 ordered pieces. //2.5e-50:467:79//AC005412
R-MAMMA1000776//Human BAC clone G5552A01 from 7q21-q22, complete s
equence. //1.0e-63:429:79//AC002454
R-MAMMA1000778//Human DNA sequence from 4PTEL, Huntington's Diseas
e Region, chromosome 4p16.3. //3.5e-25:234:81//Z95704

R-MAMMA1000782//Human DNA sequence from clone 459L4 on chromosome
6p22.3-24.1 Contains EST, STS, GSS, complete sequence. //0.0021:11
9:74//AL031120
R-MAMMA1000798//Homo sapiens 959 kb contig between AML1 and CBR1 o
n chromosome 21q22, segment 2/3. //6.3e-08:269:64//AJ229042
R-MAMMA1000802//Homo sapiens chromosome 19, cosmid R33729, complet
e sequence. //1.1e-35:261:80//AC005339
R-MAMMA1000831//CIT-HSP-2387J3.TF.1 CIT-HSP Homo sapiens genomic c
lone 2387J3, genomic survey sequence. //0.68:156:65//AQ240807
R-MAMMA1000839//Homo sapiens chromosome 17, clone hRPK.726_0.12, W
ORKING DRAFT SEQUENCE, 6 unordered pieces. //4.6e-50:335:86//AC0055
17
R-MAMMA1000841//Human Chromosome 16 BAC clone CIT987SK-A-97203, co
mplete sequence. //1.3e-40:322:77//U91323
R-MAMMA1000842//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 341D10, WORKING DRAFT SEQUENCE. //4.1e-44:471:74//Z97985
R-MAMMA1000843//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4
unordered pieces. //0.85:394:60//AC004815
R-MAMMA1000845//Plasmodium falciparum DNA *** SEQUENCING IN PROGRE
SS *** from MAL1P1, WORKING DRAFT SEQUENCE. //0.54:303:63//AL031744
R-MAMMA1000851//Homo sapiens chromosome X, MeCP2 locus, complete s
equence. //1.7e-10:115:83//AF030876
R-MAMMA1000855//Homo sapiens PAC clone 278C19 from 12q, complete s
equence. //5.0e-44:352:83//AC004263
R-MAMMA1000856//Homo sapiens chromosome 19, cosmid F24200, complet
e sequence. //1.8e-10:149:74//AC004611
R-MAMMA1000862//Hepatitis C virus genomic RNA, 3' nontranslated r
egion, partial sequence, clone #16. //8.1e-05:205:66//AF009075
R-MAMMA1000863//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12,
U115B9 (Lawrence Livermore human cosmid library) complete sequenc
e. //2.9e-49:421:80//AC002364
R-MAMMA1000865//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-32
8A3, complete sequence. //9.1e-41:302:83//AC002301
R-MAMMA1000867//Human BRCA1, Rho7 and vatl genes, complete cds, an
d ip135 gene, partial cds. //1.9e-17:500:61//L78833
R-MAMMA1000875//Homo sapiens chromosome 16, cosmid clone RT99 (LAN
L), complete sequence. //1.2e-17:211:74//AC004653
R-MAMMA1000876//Homo sapiens Xp22 BAC GS-607H18 (Genome Systems Hu
man BAC library) complete sequence. //4.7e-09:160:65//AC003658
R-MAMMA1000877//Homo sapiens DNA sequence from PAC 95883 on chromo
some Xp22.11-Xp22.22. Contains ESTs STS and CpG island. //3.2e-34:3
54:75//Z93023
R-MAMMA1000880//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-57
5C2, complete sequence. //1.4e-41:411:74//AC002425
R-MAMMA1000883
R-MAMMA1000897
R-MAMMA1000905//Homo sapiens chromosome 5, P1 clone 274A11 (LBNL H
56), complete sequence. //1.3e-73:304:91//AC004506
R-MAMMA1000906//Human DNA from chromosome 19-specific cosmid F1415
0, genomic sequence, complete sequence. //8.4e-23:194:83//AC003110
R-MAMMA1000908//Human Chromosome 15q26.1 PAC clone pDJ41616, compl
ete sequence. //1.5e-09:170:71//AC003024
R-MAMMA1000914//Homo sapiens PAC clone DJ0740L10 from 7p13-p14, co
mplete sequence. //8.3e-13:323:67//AC005247
R-MAMMA1000921//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 423B22, WORKING DRAFT SEQUENCE. //6.8e-28:333:72//AL0343
79
R-MAMMA1000931//HS 3227_B1_B03_T7 CIT Approved Human Genomic Sperm
Library D Homo sapiens genomic clone Plate=3227 Col=5 Row=0, geno
mic survey sequence. //1.4e-55:443:79//AQ191777
R-MAMMA1000940//Homo sapiens clone RG013F03, WORKING DRAFT SEQUENC
E, 6 unordered pieces. //2.0e-43:340:84//AC005046
R-MAMMA1000941//Homo sapiens chromosome 17, clone 297N7, complete
sequence. //1.8e-53:330:84//AC002347
R-MAMMA1000942//Human Chromosome X clone bWDX187, complete sequenc
e. //1.2e-39:391:74//AC004383
R-MAMMA1000943//Human PAC clone DJ327A19 from Xq25-q26, complete s
equence. //4.6e-75:566:81//AC002477
R-MAMMA1000956//Plasmodium falciparum MAL3P7, complete sequence. //
0.013:285:59//AL034559
R-MAMMA1000957//Homo sapiens clone RG339C12, WORKING DRAFT SEQUENC
E, 10 unordered pieces. //5.2e-45:288:90//AC005096
R-MAMMA1000962//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUEN
CE, 5 unordered pieces. //2.9e-108:561:96//AC006001
R-MAMMA1000968//Homo sapiens PAC clone 278C19 from 12q, complete s
equence. //3.9e-41:287:87//AC004263
R-MAMMA1000975//Homo sapiens DNA sequence from PAC 179N16 on chrom
osome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and
the alternatively spliced SAPK2 gene coding for CSaids binding prot
ein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and

【0798】

【表498】

two predicted CpG islands, complete sequence.//9.4e-65:542:79//Z95152

R-MAMMA1000979//Homo sapiens chromosome 21q22.3, PAC clones 314N7, 225L15, BAC clone 7B7, complete sequence bases 1..333303.//3.2e-34:296:80//AJ011930

R-MAMMA1000987//Homo sapiens CC chemokine gene cluster, complete sequence.//1.7e-40:255:87//AF088219

R-MAMMA1000998//Homo sapiens PAC clone DJ1152D16 from Xq23, complete sequence.//2.5e-39:315:73//AC005190

R-MAMMA1001003//Homo sapiens chromosome 10 clone CIT-HSP-1338F24 map 10p11.2-10p12.1, complete sequence.//2.4e-52:296:84//AC006101

R-MAMMA1001008//Homo sapiens *** SEQUENCING IN PROGRESS *** WORKING DRAFT SEQUENCE.//7.9e-88:432:98//AJ011929

R-MAMMA1001021//Homo sapiens PAC clone DJ0859M05 from 7q11, complete sequence.//3.8e-39:286:87//AC004910

R-MAMMA1001024//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE. 6 unordered pieces.//2.0e-31:274:80//AC004913

R-MAMMA1001030//Homo sapiens full length insert cDNA clone ZD96C01.//3.2e-99:469:99//AF088074

R-MAMMA1001035//RPC1-1-46G8Sp6 RPC1-1 Homo sapiens genomic clone RPC1-1-46G8Sp6, genomic survey sequence.//3.5e-49:270:90//AQ275285

R-MAMMA1001038//Homo sapiens chromosome 3, olfactory receptor pseudogene cluster 1, complete sequence, and myosin light chain kinase (MLCK) pseudogene, partial sequence.//1.1e-41:285:87//AF042089

R-MAMMA1001041

R-MAMMA1001050//Homo sapiens genomic DNA, 237 kb segment from 6p21.3 region including HLA genes, WORKING DRAFT SEQUENCE.//1.3e-55:334:91//D84394

R-MAMMA1001059//Mouse RNA helicase and RNA-dependent ATPase from the DEAD box family mRNA, complete cds.//1.7e-51:481:77//L25125

R-MAMMA1001067//CIT-HSP-2371K20.TF CIT-HSP Homo sapiens genomic clone 2371K20, genomic survey sequence.//7.2e-65:346:95//AQ111326

R-MAMMA1001073

R-MAMMA1001074//Homo sapiens BAC clone MH0400010 from Y, complete sequence.//8.6e-33:457:69//AC005040

R-MAMMA1001075//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-24 B77, complete sequence.//0.15:325:62//AC004605

R-MAMMA1001078//Homo sapiens chromosome 5, BAC clone 203o13 (LBML H155), complete sequence.//1.6e-45:344:84//AC005609

R-MAMMA1001082//Human genomic DNA sequence from clone 30801 on chromosome Xp11.3-11.4. Contains EST, CA repeat, STS, GSS, CpG island.//8.5e-15:413:64//Z93403

R-MAMMA1001091//Sequence 7 from patent US 5468610.//0.0027:159:64//J15499

R-MAMMA1001092//Homo sapiens chromosome 17, clone hRPK.372_K_20, complete sequence.//2.0e-51:267:82//AC005951

R-MAMMA1001105//Homo sapiens DNA sequence from PAC 119E23 on chromosome Xq25-q27.1. Contains glypican-3 precursor (intestinal protein OC1-5) (GTR2-2).5' UTR. ESTs, STS.//6.9e-22:178:85//Z99570

R-MAMMA1001110//Homo sapiens chromosome 17, clone HRPCL169K15, complete sequence.//3.0e-19:141:81//AC003963

R-MAMMA1001126//Human DNA from overlapping chromosome 7 PAC and P1 clones containing the XRCC2 gene, genomic sequence, complete sequence.//2.2e-46:462:75//AC003109

R-MAMMA1001133//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 120G22, WORKING DRAFT SEQUENCE.//1.8e-68:455:86//AL031847

R-MAMMA1001139//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//7.1e-09:100:84//AL022345

R-MAMMA1001143//Papio hamadryas lipoprotein lipase (LPL) gene, intron 7.//1.9e-49:362:85//U73684

R-MAMMA1001145//Homo sapiens chromosome 17, clone hRPK.235_1_10, complete sequence.//9.5e-49:512:74//AC005922

R-MAMMA1001154//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-88 D1, complete genomic sequence, complete sequence.//1.5e-29:305:76//AC002289

R-MAMMA1001161//Human DNA sequence from clone 681J21 on chromosome 1q23.2-24.3 Contains CpG island, complete sequence.//1.1e-64:339:90//AL031286

R-MAMMA1001162//Human DNA from cosmid DNA NMDB (f10080) and NMDC (f13544) from chromosome 19q13.3 (obtained by automated sequence analysis).//3.4e-09:243:64//M89651

R-MAMMA1001181//Human Chromosome X clone bWXD173, WORKING DRAFT SEQUENCE. 2 ordered pieces.//3.7e-29:351:74//AC004387

R-MAMMA1001186//Homo sapiens chromosome 19, cosmid R28778, complete sequence.//2.2e-25:415:68//AC006125

R-MAMMA1001191//Homo sapiens T-cell receptor alpha delta locus from bases 1000498 to 1071650 (section 5 of 5) of the Complete Nucleotide Sequence.//0.99:243:61//AE000662

R-MAMMA1001198//Mus musculus eps15R mRNA, complete cds.//8.0e-57:223:86//U29156

R-MAMMA1001202//Mus musculus clone OST13722, genomic survey sequence.//1.0e-30:220:85//AF046748

R-MAMMA1001203//Homo sapiens chromosome 17, clone hRPK.22_M_12, WORKING DRAFT SEQUENCE. 2 ordered pieces.//8.9e-61:567:78//AC005412

R-MAMMA1001206//Homo sapiens chromosome 5, P1 clone 854b11 (LBML H44), complete sequence.//4.6e-08:442:61//AC004763

R-MAMMA1001215//Homo sapiens chromosome 19, CIT-HSP BAC 470n8, complete sequence.//1.3e-117:564:97//AC005393

R-MAMMA1001220//HS-1023-A1-G10-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 802 Col=19 Row=M, genomic survey sequence.//6.0e-16:276:68//B33708

R-MAMMA1001222//F17E12TFB IGF Arabidopsis thaliana genomic clone F17E12, genomic survey sequence.//0.041:277:61//B97762

R-MAMMA1001243

R-MAMMA1001244//HS-1058-A2-G01-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 780 Col=2 Row=M, genomic survey sequence.//3.5e-05:104:74//B43862

R-MAMMA1001249//H. sapiens DNA for matrix attachment region.//0.0013:95:75//Z54221

R-MAMMA1001256//Human BAC clone GS188P18, complete sequence.//3.4e-32:356:74//AC000115

R-MAMMA1001259

R-MAMMA1001260//Homo sapiens mRNA for KIA00661 protein, complete cds.//6.3e-20:226:75//AB014561

R-MAMMA1001268//Human DNA sequence from PAC 225D2 on chromosome Xq21. Contains ESTs, CA repeat.//1.1e-47:352:85//Z95124

R-MAMMA1001271

R-MAMMA1001274//H. sapiens DNA for trapped exon (ID HMC07C06), genomic survey sequence.//3.1e-40:232:93//X88457

R-MAMMA1001280//Homo sapiens full length insert cDNA clone YW26C09.//1.9e-112:574:95//AF087976

R-MAMMA1001292//Human DNA sequence from clone 1170K4 on chromosome 22q12.2-13.1. Contains three novel genes, one of which codes for a Trypsin family protein with class A LDL receptor domains, and the IL2RB gene for interleukin 2 Receptor, Beta (IL-2 Receptor, CD12.2 antigen). Contains a putative CpG island, ESTs, and GSSs, complete sequence.//2.9e-114:582:96//AL022314

R-MAMMA1001296//Human DNA sequence from PAC 487J7 on chromosome 6q21-22.1. Contains an unknown gene coding for three alternative mRNAs. Contains ESTs, STSs, a BAC end-sequence (GSS) and a CA repeat polymorphism.//1.9e-64:268:88//AL008730

R-MAMMA1001298//Homo sapiens chromosome 17, clone hRPK.849_M_15, complete sequence.//1.5e-38:306:83//AC005703

R-MAMMA1001305//Human DNA sequence from PAC 127B20 on chromosome 22q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein, ribosomal protein L6 pseudogene, ESTs and CA repeat.//1.5e-37:306:82//Z83838

R-MAMMA1001322//Homo sapiens DNA sequence from PAC 434Q14 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2B adenosine A2b receptor LIKE pseudogene, the IRF5 gene for Interferon Regulatory Factor 5 and two novel genes. Contains ESTs and GSSs, complete sequence.//2.4e-15:260:71//AL022398

R-MAMMA1001324//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//4.0e-06:90:83//AC005614

R-MAMMA1001330//Human BAC clone RG066D11 from 7q22, complete sequence.//1.4e-45:439:74//AC002430

R-MAMMA1001341//Human DNA sequence from PAC 211D12 on chromosome 22q12-13.2. Contains Krs-2, K+ channel protein, stress responsive.//1.3e-24:137:81//Z93018

R-MAMMA1001343//Human Chromosome 16 BAC clone CIT987SK-A-17E1, complete sequence.//5.4e-51:197:89//AC002041

R-MAMMA1001346//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-233A8, complete sequence.//0.99:182:64//AC004685

R-MAMMA1001383//Homo sapiens clone 82F9, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.9e-42:303:86//AC004815

R-MAMMA1001388//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 508115, WORKING DRAFT SEQUENCE.//1.5e-44:324:83//AL021707

R-MAMMA1001397//Homo sapiens genomic DNA, chromosome 21q11.1, segment 15/28, WORKING DRAFT SEQUENCE.//2.0e-39:254:89//AP000044

R-MAMMA1001408//Homo sapiens chromosome 12q24.1, WORKING DRAFT SEQUENCE, 33 unordered pieces.//9.4e-36:251:88//AC005805

R-MAMMA1001411//T15F1-T7.1 TAML Arabidopsis thaliana genomic clone T15F1, genomic survey sequence.//1.0:98:71//AQ248928

R-MAMMA1001419//Homo sapiens translation initiation factor 4e mRNA, complete cds.//4.8e-18:117:96//AF038957

R-MAMMA1001420//Homo sapiens chromosome 5, P1 clone 1041F10 (LBML

【0799】

【表499】

H88), complete sequence.//2.8e-09:377:63//AC005179
 R-MAMMA1001435//S.pombe chromosome I cosmid c26H5.//1.0:356:59//Z9
 9126
 R-MAMMA1001442//Homo sapiens chromosome 4 clone 8150J4 map 4q25, c
 omplete sequence.//3.4e-17:259:72//AC004047
 R-MAMMA1001446//Homo sapiens BAC clone RG139P11 from Tq11-q21, com
 plete sequence.//2.9e-17:231:71//AC004491
 R-MAMMA1001452//Human DNA sequence from clone 452M16 on chromosome
 Xq21.1-21.33 Contains capping protein alpha subunit isoform 1 pse
 udogene, STS, GSS, and CA repeat, complete sequence.//6.1e-50:558:
 73//AL024493
 R-MAMMA1001465//cSRL-2F3-u cSRL flow sorted Chromosome 11 specific
 cosmid Homo sapiens genomic clone cSRL-2F3, genomic survey sequen
 ce.//3.0e-23:141:96//B04295
 R-MAMMA1001476//Mus musculus uridine kinase mRNA, partial cds.//3.
 4e-09:309:64//L31783
 R-MAMMA1001487//Homo sapiens chromosome 17, clone hRPC.1108_L_11,
 complete sequence.//5.1e-30:286:79//AC005206
 R-MAMMA1001501
 R-MAMMA1001502//Human DNA sequence *** SEQUENCING IN PROGRESS ***
 from clone 356B7, WORKING DRAFT SEQUENCE.//4.3e-19:349:64//AL03171
 4
 R-MAMMA1001510
 R-MAMMA1001522//Homo sapiens chromosome 5, BAC clone 24h24 (LBML H
 194), complete sequence.//1.5e-09:136:75//AC005352
 R-MAMMA1001547//Human Chromosome X, complete sequence.//3.5e-40:30
 0:84//AC002418
 R-MAMMA1001551//Human DNA sequence from PAC 42616 on chromosome 1p
 34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protei
 n phosphatase-1, ESTs, and a CA repeat.//1.1e-57:282:89//AL020997
 R-MAMMA1001575
 R-MAMMA1001576//Human gamma-tubulin mRNA, complete cds.//7.6e-60:5
 30:78//M61764
 R-MAMMA1001590//Homo sapiens Bruton's tyrosine kinase (BTK), alpha
 a-D-galactosidase A (GLA), L44-like ribosomal protein (L44L) and F
 TP3 (FTP3) genes, complete cds.//1.3e-29:161:86//U78027
 R-MAMMA1001600//Homo sapiens 12q24 PAC RPC11-66E7 (Roswell Park Ca
 ncer Institute Human PAC library) complete sequence.//2.1e-18:390:
 66//AC004216
 R-MAMMA1001604//Human DNA sequence from clone 1042K10 on chromosom
 e 22q13.1-13.2. Contains the ADSL gene for Adenylosuccinate lyase
 (EC 4.3.2.2, Adenylosuccinase, ASL) and 4 novel genes (one with pr
 obable rabGAP domains and Src homology domain 3). Contains ESTs, 5
 TSs, GSSs and a putative CpG island, complete sequence.//1.0:227:6
 2//AL022238
 R-MAMMA1001606//Human DNA sequence *** SEQUENCING IN PROGRESS ***
 from clone 228H13, WORKING DRAFT SEQUENCE.//1.3e-17:219:69//AL0319
 85
 R-MAMMA1001620//Human DNA sequence *** SEQUENCING IN PROGRESS ***
 from clone 1018D12, WORKING DRAFT SEQUENCE.//2.1e-51:298:84//AL031
 650
 R-MAMMA1001627//Human DNA sequence *** SEQUENCING IN PROGRESS ***
 from clone 229A8, WORKING DRAFT SEQUENCE.//7.8e-45:328:85//Z86090
 R-MAMMA1001630//, complete sequence.//2.5e-08:170:72//AC005399
 R-MAMMA1001633//Homo sapiens chromosome 10 clone CIT987SK-1057L21
 map 10q25, complete sequence.//2.2e-21:241:70//AC005386
 R-MAMMA1001635//Homo sapiens DNA sequence from PAC 230G1 on chromo
 some Xp11.3. Contains EST, STS and GSS, complete sequence.//1.1e-3
 2:346:74//Z84466
 R-MAMMA1001649
 R-MAMMA1001663//Homo sapiens clone 162B15, complete sequence.//9.4
 e-68:267:89//AC004811
 R-MAMMA1001670//Human DNA sequence from PAC 75N13 on chromosome Xq
 21.1. Contains ZNF6 like gene, ESTs, STSs and CpG islands.//1.7e-4
 9:322:88//Z82216
 R-MAMMA1001671//Homo sapiens chromosome 19, cosmid F23269, complet
 e sequence.//2.4e-114:575:96//AC005614
 R-MAMMA1001679//CIT-HSP-2335N4.TF CIT-HSP Homo sapiens genomic clo
 ne 2335N4, genomic survey sequence.//2.4e-82:400:99//AQ037393
 R-MAMMA1001683//Homo sapiens Chromosome 7 BAC Clone 239c10, WORKIN
 G DRAFT SEQUENCE, 9 unordered pieces.//5.7e-47:533:72//AC004166
 R-MAMMA1001686//Homo sapiens chromosome 19, CIT-HSP-444n24, comple
 te sequence.//6.6e-12:194:72//AC005261
 R-MAMMA1001692//Human DNA sequence *** SEQUENCING IN PROGRESS ***
 from clone Y738F9, WORKING DRAFT SEQUENCE.//9.6e-44:414:77//AL0223
 45
 R-MAMMA1001711//Homo sapiens clone BAC 9H13 chromosome 8 map 8q21,
 complete sequence.//3.1e-31:436:70//AF110324
 R-MAMMA1001715//Human DNA sequence *** SEQUENCING IN PROGRESS ***
 from clone 73E16, WORKING DRAFT SEQUENCE.//8.8e-76:524:84//Z95330
 R-MAMMA1001730
 R-MAMMA1001735//Cricetulus griseus (chinese hamster) mRNA for beta
 tubulin (clone 89T), partial.//2.7e-13:382:63//X60786
 R-MAMMA1001740//Homo sapiens genomic DNA, chromosome 21q11.1, segm
 ent 21/28, WORKING DRAFT SEQUENCE.//3.9e-47:318:87//AP000050
 R-MAMMA1001743//Homo sapiens clone DJ0981007, complete sequence.//
 4.0e-108:566:95//AC006017
 R-MAMMA1001744
 R-MAMMA1001745//Homo sapiens BAC clone 529F11 from 8q21, complete
 sequence.//3.5e-113:564:97//AF070718
 R-MAMMA1001751//Homo sapiens chromosome 19, cosmid R27328, complet
 e sequence.//3.6e-30:312:75//AC005625
 R-MAMMA1001754//Bos taurus vacuolar proton pump subunit SFD alpha
 isoform (SFD) mRNA, complete cds.//4.7e-34:320:77//AF041338
 R-MAMMA1001757//Homo sapiens chromosome 17, clone hRPC.4_G_17, com
 plete sequence.//4.7e-10:244:67//AC003688
 R-MAMMA1001760//RPC111-38L16.TV RPC11-11 Homo sapiens genomic clone
 RPC11-38L16, genomic survey sequence.//1.3e-10:236:64//AQ029432
 R-MAMMA1001764//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-42
 0 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//
 0.74:361:60//AC005140
 R-MAMMA1001768//Homo sapiens chromosome 17, clone hRPC.147_L_13, c
 omplete sequence.//1.6e-42:416:76//AC005332
 R-MAMMA1001769//Homo sapiens chromosome 17, clone hRPC.1073_F_15,
 complete sequence.//1.4e-13:129:83//AC004686
 R-MAMMA1001771//M.musculus mRNA for semaphorin B, //1.1e-34:530:69/
 X85991
 R-MAMMA1001783//Homo sapiens Chromosome 2 BAC Clone 376a1, WORKING
 DRAFT SEQUENCE, 17 unordered pieces.//1.1e-42:282:85//AC000360
 R-MAMMA1001785//Human chromosome 16p13.11 BAC clone CIT987SK-98H8
 complete sequence.//3.0e-49:282:86//U91319
 R-MAMMA1001788
 R-MAMMA1001790//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUEN
 CE, 6 unordered pieces.//9.8e-43:530:71//AC004913
 R-MAMMA1001806//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-31
 9E8, complete sequence.//1.8e-43:324:79//AC004020
 R-MAMMA1001812//Plasmodium falciparum chromosome 2, section 69 of
 73 of the complete sequence.//0.65:183:63//AE001432
 R-MAMMA1001815//Homo sapiens clone GS223D04, WORKING DRAFT SEQUENC
 E, 3 unordered pieces.//1.1e-10:417:62//AC005018
 R-MAMMA1001817//Homo sapiens Xp22-83 BAC GSHB-324M7 (Genome System
 s Human BAC Library) complete sequence.//2.6e-40:313:84//AC005859
 R-MAMMA1001818
 R-MAMMA1001820//Homo sapiens, WORKING DRAFT SEQUENCE, 52 unordered
 pieces.//2.2e-45:340:82//AC004086
 R-MAMMA1001824//Homo sapiens clone DJ1107K15, WORKING DRAFT SEQUEN
 CE, 8 unordered pieces.//1.9e-53:291:85//AC004966
 R-MAMMA1001836//HS_3164_B1_A02_MR CIT Approved Human Genomic Spem
 Library D Homo sapiens genomic clone Plate=3164 Col=3 Row=B, geno
 mic survey sequence.//6.5e-08:79:89//AQ185484
 R-MAMMA1001837//Homo sapiens chromosome 19, overlapping cosmids F1
 8547, F11133, R27945, R28830 and R32804, complete sequence.//8.4e-
 55:309:85//AC003682
 R-MAMMA1001848//Homo sapiens PAC clone DJ0296G17 from Xq23, comple
 te sequence.//1.6e-16:125:90//AC006144
 R-MAMMA1001851//Genomic sequence from Human 9q34, WORKING DRAFT SE
 QUENCE, 2 unordered pieces.//2.4e-50:516:74//AC002099
 R-MAMMA1001854//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-57
 5C2, complete sequence.//1.7e-38:308:82//AC002425
 R-MAMMA1001858//Human Xq13 3' end of PAC 92E23 containing the X in
 activation transcript (XIST) gene, complete sequence.//6.5e-50:283:
 86//U80460
 R-MAMMA1001864//Human Chromosome 15q26.1 PAC clone pDJ398g19, WORK
 ING DRAFT SEQUENCE, 21 unordered pieces.//3.4e-36:224:86//AC005143
 R-MAMMA1001868//Plasmodium falciparum chromosome 2, section 54 of
 73 of the complete sequence.//1.4e-11:495:63//AE001417
 R-MAMMA1001874//Human chromosome 1 BAC 308G1 genomic sequence, WOR
 KING DRAFT SEQUENCE, 3 unordered pieces.//3.2e-42:446:76//AC003117
 R-MAMMA1001878//Human DNA sequence from PAC 431A14 on chromosome 6
 p21. Contains CYCLOPHILIN (PEPTIDYLPROLYL ISOMERASE) like and CIP1
 (WAF1, CDKN1A, CDKN1, MDA-6, SD11, PIC1, CAP20) genes. Contains p
 robable GTPase and receptor genes and ESTs, STSs and CpG islands.//
 6.9e-44:391:78//Z85996
 R-MAMMA1001880//Human DNA sequence from fosmid F77D12 on chromosom
 e 22q12-qter contains ESTs, tRNA.//1.3e-15:181:76//Z82097
 R-MAMMA1001890//Homo sapiens Chromosome 16 BAC clone CIT987SKA-67
 0B5 -complete genomic sequence, complete sequence.//1.7e-43:283:8
 6//AC002303
 R-MAMMA1001907//Human DNA sequence *** SEQUENCING IN PROGRESS ***
 from clone 385E7, WORKING DRAFT SEQUENCE.//1.4e-48:420:79//AL03172

【0800】

【表500】

R-MAMMA1001908//Saccharomyces cerevisiae chromosome IV cosmid 948 1.//2.9e-14:505:60//U28373	R-MAMMA1002174//Homo sapiens chromosome 10 clone CIT987SK-1109P11, complete sequence.//4.4e-12:189:72//AC005871
R-MAMMA1001931//Homo sapiens NACP/alpha-synuclein gene, allele A0, intron 4, partial sequence.//0.51:162:63//AF041008	R-MAMMA1002198//Homo sapiens clone DJ0800G07, complete sequence.//1.1e-48:338:81//AC004890
R-MAMMA1001956//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.//1.4e-51:422:79//AL034380	R-MAMMA1002209//Homo sapiens chromosome 17, clone hRPK.156_L14, complete sequence.//1.2e-23:269:74//AC005821
R-MAMMA1001963//Homo sapiens clone HS19.3 Alu-Ya5 sequence.//1.9e-31:163:91//AF015149	R-MAMMA1002215//Homo sapiens clone GS250N06, WORKING DRAFT SEQUENCE. 5 unordered pieces.//3.2e-12:243:68//AC005158
R-MAMMA1001969//Human DNA from chromosome 19 cosmid F19410, genomic sequence, complete sequence.//8.7e-10:186:76//AC002128	R-MAMMA1002219//Homo sapiens 12p13.3 RPC14-773N5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//3.3e-45:295:88//AC004802
R-MAMMA1001970//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//1.0e-62:298:86//AC003071	R-MAMMA1002230//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423822, WORKING DRAFT SEQUENCE.//7.3e-41:385:78//AL034379
R-MAMMA1001982//Human Chromosome 15q26.1 PAC clone pDJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.8e-44:525:72//AC004581	R-MAMMA1002236//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//7.3e-45:363:79//U38253
R-MAMMA1002009//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 109G6, WORKING DRAFT SEQUENCE.//1.4e-43:282:79//AL023879	R-MAMMA1002243//Homo sapiens chromosome 17, clone hRPK.112_H10, complete sequence.//2.8e-119:582:98//AC005666
R-MAMMA1002011	R-MAMMA1002250//Homo sapiens chromosome 16, P1 clone 109-9G (LANL), complete sequence.//4.7e-42:319:84//AC005600
R-MAMMA1002032//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 469022, WORKING DRAFT SEQUENCE.//1.1e-39:310:84//AL031284	R-MAMMA1002267//Homo sapiens chromosome 17, clone hRPK.346_K10, complete sequence.//1.5e-33:571:67//AC006120
R-MAMMA1002033//Homo sapiens chromosome 5, Pac clone 162o17 (LBML HI47), complete sequence.//2.5e-17:170:81//AC003954	R-MAMMA1002268//Mus musculus sphingosine kinase (SPHK1b) mRNA, complete cds.//2.3e-35:462:70//AF068749
R-MAMMA1002041//Homo sapiens PAC clone DJ0728D04, complete sequence.//8.7e-79:296:85//AC004865	R-MAMMA1002269//345117.TV CIT978SKA1 Homo sapiens genomic clone A-345117, genomic survey sequence.//4.7e-05:153:69//B15590
R-MAMMA1002042//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//8.8e-46:386:80//U91318	R-MAMMA1002282//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 112K5, WORKING DRAFT SEQUENCE.//8.5e-37:467:71//Z85987
R-MAMMA1002047//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//1.9e-32:326:75//U91318	R-MAMMA1002292//Hordeum vulgare lipoxygenase 2 (LoxC) mRNA, complete cds.//0.074:178:61//L37358
R-MAMMA1002056//Homo sapiens chromosome 17, clone hRPK.506_H21, complete sequence.//6.6e-48:367:82//AC005962	R-MAMMA1002293//Homo sapiens chromosome 16, cosmid clone RT167 (LANL), complete sequence.//5.8e-26:355:71//AC005568
R-MAMMA1002058//Homo sapiens clone RGO38K21, WORKING DRAFT SEQUENCE. 3 unordered pieces.//0.25:139:69//AC005052	R-MAMMA1002294//Homo sapiens chromosome 17, clone hRPC.1110_E20, complete sequence.//1.2e-35:281:82//AC004231
R-MAMMA1002068//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//2.2e-45:406:78//AC004676	R-MAMMA1002297//Human DNA sequence from cosmid L174G8, Huntington's Disease Region, chromosome 4p16.3.//6.7e-48:381:80//Z69375
R-MAMMA1002078//Homo sapiens chromosome 17, clone hRPK.401_O9, complete sequence.//2.3e-22:357:64//AC005291	R-MAMMA1002298//Homo sapiens BAC clone RG208H19 from Tq11.23, complete sequence.//1.8e-17:296:70//AC005074
R-MAMMA1002082//Homo sapiens PAC clone 278C19 from 12q, complete sequence.//2.5e-38:304:82//AC004263	R-MAMMA1002299//HS_3116_A2_F07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3116 Col=14 Row=K, genomic survey sequence.//4.1e-60:354:91//AQ140526
R-MAMMA1002084//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1174N9, WORKING DRAFT SEQUENCE.//8.9e-41:319:83//AL031602	R-MAMMA1002308
R-MAMMA1002093//CIT-HSP-206DJ9.TF CIT-HSP Homo sapiens genomic clone 206DJ9, genomic survey sequence.//9.7e-17:129:88//B69983	R-MAMMA1002310//Human DNA sequence from cosmid B10B1 on chromosome 22 Contains ESTs, CA repeat and STS, complete sequence.//9.9e-35:283:83//Z73979
R-MAMMA1002108	R-MAMMA1002311//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence.//1.3e-86:503:90//AC006210
R-MAMMA1002118//Human DNA sequence from cosmid E116C6, on chromosome 22 Contains ESTs, complete sequence.//0.94:168:64//Z73495	R-MAMMA1002312//H.sapiens gene encoding La autoantigen.//1.3e-23:382:67//X97869
R-MAMMA1002125//Homo sapiens chromosome 17, clone hRPK.63_A1, complete sequence.//4.8e-40:313:83//AC005670	R-MAMMA1002317//Human DNA sequence from clone 48G12 on chromosome Xq27.1-27.3. Contains STSs and GSSs, complete sequence.//1.3e-59:23:87//AL031054
R-MAMMA1002132//Homo sapiens PAC clone DJ1059M17 from 7q21-q31.1, complete sequence.//2.0e-70:461:83//AC004953	R-MAMMA1002319//Homo sapiens chromosome 19, fosmid 39347, complete sequence.//2.2e-106:522:98//AC005756
R-MAMMA1002140//Human DNA sequence from PAC 465G10 on chromosome X contains Menkes Disease (ATP7A) putative Cutt+-transporting P-type ATPase exons 2 to 21, PGAM-B, ESTs.//1.1e-32:477:73//Z94801	R-MAMMA1002322//Homo sapiens genomic DNA, chromosome 21q11.1, segment 13/28, WORKING DRAFT SEQUENCE.//2.3e-48:452:76//AP000042
R-MAMMA1002143//Homo sapiens platelet-activating factor acetylhydrolase gene, promoter region and exon 1.//6.6e-06:130:73//AF027357	R-MAMMA1002329//M.musculus mRNA for semaphorin B.//2.0e-12:210:73//X85991
R-MAMMA1002145//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE.//6.0e-19:242:73//AL031447	R-MAMMA1002332//Homo sapiens PAC clone DJ1139101 from 12q23, complete sequence.//3.4e-46:393:71//AC004973
R-MAMMA1002153//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0281M17; HTGS phase 1, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.1e-51:291:75//AC006052	R-MAMMA1002333//HS_3245_A1_B04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3245 Col=7 Row=C, genomic survey sequence.//3.1e-21:146:92//AQ205759
R-MAMMA1002155//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 608E8, WORKING DRAFT SEQUENCE.//1.2e-53:461:79//AL022343	R-MAMMA1002339//Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//9.7e-39:310:79//AF001549
R-MAMMA1002156//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter, complete sequence.//5.1e-37:305:82//AC004997	R-MAMMA1002347//Homo sapiens 12q24.1 PAC RPC13-305I20 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.2e-46:443:76//AC006088
R-MAMMA1002158//Human DNA sequence from clone 1049G16 on chromosome 22q12-13.2 Contains gene similar to GLUCOSAMINE-6-SULFATASE, a nuclear receptor coactivator gene, ESTs, STSs, GSSs, complete sequence.//8.1e-34:296:81//AL034418	R-MAMMA1002351//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1059H15, WORKING DRAFT SEQUENCE.//1.1e-90:553:89//AL022100
R-MAMMA1002170//Human DNA sequence from clone 1163J1 on chromosome 22q13.2-13.33. Contains the 3' part of a gene for the ortholog of mouse transmembrane receptor Celser1, a novel gene for a protein similar to C. elegans B0035.16 and bacterial tRNA (5-Methylaminomethyl-2-thiouridylyl)-Methyltransferases, and the 3' part of a novel gene for a protein similar to mouse B99. Contains ESTs, GSSs and putative CpG islands, complete sequence.//7.9e-39:332:82//AL031558	R-MAMMA1002352//Homo sapiens mRNA for leukemia associated gene 2.//8.8e-81:388:92//Y15228
	R-MAMMA1002353//Homo sapiens 12q24 BAC RPC111-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//5.5e-35:302:80//AC002996
	R-MAMMA1002355//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 222E13, WORKING DRAFT SEQUENCE.//5.4e-52:361:76//Z93241

【表501】

R-MAMMA1002356//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence.//8.3e-28:187:91//AC004652
 R-MAMMA1002359//Human DNA sequence from cosmid L118DS, Huntington's Disease Region, chromosome 4p16.3 contains CpG islands.//6.3e-47:297:85//Z68869
 R-MAMMA1002360//HS_2163_B2_C08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2163 Col=16 Row=F, genomic survey sequence.//1.5e-20:374:66//AQ125213
 R-MAMMA1002361//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 349A12, WORKING DRAFT SEQUENCE.//2.2e-35:264:85//AL033520
 R-MAMMA1002362//H. sapiens PEX gene.//1.8e-40:243:86//Y10196
 R-MAMMA1002380//RPC111-73J4.TJ RPC111 Homo sapiens genomic clone R-73J4, genomic survey sequence.//1.7e-38:295:77//AQ268168
 R-MAMMA1002384//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.5e-37:311:81//AC004801
 R-MAMMA1002385
 R-MAMMA1002392//Human BAC clone RG066D11 from 7q22, complete sequence.//2.0e-37:365:77//AC002430
 R-MAMMA1002411//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 64K7, WORKING DRAFT SEQUENCE.//9.4e-22:496:65//AL031668
 R-MAMMA1002413//Homo sapiens 12q24.2 PAC RPC11-157K6 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.3e-15:153:77//AC005146
 R-MAMMA1002417//Human DNA sequence from PAC 42616 on chromosome 1p34.1-1p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.8e-23:508:62//AL020997
 R-MAMMA1002427//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//2.5e-37:288:84//U91321
 R-MAMMA1002428//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185MS, WORKING DRAFT SEQUENCE.//6.0e-05:130:75//AL034423
 R-MAMMA1002434//Homo sapiens DNA sequence from PAC 380E11 on chromosome 6p22.3-p24. Contains HB15 gene, ESTs, CA repeat, STS and GSS.//4.8e-18:205:78//AL022396
 R-MAMMA1002446//CIT-HSP-2021L14, TR CIT-HSP Homo sapiens genomic clone 2021L14, genomic survey sequence.//4.6e-41:387:72//B65379
 R-MAMMA1002454//Homo sapiens chromosome 19, cosmid F23259, complete sequence.//1.2e-67:491:82//AC005512
 R-MAMMA1002461//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//1.4e-28:188:85//AC003982
 R-MAMMA1002470//Saccharomyces cerevisiae chromosome VIII cosmid 9205.//6.3e-09:280:61//U10556
 R-MAMMA1002475//Human DNA sequence from PAC 306D1 on chromosome X contains ESTs.//1.5e-25:310:74//Z83822
 R-MAMMA1002480//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.2e-38:533:93//AC005077
 R-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds.//2.7e-114:560:97//AF055460
 R-MAMMA1002494//Human DNA sequence from cosmid L174G8, Huntington's Disease Region, chromosome 4p16.3.//2.1e-46:329:84//Z69375
 R-MAMMA1002498//Rat mRNA.//0.0068:223:64//M59859
 R-MAMMA1002524//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.012:460:60//AC005139
 R-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds.//1.2e-101:529:95//AF065214
 R-MAMMA1002545//Homo sapiens ribosomal protein s4 Y isoform gene, complete cds.//6.6e-50:471:77//AF041427
 R-MAMMA1002554//Homo sapiens chromosome 4 clone B227H22 map 4q25, complete sequence.//5.7e-38:279:84//AC004056
 R-MAMMA1002556//Homo sapiens chromosome 10 clone CIT-HSP-1255F20 map 10p11.2-10p12.1, complete sequence.//9.6e-13:237:67//AC005878
 R-MAMMA1002566//CITBI-E1-2509P21, TR CITBI-E1 Homo sapiens genomic clone 2509P21, genomic survey sequence.//9.7e-14:216:73//AQ261427
 R-MAMMA1002571//CITBI-E1-2516L21, TF CITBI-E1 Homo sapiens genomic clone 2516L21, genomic survey sequence.//4.6e-25:142:99//AQ279542
 R-MAMMA1002573//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 811H13, WORKING DRAFT SEQUENCE.//1.1e-30:250:82//AL023805
 R-MAMMA1002585//Rabbit angiotensin-converting enzyme (ACE) gene, 5' end.//1.0:196:61//M58580
 R-MAMMA1002590//H. sapiens CpG island DNA genomic MseI fragment, clone 8d5, forward read cpg8d5.f1g.//1.0:114:64//Z63758
 R-MAMMA1002597//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1103G7, WORKING DRAFT SEQUENCE.//9.0e-96:459:98//AL034548
 R-MAMMA1002598//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 120G22, WORKING DRAFT SEQUENCE.//0.79:362:58//ALD31847
 R-MAMMA1002603//Homo sapiens chromosome 17, clone hRPC.214_C_8, complete sequence.//1.3e-46:333:80//AC005803
 R-MAMMA1002612//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 269M15, WORKING DRAFT SEQUENCE.//7.4e-41:283:86//AL021395
 R-MAMMA1002617//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 591N18, WORKING DRAFT SEQUENCE.//1.7e-20:308:71//AL031594
 R-MAMMA1002618//Homo sapiens clone RG122E10, complete sequence.//1.2e-31:230:76//AC005067
 R-MAMMA1002619//Homo sapiens chromosome 21 PAC RPC1P704E14135Q2.//9.0e-113:551:98//AJ010598
 R-MAMMA1002622//Homo sapiens chromosome 4 clone B207D4 map 4q25, complete sequence.//2.8e-43:324:83//AC004050
 R-MAMMA1002623//Homo sapiens chromosome 17, clone hRPC.1171_1_10, complete sequence.//2.7e-80:344:84//AC004687
 R-MAMMA1002625//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1056L3, WORKING DRAFT SEQUENCE.//2.6e-34:391:72//AL031727
 R-MAMMA1002629//Human DNA from overlapping chromosome 19-specific cosmids R32543, and F15613 containing ZNF gene family member, genomic sequence, complete sequence.//5.5e-58:346:81//AC003006
 R-MAMMA1002636//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.1e-52:285:92//AC004895
 R-MAMMA1002637//Mus musculus kinesin light chain 2 (Klc2) mRNA, complete cds.//2.1e-13:359:64//AF055666
 R-MAMMA1002646//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 39417, WORKING DRAFT SEQUENCE.//2.5e-24:285:68//AL023585
 R-MAMMA1002650//Human IGF-II gene exon 2 for insulin-like growth factor II located on chromosome 11.//0.64:237:61//X03424
 R-MAMMA1002655//Homo sapiens minisatellite ceb1 repeat region.//0.18:152:65//AF048727
 R-MAMMA1002662//Homo sapiens clone DJ0739M23, complete sequence.//2.5e-46:370:82//AC004870
 R-MAMMA1002665//Human DNA sequence from PAC 435C23 on chromosome X, contains ESTs.//7.4e-55:298:92//Z92844
 R-MAMMA1002671//RPC111-45M10, TK RPC111 Homo sapiens genomic clone R-45M10, genomic survey sequence.//0.99:151:65//AQ194411
 R-MAMMA1002673//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//3.1e-38:410:76//AL022162
 R-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds.//1.4e-107:544:96//D86987
 R-MAMMA1002685//HS_2052_A1_H02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2052 Col=3 Row=0, genomic survey sequence.//1.2e-23:255:75//AQ231087
 R-MAMMA1002698//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC library) complete sequence.//1.1e-38:299:83//AC004673
 R-MAMMA1002699//Mus musculus intersectin-EH binding protein lbpl mRNA, partial cds.//3.3e-05:61:93//AF057285
 R-MAMMA1002701//Homo sapiens gene for AF-6, complete cds.//3.5e-39:317:81//AB011399
 R-MAMMA1002708//Homo sapiens 12p13.3 PAC RPC15-977L1 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.26:365:62//AC005293
 R-MAMMA1002711//Homo sapiens chromosome 21 PAC LLNLP704F18108Q13.//2.5e-31:304:77//AJ006995
 R-MAMMA1002721//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 473B4, WORKING DRAFT SEQUENCE.//2.3e-40:279:87//Z83826
 R-MAMMA1002727//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.45:183:64//AC004710
 R-MAMMA1002728//Human Chromosome 11 Overlapping Cosmids cSRL72g7 and cSRL140b8, complete sequence.//1.1e-42:410:74//AC002037
 R-MAMMA1002744//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//1.6e-19:473:63//U96629
 R-MAMMA1002746//Homo sapiens chromosome 17, clone hRPC.136_H_19, complete sequence.//2.2e-108:544:97//AC005856
 R-MAMMA1002748//Homo sapiens 3p22 Contig 7 PAC RPC14-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//5.9e-106:551:95//AC006055
 R-MAMMA1002754//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.7e-34:305:79//AC005020
 R-MAMMA1002758//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//0.00014:130:74//U95626
 R-MAMMA1002764//Homo sapiens chromosome 19, cosmid R33632, complete

【0802】

【表502】

e sequence.//8.7e-10:118:81//AC005781
 R-MAMMA1002765//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//1.2e-31:290:78//AC006128
 R-MAMMA1002769//Human DNA sequence from PAC 36J3, between markers OXS1192 and OXS102 on chromosome X.//0.94:260:62//Z82975
 R-MAMMA1002780//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 620E11, WORKING DRAFT SEQUENCE.//2.6e-21:529:62//AL031667
 R-MAMMA1002782//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 199H16, WORKING DRAFT SEQUENCE.//2.8e-30:234:72//AL022320
 R-MAMMA1002796//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 237J2, WORKING DRAFT SEQUENCE.//1.0:155:66//AL021394
 R-MAMMA1002807//Human DNA sequence from BAC 941F9 on chromosome 22 q11.2-qter. Contains ESTs, STSs and 3' part of FIBULIN-1 D PRECURSOR like gene, part of a Brain Protein E46 like gene and a CpG island, complete sequence.//5.0e-42:443:75//Z95331
 R-MAMMA1002820//345M16.TVB C1978SKA1 Homo sapiens genomic clone A-345M16, genomic survey sequence.//1.3e-14:95:87//B17487
 R-MAMMA1002830//Human PAC clone DJ515N1 from 22q11.2-q22, complete sequence.//4.1e-20:223:74//AC002073
 R-MAMMA1002833//Homo sapiens Xp22 bins 3-5 PAC RPC14-617A9 (Roswell Park Cancer Institute Human PAC Library) containing Arylsulfatase D and E genes, complete sequence.//1.8e-37:295:84//AC005295
 R-MAMMA1002835
 R-MAMMA1002838//Human gene hY3 encoding a cytoplasmic rRNA.//4.4e-14:108:92//V00585
 R-MAMMA1002842//CIT-HSP-2017022, TRB CIT-HSP Homo sapiens genomic clone 2017022, genomic survey sequence.//5.2e-43:168:85//B67141
 R-MAMMA1002843//Homo sapiens clone GS051M12, complete sequence.//8.7e-44:525:71//AC005007
 R-MAMMA1002844
 R-MAMMA1002858//H. sapiens ERF-1 mRNA 3' end.//2.8e-99:361:91//X79067
 R-MAMMA1002868//Homo sapiens clone DJ0852024, WORKING DRAFT SEQUENCE. 2 unordered pieces.//9.5e-39:288:81//AC004906
 R-MAMMA1002871//Homo sapiens BAC clone MH0539B24 from 7p15.1-p14, complete sequence.//0.0022:490:57//AC006044
 R-MAMMA1002880//Homo sapiens Xp22 Bins 35-37 BAC CSHB-214D18 (Genome Systems Human BAC Library) complete sequence.//1.3e-09:143:76//AC005296
 R-MAMMA1002881//Human thymopoietin (TMPO) gene, partial exon 6, complete exon 7, partial exon 8, and partial cds for thymopoietin beta.//5.1e-41:264:87//U18271
 R-MAMMA1002886//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, EST, GSS, STS, CpG island, complete sequence.//4.7e-32:216:90//AL022069
 R-MAMMA1002887
 R-MAMMA1002890
 3.4e-49:376:81//AG006257
 R-MAMMA1002892//Homo sapiens PAC clone DJ0765G07 from 7q11, complete sequence.//6.0e-60:344:79//AC004881
 R-MAMMA1002895//RPC111-90K13, TV RPC111 Homo sapiens genomic clone R-90K13, genomic survey sequence.//2.1e-34:300:77//AQ283502
 R-MAMMA1002908//Human Chromosome X, complete sequence.//4.2e-39:297:85//AC004070
 R-MAMMA1002909//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0442P12: HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.4e-23:344:74//AC005798
 R-MAMMA1002930//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence.//5.2e-39:261:88//AC006019
 R-MAMMA1002938//C. pasteurianus gap gene.//1.0:343:59//X72219
 R-MAMMA1002941//Homo sapiens chromosome 17, clone hRPC.346_K_10, complete sequence.//6.3e-88:556:87//AC006120
 R-MAMMA1002947
 0.48:156:69//AC005469
 R-MAMMA1002964//Human DNA sequence from PAC 42616 on chromosome 1p34.1-p35. Contains NIPP-1-like gene a nuclear inhibitor of protein phosphatase-1, ESTs, and a CA repeat.//1.2e-39:473:73//AL020997
 R-MAMMA1002970//Homo sapiens chromosome 5, P1 clone 793c5 (LBNL H57), complete sequence.//4.7e-47:420:77//AC005200
 R-MAMMA1002972//alpha 1 syntrophin [human, mRNA Partial, 1771 nt].//0.97:305:62//S61737
 R-MAMMA1002973//Human DNA sequence from cosmid Y210E9, between markers DXS366 and DXS87 on chromosome X.//2.6e-35:256:85//Z70280
 R-MAMMA1002982
 1.0e-27:110:85//AG005524
 R-MAMMA1002987//Homo sapiens PAC clone DJ1086D14, complete sequence.//1.4e-28:527:66//AC004460
 R-MAMMA1003003//Homo sapiens chromosome 10 clone CRI-JC2059 map 10 q24.1-10q24.2, WORKING DRAFT SEQUENCE, 1 ordered pieces.//7.9e-48:418:78//AC006109
 R-MAMMA1003004//, complete sequence.//2.0e-12:442:61//AC005406
 R-MAMMA1003007//Homo sapiens chromosome 10 clone CRI-JC2059 map 10 q24.1-10q24.2, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.7e-48:293:91//AC006109
 R-MAMMA1003011//A-306G8.TP C1978SK Homo sapiens genomic clone A-306G8, genomic survey sequence.//0.45:168:64//B18092
 R-MAMMA1003015//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//2.9e-44:399:77//AC005740
 R-MAMMA1003019//RPC111-9J9, TV RPC111 Homo sapiens genomic clone R-PC111-9J9, genomic survey sequence.//2.7e-14:294:68//B71583
 R-MAMMA1003026//HS_2166_B2_C12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2166 Col=24 Row=F, genomic survey sequence.//0.021:189:64//AQ125639
 R-MAMMA1003031//Homo sapiens chromosome 5, BAC clone 319C17 (LBNL H159), complete sequence.//1.8e-98:525:95//AC005214
 R-MAMMA1003035//Homo sapiens 12q13.1 Cosmid C174F5 (Lawrence Livermore LL12NC01 or LL12NC02 human cosmid libraries) complete sequence.//6.7e-06:297:63//AC004550
 R-MAMMA1003039//RPC111-56J17.TJ RPC111 Homo sapiens genomic clone R-56J17, genomic survey sequence.//0.21:375:59//AQ081889
 R-MAMMA1003040//Human DNA sequence from cosmid L108f12, Huntington's Disease Region, chromosome 4p16.3.//2.7e-29:298:67//Z49235
 R-MAMMA1003044//Homo sapiens chromosome 19, cosmid R30676, complete sequence.//2.9e-14:113:91//AC004560
 R-MAMMA1003047
 R-MAMMA1003049
 R-MAMMA1003055//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 377F16, WORKING DRAFT SEQUENCE.//2.3e-45:317:86//Z93783
 R-MAMMA1003056//Homo sapiens chromosome 19, cosmid R34275, complete sequence.//1.0:229:63//AC005305
 R-MAMMA1003057//M. domesticus MD6 mRNA.//6.2e-42:326:82//X54352
 R-MAMMA1003066//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 473B4, WORKING DRAFT SEQUENCE.//3.1e-49:299:87//Z83826
 R-MAMMA1003089//Homo sapiens BAC clone RG298G08 from 7p15-p21, complete sequence.//2.7e-30:520:67//AC005084
 R-MAMMA1003099//RPC111-8N9, TP RPC111 Homo sapiens genomic clone R-PC111-8N9, genomic survey sequence.//4.2e-44:338:82//B71494
 R-MAMMA1003104//Mus musculus rostral cerebellar malformation protein (rcm) mRNA, complete cds.//3.4e-48:423:79//U72634
 R-MAMMA1003113//Homo sapiens chromosome 12p13.3 clone RPC111-433J, 6, WORKING DRAFT SEQUENCE, 100 unordered pieces.//4.8e-114:567:97//AC006087
 R-MAMMA1003127//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 250D10, WORKING DRAFT SEQUENCE.//1.4e-34:283:83//Z99716
 R-MAMMA1003135//P. knowlesi Mbn-cutting sites in lambda KBS50.//0.010:243:62//W38776
 R-MAMMA1003140//Homo sapiens chromosome 17, clone HC1T87G17, complete sequence.//6.7e-34:288:81//AC003663
 R-MAMMA1003146//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds.//4.8e-08:438:59//M97514
 R-MAMMA1003150//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 598F2, WORKING DRAFT SEQUENCE.//1.7e-63:149:94//AL021579
 R-MAMMA1003166//HS_3128_A1_B01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3128 Col=1 Row=C, genomic survey sequence.//3.0e-17:261:70//AQ140766
 R-NT2RM2002580//Homo sapiens clone 24781 mRNA sequence.//2.6e-111:593:94//AF070640
 R-NT2RM4000024
 R-NT2RM4000027//Homo sapiens PAC clone DJ1194E14 from 7p21, complete sequence.//0.026:476:56//AC004993
 R-NT2RM4000030//Mus musculus sex determining protein (Sry) gene, complete cds.//0.00044:378:59//U70653
 R-NT2RM4000046//M. mulatta MHC DR beta 6 gene encoding major histocompatibility complex.//0.27:130:64//Z26239
 R-NT2RM4000061
 R-NT2RM4000085//Homo sapiens clone 24700 unknown mRNA, partial cds.//7.2e-112:550:97//AF070639
 R-NT2RM4000086//RPC111-6J23.TV RPC111 Homo sapiens genomic clone R-PC111-6J23, genomic survey sequence.//7.2e-18:277:71//B49463
 R-NT2RM4000104//F. rubripes GSS sequence, clone 063K10aGS, genomic survey sequence.//3.6e-08:287:61//Z88817
 R-NT2RM4000139//Homo sapiens chromosome 16, cosmid clone 330D11 (LANL), complete sequence.//9.4e-08:336:65//AC005199
 R-NT2RM4000155
 R-NT2RM4000156//Homo sapiens chromosome 17, clone hRPC.136_H_19, c

【0803】

【表503】

complete sequence.//3.4e-23:335:72//AC005856
R-NT2RM4000167//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//1.6e-87:551:87//D12646
R-NT2RM4000169//Human ribosomal protein L37a mRNA sequence.//5.9e-14:122:88//L22154
R-NT2RM4000191
R-NT2RM4000197//HS_3241_A2_H05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3241 Col=10 Row=D, genomic survey sequence.//2.8e-86:430:97//AQ206812
R-NT2RM4000199//Mus musculus Yp BAC GSNB-368G7 (Genome Systems Mouse BAC Library) complete sequence.//0.0047:193:63//AC006056
R-NT2RM4000200
R-NT2RM4000202//Homo sapiens chromosome 16, cosmid clone 378E2 (LA NL), complete sequence.//2.1e-40:334:76//AC004035
R-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//5.2e-102:546:94//AB018255
R-NT2RM4000215
R-NT2RM4000229//Homo sapiens chromosome 10 clone CIT987SK-1144G6 map 10q25.1, complete sequence.//2.1e-55:303:86//AC005383
R-NT2RM4000233//Struthio camelus microsatellite sequence OSM 7.//1.2e-07:198:67//AF003735
R-NT2RM4000244//Homo sapiens chromosome 19, BAC CIT-8-393i15 (BC30 1323), complete sequence.//1.7e-49:322:88//AC006116
R-NT2RM4000251//Homo sapiens Chromosome 22q11.2 BAC Clone 7218 in DGCR Region, complete sequence.//0.97:184:66//AC000085
R-NT2RM4000265//Human PAC clone DJ073F11 from Xq23, complete sequence.//6.2e-66:552:78//AC000055
R-NT2RM4000290//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 39417, WORKING DRAFT SEQUENCE.//1.4e-05:229:65//AL023585
R-NT2RM4000324
R-NT2RM4000327//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 75N14, WORKING DRAFT SEQUENCE.//3.3e-42:443:75//Z97199
R-NT2RM4000344//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//6.4e-64:433:84//AC004826
R-NT2RM4000349//Human mRNA for KIAA0005 gene, complete cds.//7.7e-11:210:69//D13630
R-NT2RM4000354//Caenorhabditis elegans cosmid T14A8.//0.084:257:60//U50066
R-NT2RM4000356
R-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds.//8.7e-112:577:95//AB014542
R-NT2RM4000368
1.6e-48:348:85//AC006257
R-NT2RM4000386//Rat mRNA for growth potentiating factor, complete cds.//4.4e-35:141:87//D42148
R-NT2RM4000395//RPC111-8N9, TP RPC111 Homo sapiens genomic clone R PCI-11-BN9, genomic survey sequence.//1.4e-25:207:75//B71494
R-NT2RM4000414//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 228H13, WORKING DRAFT SEQUENCE.//7.1e-17:492:64//AL031985
R-NT2RM4000421//RPC111-66B1, TK RPC111 Homo sapiens genomic clone R-66B1, genomic survey sequence.//1.8e-40:311:82//AQ241167
R-NT2RM4000425//Homo sapiens chromosome Xp22-135-136 clone GSHB-56711, WORKING DRAFT SEQUENCE, 35 unordered pieces.//2.5e-47:316:87//AC005867
R-NT2RM4000433//Mus musculus retinoic acid-responsive protein (Str a6) mRNA, complete cds.//1.6e-17:133:78//AF062476
R-NT2RM4000457
R-NT2RM4000471//Homo sapiens mRNA for putative tRNA splicing protein, partial.//4.6e-113:559:96//AJ010952
R-NT2RM4000486//Homo sapiens mRNA, complete cds, clone:RES4-22C.//0.00015:170:67//AB000461
R-NT2RM4000496
R-NT2RM4000511//Rat troponin T cardiac isoform gene, complete cds.//0.21:290:58//M80829
R-NT2RM4000514//CIT-HSP-2169K4, TR CIT-HSP Homo sapiens genomic clone 2169K4, genomic survey sequence.//1.5e-20:150:89//B95717
R-NT2RM4000515//HS-1024-B2-G01-MR, abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 803 Col=2 Row=N, genomic survey sequence.//6.3e-10:74:98//B34556
R-NT2RM4000520//Caenorhabditis elegans cosmid F36H12.//0.15:406:61//AF078790
R-NT2RM4000531
R-NT2RM4000532//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete sequence.//1.0:119:66//AE001391
R-NT2RM4000534//paramecium species 4.51er mt dna dimer: replication init. region, clone 2.//9.8e-05:326:60//K00909
R-NT2RM4000585//HS_3252_A2_G08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=16 Row=M, genomic survey sequence.//1.9e-69:376:93//AQ219890
R-NT2RM4000590//CIT-HSP-539024, TV CIT-HSP Homo sapiens genomic clone 539024, genomic survey sequence.//1.7e-38:226:93//B50657
R-NT2RM4000595//Human Chromosome X clone BWD342, complete sequence.//1.0:239:61//AC004072
R-NT2RM4000603//RPC111-49P13, TK RPC111 Homo sapiens genomic clone R-49P13, genomic survey sequence.//0.77:139:64//AQ051950
R-NT2RM4000611
R-NT2RM4000616//HS_3107_A2_B03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3107 Col=5 Row=C, genomic survey sequence.//1.3e-54:272:99//AQ210034
R-NT2RM4000674
R-NT2RM4000689//Mus musculus pericentri mRNA, complete cds.//3.5e-70:551:80//U05823
R-NT2RM4000698
R-NT2RM4000700
R-NT2RM4000712//Homo sapiens clone NH0512E16, complete sequence.//0.54:294:58//AC005039
R-NT2RM4000717//Plasmodium falciparum MAL3P8, complete sequence.//0.050:387:58//AL034560
R-NT2RM4000733//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//1.0e-107:566:95//AL034379
R-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds.//1.1e-103:536:95//AB018303
R-NT2RM4000741//CIT-HSP-2294N4, TR CIT-HSP Homo sapiens genomic clone 2294N4, genomic survey sequence.//5.2e-41:244:93//AQ006361
R-NT2RM4000751//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 537K23, WORKING DRAFT SEQUENCE.//2.7e-28:416:67//AL034405
R-NT2RM4000764//Human HepG2 3' region Mbol cDNA, clone hmd3g01m3.//2.1e-33:199:96//D17217
R-NT2RM4000778//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC library) complete sequence.//0.00060:241:62//AC002980
R-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds.//2.9e-104:546:94//AB007920
R-NT2RM4000787//Homo sapiens, clone hRPK.3_A.1, complete sequence.//5.3e-32:321:77//AC006198
R-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216, complete sequence.//1.9e-111:552:97//AC005306
R-NT2RM4000795//Homo sapiens Chromosome 17p13 Cosmid Clone cos39, complete sequence.//0.74:364:57//U58675
R-NT2RM4000796//Homo sapiens full length insert cDNA clone ZD62D10.//2.7e-105:510:98//AF08348
R-NT2RM4000798//Human polymorphic epithelial mucin core protein mRNA, 3' end.//7.7e-27:158:96//M21868
R-NT2RM4000813
R-NT2RM4000820//. complete sequence.//2.0e-104:432:97//AC005406
R-NT2RM4000833//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MX122, complete sequence.//2.0e-07:166:68//AB012248
R-NT2RM4000848//Rabies virus matrix (M) protein mRNA, complete cds.//0.073:70:84//M22013
R-NT2RM4000852//Plasmodium falciparum 3D7 chromosome 12 PFYAC122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:237:62//AC004709
R-NT2RM4000855
R-NT2RM4000887//HS_3189_B2_B08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3189 Col=16 Row=D, genomic survey sequence.//2.1e-06:114:73//AQ300597
R-NT2RM4000895//Pan troglodytes HS19.8-similar locus and Y Alu element, genomic survey sequence.//3.8e-46:207:91//AF077058
R-NT2RM4000950//Human BAC clone RG341D10 from 7p15-p21, complete sequence.//1.0:336:60//AC002530
R-NT2RM4000971//Human Xq28 cosmids U126G1, U142F2, U6986, U145C10, U169A5, U84H1, U24D12, U80A7, U153E6, L35485, and R7-163AB containing iduronate 2-sulfatase gene and pseudogene, complete sequence.//7.1e-09:259:64//AF011889
R-NT2RM4000979
R-NT2RM4000996//HS_3164_A1_E02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3164 Col=3 Row=I, genomic survey sequence.//2.0e-82:443:94//AQ141622
R-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds.//1.2e-112:545:97//AB018272
R-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds.//7.9e-113:556:97//AB014539
R-NT2RM4001032//Homo sapiens Surf-5 and Surf-6 genes.//1.2e-10:12:0:82//AJ224639
R-NT2RM4001047//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 163C9, WORKING DRAFT SEQUENCE.//1.0:158:67//AL008733
R-NT2RM4001054//CIT-HSP-2292N8, TR CIT-HSP Homo sapiens genomic clone

【0804】

【表504】

ne 2292N8, genomic survey sequence.//5.8e-19:118:97//AQ004096
R-NT2RM4001084//Mouse DNA with homology to EBV IR3 repeat, segment 1, clone Mu2.//1.0e-05:271:64//M10296
R-NT2RM4001092//CITBI-EI-2524J20.TR CITBI-EI Homo sapiens genomic clone 2524J20, genomic survey sequence.//1.0:186:63//AQ277294
R-NT2RM4001116
R-NT2RM4001140//Homo sapiens PAC clone DJ0964C11 from 7p14-pl5, complete sequence.//3.6e-79:468:90//AC004593
R-NT2RM4001151//HS_2270_B1_E05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=9 Row=J, genomic survey sequence.//5.5e-62:312:98//AQ163739
R-NT2RM4001155//Homo sapiens chromosome 12p13.3 clone RPC14-816N1, WORKING DRAFT SEQUENCE, 31 unordered pieces.//1.4e-107:536:97//AC005841
R-NT2RM4001160//HS_3015_B1_H10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3015 Col=19 Row=P, genomic survey sequence.//7.1e-35:201:95//AQ118712
R-NT2RM4001187//X.laevis xUBFbeta2 mRNA for upstream binding factor 1.//0.019:177:63//X57201
R-NT2RM4001191//HS_3002_A1_F05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=9 Row=K, genomic survey sequence.//3.9e-33:230:75//AQ088791
R-NT2RM4001200//Homo sapiens full length insert cDNA clone YL3SHO 3.//7.5e-69:335:99//AF085857
R-NT2RM4001203
R-NT2RM4001204
R-NT2RM4001217
R-NT2RM4001256
R-NT2RM4001258
R-NT2RM4001309
R-NT2RM4001313//Homo sapiens 12q24.1 PAC RPC11-71H24 (Roswell Park Cancer Institute Human PAC library) complete sequence.//0.00055:183:63//AC004551
R-NT2RM4001316//Homo sapiens chromosome 17, clone hCIT.117_K_16, complete sequence.//4.5e-21:212:79//AC004757
R-NT2RM4001320//CIT-HSP-2303E22.TR CIT-HSP Homo sapiens genomic clone 2303E22, genomic survey sequence.//3.8e-30:86:89//AQ021084
R-NT2RM4001340
0.0027:493:60//AC005133
R-NT2RM4001344
R-NT2RM4001347//CITBI-EI-2506120.TR CITBI-EI Homo sapiens genomic clone 2506120, genomic survey sequence.//6.5e-16:101:99//AQ262797
R-NT2RM4001371//CITBI-EI-2503G21.TR CITBI-EI Homo sapiens genomic clone 2503G21, genomic survey sequence.//0.063:140:65//AQ265776
R-NT2RM4001382//HS_3044_A1_F02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3044 Col=3 Row=K, genomic survey sequence.//0.96:103:66//AQ098668
R-NT2RM4001384//R.norvegicus mRNA for dendrin.//8.5e-07:120:75//Y09000
R-NT2RM4001410//Bovine cytochrome P450-scc mRNA fragment.//2.3e-15:199:75//M25920
R-NT2RM4001411//Rattus norvegicus FcR1 gamma-chain interacting protein SH2-B (SH2-B) mRNA, complete cds.//1.7e-55:235:83//U57391
R-NT2RM4001412
R-NT2RM4001414//Homo sapiens Xp22 Cosmids U98B4 and U24F2 (Lawrence Livermore human cosmid library) complete sequence.//1.7e-80:489:89//U69730
R-NT2RM4001437//RPC111-56D2.TJ RPC111 Homo sapiens genomic clone R-56D2, genomic survey sequence.//3.8e-43:250:93//AQ081969
R-NT2RM4001444//Homo sapiens Xp22-171-173 BAC GSHB-31214 (Genome Systems Human BAC Library) complete sequence.//0.0034:224:63//AC005926
R-NT2RM4001454//Homo Sapiens Chromosome X clone bWDX90, complete sequence.//2.4e-33:360:68//AC004075
R-NT2RM4001455//HS_3229_B1_E04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3229 Col=7 Row=J, genomic survey sequence.//1.0:183:61//AQ191289
R-NT2RM4001483//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.2e-51:451:79//AC005282
R-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds.//2.2e-102:547:93//AB014585
R-NT2RM4001519//HS_2208_A1_F07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=13 Row=K, genomic survey sequence.//0.25:214:63//AQ091836
R-NT2RM4001522//H.sapiens gene for Cu/Zn-superoxide dismutase.//3.6e-13:246:70//Z29336
R-NT2RM4001557//Plasmodium falciparum MAL3P4, complete sequence.//0.055:320:58//AL008970
R-NT2RM4001565//Homo sapiens chromosome 12p13.3 clone RPC111-189M2, WORKING DRAFT SEQUENCE, 39 unordered pieces.//3.9e-26:329:72//A005910
R-NT2RM4001566//Human trophinin mRNA, complete cds.//6.3e-38:296:86//U04811
R-NT2RM4001569//Human DNA sequence from clone 461P17 on chromosome 20q12-13.2. Contains four novel (pseudo)genes for proteins with Kunitz/Bovine pancreatic trypsin inhibitor and/or WAP-type (Whey Acidic Protein) 'four-disulfide core' domains, COX6C (Cytochrome C oxidase Polypeptide VIC, EC 1.9.3.1) and RPL5 (60S Ribosomal Protein L5) pseudogenes, a pseudogene similar to part of the HSPD1 (HSP60, Mitochondrial Matrix Protein P1 precursor, Heat Shock Protein 60, GROEL protein, HUCHA60) gene, and the Major Epididymis-specific protein E4 precursor (HE4, Epididymis Secretory protein E4, WAP-type (Whey Acidic Protein) 'four-disulfide core' domain) gene. Contains ESTs, an STS, GSSs and a putative CpG island, complete sequence.//2.0e-35:213:89//AL031663
R-NT2RM4001582//Mus musculus COP9 complex subunit 7b (COPS7b) mRNA, complete cds.//5.4e-60:558:77//AF071317
R-NT2RM4001592//M.musculus mRNA of enhancer-trap-locus 1.//4.8e-86:565:85//X69942
R-NT2RM4001594//Human interleukin-13 (IL-13) precursor gene, complete cds.//0.083:283:61//U31120
R-NT2RM4001597//HS_2059_A1_G11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2059 Col=21 Row=M, genomic survey sequence.//4.4e-09:105:83//AQ245136
R-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds.//6.7e-111:565:95//AB018334
R-NT2RM4001611//Homo sapiens ryanodine receptor (RyR) mRNA, partial cds.//1.0:364:61//AF051936
R-NT2RM4001629//RPC111-54G14.TJ RPC111 Homo sapiens genomic clone R-54G14, genomic survey sequence.//0.0018:347:61//AQ083173
R-NT2RM4001650
R-NT2RM4001662//Homo sapiens DNA sequence from PAC 159A15 on chromosome Xp11.21-p11.23. Contains inter-alpha-trypsin inhibitor heavy chain H3 precursor-like protein.//0.75:212:62//AL022575
R-NT2RM4001666//Homo sapiens Chromosome 16 BAC clone C1987SK-A-233A8, complete sequence.//2.6e-26:461:65//AC004685
R-NT2RM4001682//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//1.5e-107:544:96//AL031775
R-NT2RM4001710//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE.//1.8e-110:580:95//AL031447
R-NT2RM4001714//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.1e-10:543:59//AC004153
R-NT2RM4001715//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//8.7e-111:577:94//AL034430
R-NT2RM4001731//Ovis aries dinucleotide repeat polymorphism at MAF 92 locus.//0.017:93:73//M80527
R-NT2RM4001741//Mouse mRNA for talin.//2.4e-34:273:83//X56123
R-NT2RM4001746//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 316G12, WORKING DRAFT SEQUENCE.//1.7e-112:567:96//AL031709
R-NT2RM4001754//Homo sapiens PAC clone 248015 from 13q12-q13, complete sequence.//1.4e-64:475:83//AC002483
R-NT2RM4001758//R.norvegicus mRNA for serine/threonine kinase MARK 1.//1.9e-18:202:78//Z83868
R-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds.//2.0e-22:236:80//AB018270
R-NT2RM4001783//Homo sapiens clone DJ0981007, complete sequence.//4.4e-106:551:95//AC006017
R-NT2RM4001810//T28D3TF TAMU Arabidopsis thaliana genomic clone T28D3, genomic survey sequence.//0.76:279:60//B27089
R-NT2RM4001813
R-NT2RM4001823
R-NT2RM4001828//HS_3073_A2_E01_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3073 Col=2 Row=I, genomic survey sequence.//1.6e-46:255:96//AQ121030
R-NT2RM4001836//Sus scrofa microsatellite S0398 sequence.//9.4e-06:141:69//U78024
R-NT2RM4001841//Salmo salar microsatellite Ssa65 DNA.//1.5e-06:175:65//AF019184
R-NT2RM4001842//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.0e-07:332:61//AC005077
R-NT2RM4001856//Mus musculus clone OST16642, genomic survey sequence.//4.8e-30:235:85//AF046633

【0805】

【表505】

R-NT2RM4001858//HS_3244_B1_F10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3244 Col=19 Row=L, genomic survey sequence.//3.0e-40:263:89//AQ252798

R-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CA LC.//5.0e-119:592:97//Y17711

R-NT2RM4001876//Megastigmus wachtlit dinucleotide microsatellite, clone MNA47CT.//0.13:134:64//AJ001069

R-NT2RM4001880

R-NT2RM4001905//HS_2016_B1_H11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2016 Col=21 Row=P, genomic survey sequence.//0.0066:264:59//AQ226877

R-NT2RM4001922//HS_2228_B2_B07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2228 Col=14 Row=D, genomic survey sequence.//2.5e-35:205:96//AQ065498

R-NT2RM4001930//Homo sapiens chromosome 17, clone hRPC.34_M_24, complete sequence.//0.26:325:63//AC004562

R-NT2RM4001938//Homo sapiens chromosome 17, clone hRPC.1081_P_3, complete sequence.//2.9e-85:421:98//AC005207

R-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds.//6.2e-109:556:95//AF098162

R-NT2RM4001953//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 473B4, WORKING DRAFT SEQUENCE.//1.3e-08:175:70//Z83826

R-NT2RM4001965//CIT-HSP-385N14.TR CIT-HSP Homo sapiens genomic clone 385N14, genomic survey sequence.//5.7e-69:532:81//B55044

R-NT2RM4001969//R.norvegicus mRNA for IP63 protein.//1.9e-61:352:83//X99330

R-NT2RM4001979//Homo sapiens full length insert cDNA clone ZD29F04.//1.1e-98:465:100//AF086241

R-NT2RM4001984//Borrelia burgdorferi (section 47 of 70) of the complete genome.//0.14:461:60//AE001161

R-NT2RM4001987

R-NT2RM4002013

R-NT2RM4002018

R-NT2RM4002034//Homo sapiens chromosome 5, BAC clone 24p24 (LBNL H 195), complete sequence.//3.6e-42:277:89//AC005353

R-NT2RM4002044//Homo sapiens PAC clone DJ1102B04 from 7q11.23-7q21, complete sequence.//0.83:476:57//AC006204

R-NT2RM4002054

R-NT2RM4002062//Human mitochondrial epoxide hydrolase gene, exons 5 and 6.//0.11:136:67//U06659

R-NT2RM4002063//Oryctolagus cuniculus sarcosine oxidase (SOX) mRNA, complete cds.//2.9e-99:503:96//U82267

R-NT2RM4002066//Homo sapiens CAGH45 mRNA, complete cds.//9.6e-41:554:68//U80742

R-NT2RM4002067//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 329A5, WORKING DRAFT SEQUENCE.//7.7e-64:476:81//Z97832

R-NT2RM4002073//Mus musculus fatty acid transport protein 3 mRNA, partial cds.//1.1e-33:238:85//AF072758

R-NT2RM4002075//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.031:403:57//AC005504

R-NT2RM4002093//Human Chromosome 11 pac pDJ227b23, WORKING DRAFT SEQUENCE, 19 unordered pieces.//9.4e-07:322:62//AC000383

R-NT2RM4002109//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//5.6e-44:432:74//D12646

R-NT2RM4002128//Human HepG2 partial cDNA, clone hmd2e12m5.//2.0e-26:186:90//D17000

R-NT2RM4002140

R-NT2RM4002145//Homo sapiens full length insert cDNA clone ZD38E12.//1.4e-15:193:76//AF086247

R-NT2RM4002146//Human ABL gene, intron 1b, partial sequence.//0.66:170:63//U07562

R-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds.//4.5e-110:560:96//AF084535

R-NT2RM4002174//Homo sapiens chromosome 17, clone hRPK.74_E_22, complete sequence.//8.0e-43:302:85//AC005696

R-NT2RM4002189

R-NT2RM4002194//Human Cosmid g5129g129 from 7q31.3, complete sequence.//0.29:382:60//AC003960

R-NT2RM4002205//Spiroplasma virus (SpV1-RBA2 B) complete genome.//3.5e-05:432:56//X51344

R-NT2RM4002213

R-NT2RM4002226//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//0.94:198:61//AC004448

R-NT2RM4002251

R-NT2RM4002256//Homo sapiens PAC clone DJ0570D02 from 7p13-p14, complete sequence.//2.3e-58:299:85//AC004837

R-NT2RM4002266//H. sapiens CpG island DNA genomic MseI fragment, clone 179f11, forward read cpg179f11.f1ta.//0.72:97:69//Z57487

R-NT2RM4002278//Homo sapiens clone RC140B11, WORKING DRAFT SEQUENCE, 1 unordered pieces.//7.5e-49:405:84//AC005069

R-NT2RM4002281//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 702J19, WORKING DRAFT SEQUENCE.//1.7e-13:168:77//AL033531

R-NT2RM4002287

R-NT2RM4002294//Homo Sapiens Chromosome X clone bWXD171, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.98:208:65//AC004676

R-NT2RM4002301//HS_2028_A1_E10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2028 Col=19 Row=I, genomic survey sequence.//0.94:321:57//AQ233262

R-NT2RM4002323//Human DNA sequence from clone 59B16 on chromosome 6p22.1-22.3. Contains a pseudogene similar to GP1SG20 and other exonucleases. Contains ESTs, STSs, GSSs, genomic markers D6S1691 and D6S299 and a ca repeat polymorphism, complete sequence.//1.9e-35:265:84//AL032822

R-NT2RM4002339//Human mRNA for KIAA0319 gene, complete cds.//2.4e-42:569:68//AB002317

R-NT2RM4002344//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.013:391:59//AC004709

R-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds.//8.6e-121:593:97//AB014549

R-NT2RM4002374//Human DNA sequence from cosmid U131B10, between markers DXS366 and DXS87 on chromosome X contains XK membrane transport protein, ESTs and STS.//3.8e-44:258:86//Z73417

R-NT2RM4002383//Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence.//0.00084:345:60//AC005316

R-NT2RM4002390

R-NT2RM4002409//RPC111-45M10.TK RPC111 Homo sapiens genomic clone R-45M10, genomic survey sequence.//0.99:151:66//AQ194411

R-NT2RM4002438

R-NT2RM4002446//Human DNA sequence from clone 360A4 on chromosome 16. Contains ESTs, complete sequence.//2.8e-103:533:95//AL031008

R-NT2RM4002452

R-NT2RM4002457//Homo sapiens chromosome 16, cosmid clone 32104 (LA NL), complete sequence.//0.99:171:64//AC004034

R-NT2RM4002460//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//0.96:94:71//Z92545

R-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds.//2.9e-102:508:97//AF083255

R-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds.//7.0e-31:172:98//AB014591

R-NT2RM4002493//CIT-HSP-2296C24.TF CIT-HSP Homo sapiens genomic clone 2296C24, genomic survey sequence.//0.46:182:62//AQ006882

R-NT2RM4002499//Human v-fos transformation effector protein (Fte-1), mRNA complete cds.//7.3e-24:134:99//M84711

R-NT2RM4002504//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1, 2, and 3, complete sequence.//3.9e-11:334:63//AC002368

R-NT2RM4002527

R-NT2RM4002532//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 341D10, WORKING DRAFT SEQUENCE.//3.4e-17:171:79//Z97985

R-NT2RM4002534

R-NT2RM4002567//Homo sapiens chromosome 7 clone UWCC:g1564a040 from 7p14-15, complete sequence.//2.2e-26:181:76//AC005271

R-NT2RM4002571

R-NT2RM4002593//CIT-HSP-2303L15.TF CIT-HSP Homo sapiens genomic clone 2303L15, genomic survey sequence.//0.034:73:82//AQ015579

R-NT2RM4002623//Homo sapiens clone UWCC:g1564a209 from 7p14-15, complete sequence.//0.0014:670:55//AC005862

R-NT2RP2000001//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.00087:251:59//AE001422

R-NT2RP2000006//Human DNA sequence from PAC 155D22 on chromosome 6 q27. Contains EST, STSs and a GSS.//2.7e-37:259:86//Z97205

R-NT2RP2000008//RPC111-41G16.TP RPC111 Homo sapiens genomic clone RPC111-41G16, genomic survey sequence.//4.1e-25:365:70//AQ029090

R-NT2RP2000027//Homo sapiens chromosome 17, clone HCIT305D20, complete sequence.//6.0e-05:307:62//AC004098

R-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds.//8.4e-41:223:96//AB018290

R-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//5.8e-63:325:96//AF061749

R-NT2RP2000054//Human tyrosinase gene, 5'-flanking region (containing enhancer element responsible for pigment cell-specific transcription).//0.88:210:60//D26163

R-NT2RP2000056//Mus musculus epsilon tyrosine phosphatase cytoplasmic isoform (Ptpre) mRNA, complete cds.//4.7e-38:377:78//U36758

【0806】

【表506】

R-NT2RP2000067//Rat mRNA for growth potentiating factor, complete cds.//5.0e-10:137:79//D42148	R-NT2RP2000337//Anopheles quadrimaculatus NADH dehydrogenase subunit 1 (1-4, 4L, 5-6): cytochrome oxidase subunits (1-3): adenosine triphosphatase subunits (6,8): cytochrome b: transfer RNA: ribosomal RNA (large and small subunits).//4.9e-08:494:58//L04272
R-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H 169), complete sequence.//3.1e-76:381:98//AC005754	R-NT2RP2000346//Homo sapiens apoptosis associated protein (CADD34) mRNA, complete cds.//3.4e-46:262:94//U83981
R-NT2RP2000076//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//2.3e-06:380:60//AE001372	R-NT2RP2000369//Homo sapiens chromosome 17, clone HCIT169H9, WORKING DRAFT SEQUENCE, 6 unordered pieces.//3.0e-07:334:61//AC002993
R-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds.//3.5e-77:379:97//AF050079	R-NT2RP2000414//Mouse DNA sequence *** SEQUENCING IN PROGRESS *** from clone BAC394, WORKING DRAFT SEQUENCE.//7.0e-08:98:83//AJ004828
R-NT2RP2000079//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1125A11, WORKING DRAFT SEQUENCE.//6.5e-32:314:78//AL034549	R-NT2RP2000420//Homo sapiens chromosome 17, clone hRPK.640_1_15, complete sequence.//0.99:150:62//AC005324
R-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//5.6e-74:378:96//AB018338	R-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//4.6e-19:142:90//AF102265
R-NT2RP2000091//Homo sapiens clone RGD15P03, complete sequence.//9.3e-21:226:76//AC005048	R-NT2RP2000438//RPC111-62113.TK RPC111 Homo sapiens genomic clone R-62113, genomic survey sequence.//3.1e-06:103:79//AQ199572
R-NT2RP2000097//Human DNA sequence from cosmid U209G1 on chromosome X.//9.2e-40:278:81//Z68873	R-NT2RP2000448//Homo sapiens PAC clone DJ0740D02 from 7p14-p15, complete sequence.//2.0e-22:276:73//AC004691
R-NT2RP2000098//Human BAC clone RC33F24 from 7q11.2-q21, complete sequence.//0.34:132:65//AC004015	R-NT2RP2000459//CIT-HSP-2013N9.TR CIT-HSP Homo sapiens genomic clone 2013N9, genomic survey sequence.//5.5e-27:205:87//B53940
R-NT2RP2000108//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//3.1e-09:259:67//AC003973	R-NT2RP2000498//Homo sapiens Chromosome 11q23 PAC clone pDJ149k2 c containing PLZF gene encoding kruppel-like zinc finger protein, complete sequence.//6.0e-12:119:84//AC001234
R-NT2RP2000114//Homo sapiens mRNA for CM3 synthase, complete cds.//1.8e-74:386:95//AB018356	R-NT2RP2000503//Human CYP11B2 gene for steroid 18-hydroxylase (P-450 C18), 5'-flanking region and exon 1.//0.48:201:64//D10170
R-NT2RP2000120//CITBI-E1-2503MB.TR CITBI-E1 Homo sapiens genomic clone 2503MB, genomic survey sequence.//5.1e-05:87:77//AQ263909	R-NT2RP2000510//Bactrocera dorsalis strain Tahiti mitochondrial D-loop region, complete sequence.//3.6e-07:472:59//AF033929
R-NT2RP2000126	R-NT2RP2000516
R-NT2RP2000133//Homo sapiens PAC clone DJ044L15 from Xq23, complete sequence.//4.9e-11:153:69//AC004827	R-NT2RP2000523//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 150C2, WORKING DRAFT SEQUENCE.//2.3e-61:317:97//AL022318
R-NT2RP2000147	R-NT2RP2000603//Homo sapiens mRNA for MCM3 import factor, complete cds.//6.6e-29:167:97//AB005543
R-NT2RP2000153//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//0.0058:261:57//U95626	R-NT2RP2000617
R-NT2RP2000157//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.5e-119:603:96//AC005924	R-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//2.5e-64:335:96//AB014514
R-NT2RP2000161//CIT-HSP-2045P7.TR CIT-HSP Homo sapiens genomic clone 2045P7, genomic survey sequence.//0.89:173:63//B79728	R-NT2RP2000644//Human DNA sequence from PAC 50A13 on chromosome Xp11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//1.8e-28:383:70//Z92545
R-NT2RP2000175	R-NT2RP2000656//Homo sapiens DNA sequence from PAC 874C20 on chromosome 6p22.1-22.3. Contains a Zinc Finger Protein ZFP47 LIKE gene, a Zinc Finger Protein pseudogene and a Zinc Finger Protein SRE-ZB P pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//0.0093:110:70//AL021997
R-NT2RP2000183	R-NT2RP2000658//Bacillus thuringiensis chitinase (chi) gene, complete cds.//0.73:301:60//U89796
R-NT2RP2000195//Homo sapiens chromosome 17, clone hRPK.60_A_24, complete sequence.//4.3e-39:306:83//AC005325	R-NT2RP2000668
R-NT2RP2000205//Human DNA sequence from clone 302L24 on chromosome Xq21-22, complete sequence.//7.5e-05:101:78//AL022155	R-NT2RP2000678//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 8/15, WORKING DRAFT SEQUENCE.//2.8e-11:256:66//AF000015
R-NT2RP2000224//Homo sapiens chromosome 16 BAC clone CIT987SK-A-15 ZES, complete sequence.//7.3e-55:306:94//AC004382	R-NT2RP2000710//Genomic sequence from Human 17, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.036:176:69//AC002346
R-NT2RP2000232	R-NT2RP2000715//Homo sapiens PAC clone DJ1066K24 from 7p15, complete sequence.//2.7e-110:555:96//AC004540
R-NT2RP2000233//Mus musculus tumor metastasis associated gene product (MAC) mRNA, complete cds.//7.6e-13:144:75//U88401	R-NT2RP2000731//Human DNA sequence from clone 497J21 on chromosome 6q26-27. Contains a KOC (KH-domain containing transcript overexpressed in cancer) pseudogene, genomic marker D6S193, ESTs, STSs and GSSs, and a ca repeat polymorphism, complete sequence.//2.6e-18:319:68//AL023775
R-NT2RP2000239//Homo sapiens chromosome 4 clone B353C18 map 4q25, complete sequence.//9.6e-63:410:86//AC004066	R-NT2RP2000758//CIT-HSP-507A14.TP CIT-HSP Homo sapiens genomic clone 507A14, genomic survey sequence.//1.0:189:60//B50590
R-NT2RP2000248//Caenorhabditis elegans cosmid T01C8.//1.0:282:58//US8726	R-NT2RP2000764
R-NT2RP2000257//Homo sapiens PAC clone DJ0808G16 from 7q11.23-q21, complete sequence.//2.5e-11:163:72//AC004894	R-NT2RP2000809//Human BAC clone RG356F09 from 7p21, complete sequence.//1.7e-24:215:81//AC004002
R-NT2RP2000258//Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence.//0.58:442:58//AC004077	R-NT2RP2000812//CIT-HSP-2281C3.TR CIT-HSP Homo sapiens genomic clone 2281C3, genomic survey sequence.//9.5e-32:176:97//B99575
R-NT2RP2000270//Homo sapiens DNA sequence from PAC 97D16 on chromosome 6p21.3-22.2. Contains an unknown pseudogene, a 60S Ribosomal protein L24 (L30) LIKE pseudogene and histone genes H2BFC (H2B/c), H4FFP (H4/f pseudogene), H2AFC (H2A/c), H3FIK (H3.1/k) and a tRNA A-Val pseudogene and tRNA-Thr gene. Contains ESTs, STSs, GSSs and genomic marker D6S464, complete sequence.//1.1e-39:292:84//AL009179	R-NT2RP2000814//paramecium species 5.87 mt dna dimer: replication init. region.//0.0077:418:57//K00916
R-NT2RP2000274//CIT-HSP-237901.TR CIT-HSP Homo sapiens genomic clone 237901, genomic survey sequence.//6.9e-10:121:81//AQ109409	R-NT2RP2000816//F.rubripes GSS sequence, clone 011H02aA6, genomic survey sequence.//0.61:52:73//AL010103
R-NT2RP2000288	R-NT2RP2000819
R-NT2RP2000289	R-NT2RP2000841//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 43408, WORKING DRAFT SEQUENCE.//0.00012:181:70//AL033504
R-NT2RP2000297//Homo sapiens full length insert cDNA clone ZB81C03.//7.7e-109:519:99//AF086165	R-NT2RP2000842//Mus musculus (C57BL/10 X C3H)F2 clone 4.9 novel mRNA from renin-expressing kidney tumor cell line, partial sequence.//3.7e-27:388:72//U13370
R-NT2RP2000298	R-NT2RP2000845//Homo sapiens chromosome 17, clone hRPK.849_N_15, c
R-NT2RP2000310//Homo sapiens p53 induced protein mRNA, partial cds.//1.5e-38:224:93//AF010310	
R-NT2RP2000327//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//4.3e-13:580:96//AL022398	
R-NT2RP2000329//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.4e-47:367:77//AC006039	

【0807】

【表507】

complete sequence.//0.0022:200:68//AC005703
R-NT2RP2000863
R-NT2RP2000880//Homo sapiens mRNA for putative GTP-binding protein, partial.//2.3e-43:279:89//AJ006412
R-NT2RP2000892//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 7/10.//0.0028:221:62//AB020875
R-NT2RP2000931//Homo sapiens mRNA for KIAA0723 protein, complete cds.//2.2e-55:290:96//AB018266
R-NT2RP2000938//Homo sapiens full length insert cDNA clone ZD55G12.//2.1e-37:215:93//AF086336
R-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//3.0e-96:494:96//AB018298
R-NT2RP2000965
R-NT2RP2000970//Homo sapiens DNA sequence from BAC 747E2 on chromosome 22q12.1. Contains ESTs, STSs and GSSs and genomic marker D2S56, complete sequence.//4.5e-87:440:97//AL021393
R-NT2RP2000985//Homo sapiens chromosome 17, clone hRPK.597_M12, complete sequence.//5.4e-93:484:95//AC005277
R-NT2RP2000987//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//2.1e-06:318:62//AE001372
R-NT2RP2001036//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 41018, WORKING DRAFT SEQUENCE.//2.0e-24:273:73//AL031732
R-NT2RP2001044//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-42.0 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//3.3e-07:365:65//AC005140
R-NT2RP2001065//Caenorhabditis elegans cosmid F10G7.//9.2e-06:273:59//U40029
R-NT2RP2001070//CITBI-E1-2503F4.TF CITBI-E1 Homo sapiens genomic clone 2503F4, genomic survey sequence.//0.13:97:72//AQ265973
R-NT2RP2001094//Mycoplasma mycoides SC immunodominant protein P72 (p72) gene, complete cds, mannitol-1-phosphate dehydrogenase (mtld) gene, partial cds and insertion sequence IS1296, complete sequence.//0.018:373:57//U61140
R-NT2RP2001119
R-NT2RP2001127//Homo sapiens HRHFB2060 mRNA, partial cds.//4.5e-55:304:94//AB015348
R-NT2RP2001137//Homo sapiens DNA sequence from clone 511B24 on chromosome 20q11.2-12. Contains the TOP1 gene for Topoisomerase I, the PLCG1 gene for 1-Phosphatidylinositol-4,5-Bisphosphate Phosphodiesterase Gamma 1 (EC 3.1.4.11, PLC-Gamma-1, Phospholipase C-Gamma-1 PLC-II, PLC-148), the KIAA0395 gene for a probable Zinc Finger Homeobox protein and a 60S Ribosomal Protein L23 LIKE pseudogene. C contains a predicted CpG island, ESTs, STSs and GSSs, complete sequence.//0.69:129:65//AL022394
R-NT2RP2001149//Sequence 5 from Patent US 4798885.//8.5e-28:322:77//U101838
R-NT2RP2001168
R-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds.//4.8e-95:490:96//AB007949
R-NT2RP2001174//CIT-HSP-2170B18.TR CIT-HSP Homo sapiens genomic clone 2170B18, genomic survey sequence.//1.3e-33:204:93//B89680
R-NT2RP2001196//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-65, complete sequence.//1.7e-06:413:61//AL010134
R-NT2RP2001218//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//0.5e-15:278:68//AL022153
R-NT2RP2001226//Human DNA sequence from clone 1170D6 on chromosome Xq22.3-23. Contains a pseudogene similar to U-SMRNP-associated Cyclophilin (USA-CYP, EC 5.2.1.8), ESTs, an STS and a GSS, complete sequence.//0.0020:462:57//AL030995
R-NT2RP2001233//CIT-HSP-2356P23.TR CIT-HSP Homo sapiens genomic clone 2356P23, genomic survey sequence.//8.0e-108:547:96//AQ081110
R-NT2RP2001245//Spodoptera frugiperda 16S.rRNA gene, Val-tRNA, and Leu-tRNA genes, and ND-1 protein gene, 5' end.//0.0052:350:58//M76713
R-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds.//4.6e-111:544:97//AB018353
R-NT2RP2001277//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y59A8, WORKING DRAFT SEQUENCE.//0.0058:327:59//Z98870
R-NT2RP2001290//Plasmodium falciparum 3D7 chromosome 12 PFYAC112 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.96:187:65//AC004709
R-NT2RP2001295//Homo sapiens BAC clone NH0491B03 from Tp21-p15, complete sequence.//0.59:218:62//AC005041
R-NT2RP2001312//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 349A12, WORKING DRAFT SEQUENCE.//0.12:117:64//AL033520
R-NT2RP2001327//Caenorhabditis elegans cosmid R04D3, complete sequence.//0.31:119:66//Z70212
R-NT2RP2001328//HS_2213_A1_D07.MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2213 Col=13 Row=G, genomic survey sequence.//1.7e-22:200:83//AQ136874
R-NT2RP2001347//Plasmodium falciparum MAL3P8, complete sequence.//0.81:509:56//AL034560
R-NT2RP2001378//H. sapiens DNA sequence.//0.94:147:63//Z22404
R-NT2RP2001381//Homo sapiens cyclin E2 mRNA, complete cds.//3.2e-09:75:97//AF091433
R-NT2RP2001392//Nyxococcus xanthus ATP-dependent protease (bsgA) gene, complete cds.//0.079:178:62//L19301
R-NT2RP2001394//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//3.4e-60:351:90//Z93242
R-NT2RP2001397//Hamster mRNA for cyclinB2, complete cds.//5.4e-55:320:83//D17294
R-NT2RP2001420//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1108D11, WORKING DRAFT SEQUENCE.//1.0e-44:246:85//AL034419
R-NT2RP2001423//Human DNA sequence from clone 726F20 on chromosome 1p36.11-36.23. Contains ESTs and a GSS, complete sequence.//3.7e-05:417:61//AL031273
R-NT2RP2001427//Human Chromosome 11 Cosmid cSRL34e5, complete sequence.//0.94:287:59//U73643
R-NT2RP2001436//Mus musculus clone OST1784, genomic survey sequence.//5.2e-31:299:77//AF046702
R-NT2RP2001440//Rattus norvegicus mRNA for 14-3-3 protein gamma-su type, complete cds.//7.8e-75:548:83//D17447
R-NT2RP2001445//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0e-06:452:59//AC004801
R-NT2RP2001449//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUENCE. 21 unordered pieces.//5.1e-08:218:67//AC004846
R-NT2RP2001450
R-NT2RP2001467//Human BAC clone RG343P13 from Tq31, complete sequence.//3.8e-31:254:83//AC002465
R-NT2RP2001506//C.barati p-47, ntth, bont genes.//1.2e-06:415:60//Y12091
R-NT2RP2001511//Plasmodium falciparum MAL3P7, complete sequence.//0.11:155:63//AL034559
R-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALARI.//2.1e-104:545:95//Y14494
R-NT2RP2001526//Homo sapiens chromosome 17, clone hCIT.175_E5, complete sequence.//7.0e-16:283:68//AC004596
R-NT2RP2001536//Human DNA from chromosome 14-specific cosmid containing XRCC3 DNA repair gene, genomic sequence, complete sequence.//7.7e-16:108:96//AF037222
R-NT2RP2001560//CIT978SK-A-56H4.TP CIT978SK Homo sapiens genomic clone A-56H4, genomic survey sequence.//0.052:112:66//B73597
R-NT2RP2001569//CIT-HSP-2335F8.TR CIT-HSP Homo sapiens genomic clone 2335F8, genomic survey sequence.//6.0e-78:383:98//AQ042029
R-NT2RP2001576//Homo sapiens sulfonilylurea receptor (SUR2) gene, exon 37.//0.33:135:66//AF061322
R-NT2RP2001581//Homo sapiens (clone MFD220) PCR primer.//2.7e-07:240:63//L15407
R-NT2RP2001597//HS_3016_B2_F06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3016 Col=12 Row=L, genomic survey sequence.//5.3e-45:310:87//AQ118854
R-NT2RP2001601//Homo sapiens chromosome 17, clone hRPK.855_D21, complete sequence.//0.015:445:58//AC006079
R-NT2RP2001613//Mus musculus orphan nuclear hormone receptor (CAR) gene, complete sequence.//3.5e-16:413:63//AF009326
R-NT2RP2001628//Phytomonas serpens kinetoplast maxicircle ribosomal protein S12 (G6) edited mRNA, complete cds.//0.11:190:63//AF034626
R-NT2RP2001663//Homo sapiens Chromosome 16 BAC clone CIT987SK-625P11, complete sequence.//3.0e-26:157:81//AC004125
R-NT2RP2001677//Homo sapiens chromosome 9, PI clone 11659, complete sequence.//3.0e-58:305:96//AC004472
R-NT2RP2001678//Human BAC clone RG222A16 from Tq31, complete sequence.//0.95:107:66//AC002385
R-NT2RP2001699//Mus musculus erythroid ankyrin and two alternative ly spliced erythroid ankyrins (Ankl) gene, putative exon 41 and partial cds.//8.8e-05:211:63//U76758
R-NT2RP2001720//Homo sapiens PAC clone DJ0167F23 from Tq15, complete sequence.//4.7e-68:352:97//AC004079
R-NT2RP2001721//HS-1052-B1-G06-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 774 Col=11 Row=N, genomic survey sequence.//7.7e-05:346:59//B40914
R-NT2RP2001740//HS_3213_A2_D02_T7 CIT Approved Human Genomic Sperm

【0808】

【表508】

Library D Homo sapiens genomic clone Plate=3213 Col=4 Row=G, genomic survey sequence.//1.1e-16:162.82//AQ175104	omic survey sequence.//1.9e-15:249.71//AQ178491
R-NT2RP2001748//Human gene for L-histidine decarboxylase, complete cds.//2.0e-33:312.77//D16583	R-NT2RP2002193//Rattus norvegicus potassium channel regulatory protein KCHAP mRNA, complete cds.//4.7e-35:438.73//AF032872
R-NT2RP2001762//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC26 2482), complete sequence.//2.3e-100:435.97//AC004783	R-NT2RP2002208//Hansenula wingei mitochondrial DNA, complete sequence.//0.00057:468.57//D31785
R-NT2RP2001813//Human leukocyte common antigen T200 (CD45, LCA) gene, exon 9.//0.031:261.60//M23468	R-NT2RP2002219//HS_2058_A1_C09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=17 Row=E, genomic survey sequence.//3.4e-55:512.77//AQ214380
R-NT2RP2001861	R-NT2RP2002231//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-31, complete sequence.//1.5e-06:398.61//Z98557
R-NT2RP2001869//Sequence 5 from patent US 5595900.//4.2e-21:194.77//134189	R-NT2RP2002252//Sequence 11 from patent US 5624818.//3.3e-91:553.87//141141
R-NT2RP2001876	R-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds.//3.0e-14:132.84//AF005418
R-NT2RP2001883//Human DNA sequence from clone 612818 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNII). ESTs, STS, GSS, CpG island, complete sequence.//5.0e-111:485.97//AL031864	R-NT2RP2002259//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 118J21, WORKING DRAFT SEQUENCE.//1.6e-96:548.91//AL033527
R-NT2RP2001900	R-NT2RP2002270//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-24 BFT, complete sequence.//5.1e-06:391.60//AC004605
R-NT2RP2001907//Human proto-oncogene tyrosine-protein kinase (ABL) gene, exon 1a and exons 2-10, complete cds.//5.4e-42:382.77//U07563	R-NT2RP2002292//Genomic sequence from Human 13, complete sequence.//0.91:159.64//AC001226
R-NT2RP2001926//HS_3180_B2_F02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3180 Col=4 Row=L, genomic survey sequence.//2.8e-25:138.80//AQ185415	R-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds.//1.3e-101:527.94//AF069532
R-NT2RP2001936//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:320.60//AC005504	R-NT2RP2002316//Plasmodium falciparum chromosome 2, section 45 of 73 of the complete sequence.//0.00052:389.59//AE001408
R-NT2RP2001943//Dictyostelium discoideum PkgA (pkgA) gene, partial cds.//1.4e-08:378.59//AF020280	R-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a) mRNA, complete cds.//2.3e-112:567.95//AF093668
R-NT2RP2001946//Homo sapiens clone NHD140K04, complete sequence.//3.6e-85:409.100//AC005033	R-NT2RP2002333//Rat POU domain factor (Brn-5) mRNA.//1.5e-22:323.73//L23204
R-NT2RP2001947//Human mRNA for KIAA0390 gene, complete cds.//0.85:140.64//AB002388	R-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//3.7e-102:600.89//AF038958
R-NT2RP2001969	R-NT2RP2002394//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.039:399.59//AC005308
R-NT2RP2001976//CIT-HSP-2281C3.TR CIT-HSP Homo sapiens genomic clone 2281C3, genomic survey sequence.//2.0e-60:307.98//B99575	R-NT2RP2002408//HS_2212_A1_E09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2212 Col=17 Row=1, genomic survey sequence.//9.6e-35:231.88//AQ184632
R-NT2RP2001985//Arabidopsis thaliana DNA chromosome 4, BAC clone F1W20 (ESSA11 project).//0.031:282.61//AL022140	R-NT2RP2002426//Human DNA sequence from clone 10IG11 on chromosome 22q12. Contains an ACO2 (Mitochondrial Aconitate Hydratase (Aconitase, Citrate Hydro-Lyase, EC 4.2.1.3)) pseudogene, ESTs, STSs, GSSs and a putative CpG island, complete sequence.//2.8e-39:308.82//AL021877
R-NT2RP2002025	R-NT2RP2002439//Leishmania tarentolae mitochondrial electron transport chain component mRNA.//0.022:102.71//M74225
R-NT2RP2002032//CITB1-E1-2502C19.TF CITB1-E1 Homo sapiens genomic clone 2502C19, genomic survey sequence.//1.2e-52:285.95//AQ264715	R-NT2RP2002457//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudogene, a Connective tissue growth factor (NOV, GIG) LIKE gene, a predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence.//0.00099:354.59//Z99289
R-NT2RP2002033//Human (lambda) DNA for immunoglobulin light chain.//1.1e-08:389.61//D88270	R-NT2RP2002464//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 6/15, WORKING DRAFT SEQUENCE.//0.0015:219.67//AP000013
R-NT2RP2002041//Homo sapiens 12p13.3 BAC RPC111-319E16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//1.1e-49:264.97//AC006206	R-NT2RP2002475
R-NT2RP2002046//Human BAC clone GS119P05 from Tq21, complete sequence.//0.0023:429.61//AC004011	R-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//3.1e-113:605.92//AB005289
R-NT2RP2002047//P. falciparum PK1 gene.//0.00015:239.62//X83707	R-NT2RP2002498//Human DNA sequence from PAC 162H14 on chromosome 2. Contains 3' part of a FIBULIN 1 like gene and ESTs, complete sequence.//0.32:210.64//Z98047
R-NT2RP2002058//HS_2183_A1_C01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=1 Row=M, genomic survey sequence.//1.2e-21:185.84//AQ022560	R-NT2RP2002503//Homo sapiens, clone hRPC.15_A_1, complete sequence.//4.0e-85:429.98//AC006213
R-NT2RP2002066//G.gallus microsatellite DNA (LE10222 (=T15iv004)).//0.18:102.70//Z83792	R-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds.//2.7e-105:583.91//AB018334
R-NT2RP2002070//P. falciparum major merozoite surface antigen (PMMSA) mRNA, complete cds, isolate FC27.//0.95:192.61//M19143	R-NT2RP2002520//Saccharomyces cerevisiae mitochondrial tRNA-Tyr, tRNA-Asn, & tRNA-Met genes.//0.14:406.58//AJ223323
R-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence.//3.8e-25:182.86//AF052183	R-NT2RP2002537//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 500L14, WORKING DRAFT SEQUENCE.//2.8e-16:188.78//AL023583
R-NT2RP2002079//Human DNA sequence from clone 431P23 on chromosome 6q27. Contains the first coding exon of the MLLT4 gene for myeloid/lymphoid or mixed-lineage leukemia (trithorax (Drosophila) homolog): translocated to, 4 (AF-6, Afadin, MLLT-4, ALL-1 fusion partner), and a Serine Palmitoyltransferase 2 (EC 2.3.1.50, Long Chain Base Biosynthesis protein 2, LCB-2, SPT-2) pseudogene. Contains ESTs, STSs, GSSs, and a putative CpG island, complete sequence.//1.7e-10:97.90//AL009178	R-NT2RP2002546//Homo sapiens clone TUA8 Cri-du-chat region mRNA.//4.7e-108:571.93//AF009314
R-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein.//4.6e-59:376.89//AJ007509	R-NT2RP2002549//Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence.//1.1e-103:422.95//AC005316
R-NT2RP2002105	R-NT2RP2002591//Human DNA binding protein (HPF2) mRNA, complete cds.//1.8e-36:526.67//M27878
R-NT2RP2002124//RPC111-75J16.TJ RPC111 Homo sapiens genomic clone R-75J16, genomic survey sequence.//0.58:191.64//AQ266779	R-NT2RP2002595
R-NT2RP2002137//Homo sapiens Xp22-175-176 BAC GSHB-484017 (Genome Systems Human BAC Library) complete sequence.//0.0065:294.61//AC005913	R-NT2RP2002606//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 2705, WORKING DRAFT SEQUENCE.//7.2e-10:211.71//AL033529
R-NT2RP2002154	R-NT2RP2002609
R-NT2RP2002172//RPC111-90C20.TJ RPC111 Homo sapiens genomic clone R-90C20, genomic survey sequence.//0.049:160.65//AQ282591	
R-NT2RP2002185//CIT-HSP-234115.TF CIT-HSP Homo sapiens genomic clone 234115, genomic survey sequence.//6.0e-36:230.90//AQ053355	
R-NT2RP2002192//HS_2222_B1_F08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2222 Col=15 Row=L, genomic survey sequence.//1.9e-15:249.71//AQ178491	

【0809】

【表509】

R-NT2RP2002618//Plasmodium falciparum MAL3P6, complete sequence.//2.9e-05:566:60//Z98551	R-NT2RP2003117//Homo sapiens clone DJ1137M13, complete sequence.//2.0e-51:323:88//AC005378
R-NT2RP2002621//Human DNA sequence from PAC 341110 on chromosome 6 q22.2-22.33. Contains 60S ribosomal protein L5 like (pseudo) gene, ESTs and STSs.//1.1e-38:348:78//Z97352	R-NT2RP2003121//HS_2238_A1_E08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2238 Col=15 Row=1, genomic survey sequence.//0.00055:324:61//AQ293058
R-NT2RP2002643//Homo sapiens chromosome 11 clone pTWB15.28 map 11p15.4-p15.5, genomic survey sequence.//1.2e-35:414:66//AF074030	R-NT2RP2003125
R-NT2RP2002672//Homo sapiens chromosome 10 clone CIT-HSP-1326H7 map 10q24.3-10q25.1, complete sequence.//1.3e-77:403:95//AC005384	R-NT2RP2003129
R-NT2RP2002701	R-NT2RP2003137//Human BAC clone RG084D04 from Tq31, complete sequence.//1.1e-46:521:74//AC003084
R-NT2RP2002706//Homo sapiens chromosome 19, cosmid F22676, complete sequence.//4.0e-42:147:90//AC005778	R-NT2RP2003161//Homo sapiens chromosome 10 clone CIT-HSP-1287C20, complete sequence.//1.0:368:59//AC005879
R-NT2RP2002710//P. falciparum serine rich protein (SERP I) gene.//0.84:135:67//J03983	R-NT2RP2003164//Dictyostelium discoideum actin 4 gene, 3' UTR.//1.0:120:64//M25581
R-NT2RP2002727//, complete sequence.//1.0:363:59//AC005815	R-NT2RP2003165//Homo sapiens chromosome 17, clone hRPC.1018_M_14, complete sequence.//2.2e-71:467:86//AC005823
R-NT2RP2002736//Arabidopsis thaliana chromosome 11 BAC T17M13 genomic sequence, complete sequence.//0.44:267:60//AC004138	R-NT2RP2003177
R-NT2RP2002740//Homo sapiens Xp22 BAC GSHB-600C8 (Genome Systems Human BAC library), complete sequence.//0.0016:474:60//AC004674	R-NT2RP2003194//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 996D20, WORKING DRAFT SEQUENCE.//1.1e-95:585:88//AL031597
R-NT2RP2002741//HS_3051_B1_H11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=21 Row=P, genomic survey sequence.//1.1e-38:217:86//AQ106283	R-NT2RP2003205//P. falciparum interspersed repeat antigen (FIRA) gene.//0.039:338:60//M17877
R-NT2RP2002750//Homo sapiens 12q24.1 PAC RPC11-315L5 (Roswell Park Cancer Institute Human PAC library) complete sequence.//5.0e-36:430:75//AC002395	R-NT2RP2003230//Plasmodium falciparum MAL3P6, complete sequence.//1.9e-11:542:60//Z98551
R-NT2RP2002752//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 366L4, WORKING DRAFT SEQUENCE.//8.2e-41:437:76//AL023494	R-NT2RP2003237//Arabidopsis thaliana genomic DNA, chromosome 5, PI clone: MDH9, complete sequence.//1.0:311:60//ABD16888
R-NT2RP2002753//Homo sapiens clone DJ076B20, WORKING DRAFT SEQUENCE. 6 unordered pieces.//6.8e-100:495:97//AC004882	R-NT2RP2003243//CIT-HSP-236B012, TR CIT-HSP Homo sapiens genomic clone 236B012, genomic survey sequence.//0.39:112:66//AQ077738
R-NT2RP2002769//paramusci species 5.311 mt dna dimer: replication init. region.//7.4e-10:404:60//K00917	R-NT2RP2003265//Muridae sp. (mouse-rat, neuroblastoma-glioma hybrid cell line NGD5) mRNA, complete cds.//1.3e-38:273:83//L38481
R-NT2RP2002778//Homo sapiens clone 24606 mRNA sequence.//1.2e-63:41:94//AF070537	R-NT2RP2003272//Homo sapiens clone UMGCI-y1c131 from 6p21, complete sequence.//4.4e-15:181:66//AC004187
R-NT2RP2002800//RPC111-37C8.TV RPC1-11 Homo sapiens genomic clone RPC1-11-37C8, genomic survey sequence.//4.9e-60:321:95//AQ029850	R-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds.//4.2e-110:565:95//AB014525
R-NT2RP2002839//Homo sapiens Chromosome 11q12.2 PAC clone pJ1688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//2.9e-100:492:98//AC006078	R-NT2RP2003280//Homo sapiens 12p13.3 PAC RPC15-1180D12 (Roswell Park Cancer Institute Human PAC library) complete sequence.//3.2e-12:221:70//AC005831
R-NT2RP2002857//HS_3026_B2_H07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3026 Col=14 Row=P, genomic survey sequence.//8.9e-06:242:62//AQ128697	R-NT2RP2003286//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//0.86:379:60//AC005261
R-NT2RP2002862//RPC111-42115.TJ RPC111 Homo sapiens genomic clone R-42115, genomic survey sequence.//1.5e-44:270:85//AQ052700	R-NT2RP2003293//Homo sapiens clone RG252P22, WORKING DRAFT SEQUENCE. 3 unordered pieces.//1.0e-39:418:74//AC005079
R-NT2RP2002880//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 150C2, WORKING DRAFT SEQUENCE.//1.0:295:58//AL022318	R-NT2RP2003295//HS_2053_B1_A10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2053 Col=19 Row=B, genomic survey sequence.//0.0016:346:61//AQ235251
R-NT2RP2002891	R-NT2RP2003297//Arabidopsis thaliana chromosome 11 BAC F4P9 genomic sequence, complete sequence.//0.74:397:56//AC002332
R-NT2RP2002925//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 243L18, WORKING DRAFT SEQUENCE.//2.0e-24:395:67//AL034395	R-NT2RP2003308//Homo sapiens PAC clone DJ1098B01 from 7q11.23-q21, complete sequence.//0.99:447:60//AC004960
R-NT2RP2002928//Plasmodium falciparum MAL3P5, complete sequence.//0.044:461:55//AL034556	R-NT2RP2003329//C. reinhardtii psbB 5' flanking region.//0.79:161:59//X59731
R-NT2RP2002929//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.35:491:56//AC005140	R-NT2RP2003339//RPC111-57H15.TK RPC111 Homo sapiens genomic clone R-57H15, genomic survey sequence.//0.13:184:64//AQ116039
R-NT2RP2002954//Homo sapiens chromosome 17, clone hRPC.628_E_12, complete sequence.//1.0:275:61//AC005701	R-NT2RP2003347//RPC111-15B19.TV RPC1-11 Homo sapiens genomic clone RPC1-11-15B19, genomic survey sequence.//6.4e-31:218:89//B76357
R-NT2RP2002959//Mus musculus ubiquitin conjugating enzyme (ubc4) mRNA, complete cds.//2.7e-61:508:79//U62483	R-NT2RP2003367//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//9.0e-11:101:84//U91321
R-NT2RP2002979//RPC111-20F13.TPK RPC1-11 Homo sapiens genomic clone RPC1-11-20F13, genomic survey sequence.//0.88:110:72//AQ008132	R-NT2RP2003391//HS_2255_B2_B04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2255 Col=8 Row=D, genomic survey sequence.//1.6e-38:247:90//AQ068937
R-NT2RP2002980//Homo sapiens PAC clone DJ0841B21 from 7q21.1-q31.1, complete sequence.//1.1e-102:433:95//AC004140	R-NT2RP2003393//RPC111-44K6.TJ RPC111 Homo sapiens genomic clone R-44K6, genomic survey sequence.//3.9e-31:290:79//AQ020481
R-NT2RP2002986//Human DNA sequence from clone 1147016 on chromosome Xp21.1-21.3. Contains 13 exons of the DMD muscular dystrophy gene. Contains an STS and GSSs, complete sequence.//0.31:219:62//AL031542	R-NT2RP2003394//Yeast mitochondrial ox13 gene exon 1 for cytochrome c oxidase subunit 1.//5.1e-14:579:61//X14910
R-NT2RP2002987//Homo sapiens chromosome 18, clone hRPC.24_A_23, complete sequence.//1.3e-51:283:88//AC005968	R-NT2RP2003401//Caprine arthritis-encephalitis virus tat protein (tat) and envelope glycoprotein (env) gene, partial cds.//0.32:174:66//U81429
R-NT2RP2002993//Human DNA sequence from PAC 106B9 on chromosome Xq21.//4.3e-11:430:63//AL021307	R-NT2RP2003433//Ascidian mRNA for HRSec61, complete cds.//1.5e-10:193:69//D25536
R-NT2RP2003000//Saccharomyces cerevisiae mitochondrion transfer RNA A-Leu, Gln, Lys, Arg, Gly, Asp, Ser2, Arg2, Ala, Ile, Tyr, Asn genes.//0.00088:347:62//L36887	R-NT2RP2003445//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//4.4e-99:585:89//AL023808
R-NT2RP2003034//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 2/10.//3.5e-33:271:82//AB020870	R-NT2RP2003446
R-NT2RP2003073	R-NT2RP2003456//Plasmodium falciparum MAL3P7, complete sequence.//0.98:399:57//AL034559
R-NT2RP2003099//Homo sapiens PAC clone DJ0886008 from 7q32-q35, complete sequence.//1.5e-45:548:69//AC004914	R-NT2RP2003480//Homo sapiens full length insert cDNA clone ZE09A1.//4.7e-111:540:98//AF086540
R-NT2RP2003108	R-NT2RP2003499
	R-NT2RP2003506
	R-NT2RP2003511
	R-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds.//4.1e-107:566:93//D87460

【0810】

【表510】

R-NT2RP2003517//Human c-sis/platelet-derived growth factor 2 (SIS/PDGF2) mRNA, complete cds.//1.5e-60:518:79//M12783

R-NT2RP2003522//HS_2182_A1_D05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=9 Row=G, genomic survey sequence.//0.053:251:60//AQ024304

R-NT2RP2003533//Homo sapiens chromosome 12p13.3 clone RPC14-816N1, WORKING DRAFT SEQUENCE, 31 unordered pieces.//1.5e-37:328:80//ACD05841

R-NT2RP2003543//HS_3028_A2_C12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3028 Col=24 Row=E, genomic survey sequence.//2.0e-39:203:100//AQ094957

R-NT2RP2003559//Homo sapiens full length insert cDNA clone ZD65E09.//2.3e-59:325:95//AF088055

R-NT2RP2003564

R-NT2RP2003581

R-NT2RP2003596//HS_2163_B1_D11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2163 Col=21 Row=H, genomic survey sequence.//0.0011:212:67//AQ125143

R-NT2RP2003604//Homo sapiens alpha-catenin-like protein mRNA, complete cds.//5.4e-102:501:97//U97067

R-NT2RP2003629//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-62 8 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0012:363:61//AC005507

R-NT2RP2003643//Mus musculus mRNA for CMP-N-acetylneuraminic acid synthetase.//5.1e-37:561:68//AJ006215

R-NT2RP2003668//Human DNA sequence from PAC 24608, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//0.0053:395:58//Z76735

R-NT2RP2003687//Human BAC clone RG222A16 from 7q31, complete sequence.//8.0e-10:205:67//AC002385

R-NT2RP2003691//HS_3252_A2_A11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=22 Row=A, genomic survey sequence.//5.3e-05:332:60//AQ219783

R-NT2RP2003702//CIT-HSP-2333P5, TF CIT-HSP Homo sapiens genomic clone 2333P5, genomic survey sequence.//3.9e-43:431:75//AQ035000

R-NT2RP2003704

R-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds.//2.6e-45:265:93//AB011097

R-NT2RP2003713//Human DNA sequence from PAC 411B6 on chromosome X.//0.64:169:67//Z84470

R-NT2RP2003714//Human DNA sequence from 4PTEL, Huntington's Disease Region, chromosome 4p16.3.//4.6e-11:152:73//Z95704

R-NT2RP2003727//H. sapiens mRNA for PIBF1 protein, complete.//0.94:443:59//Y09631

R-NT2RP2003737//Homo sapiens clone DJ1022114, WORKING DRAFT SEQUENCE, 14 unordered pieces.//2.2e-109:547:96//ACD04951

R-NT2RP2003751//Homo sapiens chromosome 16 BAC clone CIT987SK-A-42 7H10, complete sequence.//4.1e-109:545:97//ACD04626

R-NT2RP2003760//B. taurus mRNA for gamma-COP.//6.3e-28:400:69//X70019

R-NT2RP2003764//Mouse preprosomatostatin gene.//0.90:285:62//X51468

R-NT2RP2003769//Schizosaccharomyces pombe gene for protein involved in sexual development, complete cds.//0.96:446:58//D87956

R-NT2RP2003770//Homo sapiens sperm acrosomal protein mRNA, complete cds.//1.8e-104:531:96//AF047437

R-NT2RP2003777

R-NT2RP2003781//HS_3109_B1_B04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3109 Col=7 Row=D, genomic survey sequence.//1.3e-60:346:92//AQ186749

R-NT2RP2003793

R-NT2RP2003840

R-NT2RP2003857//HS_2205_A2_H12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2205 Col=24 Row=O, genomic survey sequence.//8.1e-22:127:99//AQ151299

R-NT2RP2003859//RPC111-37G8, TV RPC111 Homo sapiens genomic clone RPC111-37G8, genomic survey sequence.//8.3e-60:320:95//AQ029850

R-NT2RP2003871//HS_3210_A1_C08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3210 Col=15 Row=E, genomic survey sequence.//8.6e-09:322:61//AQ175028

R-NT2RP2003885//RPC111-7M10, TP RPC111 Homo sapiens genomic clone RPC111-7M10, genomic survey sequence.//4.7e-67:380:92//B72214

R-NT2RP2003912//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 32B1, WORKING DRAFT SEQUENCE.//1.2e-33:379:75//AL023693

R-NT2RP2003952

R-NT2RP2003968//Homo sapiens HUBP mRNA for ubiquitin specific protease, complete cds.//2.3e-114:568:97//AB014458

R-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds.//1.1e-107:540:97//AB007916

R-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds.//7.7e-114:568:96//AB018347

R-NT2RP2003984

R-NT2RP2003986//Human Chromosome 11 pac pDJ197h17, WORKING DRAFT SEQUENCE, 11 unordered pieces.//6.6e-99:551:92//AC000382

R-NT2RP2003988

R-NT2RP2004014

R-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127, complete sequence.//4.9e-114:568:97//AC004780

R-NT2RP2004042//nbxb0020F03r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0020F03r, genomic survey sequence.//0.11:195:64//AQ258389

R-NT2RP2004066//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 134019, WORKING DRAFT SEQUENCE.//7.6e-110:564:95//AL034555

R-NT2RP2004081//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.012:503:57//AC005308

R-NT2RP2004098//H. sapiens CpG island DNA genomic MseI fragment, clone 133h3, reverse read cpgl33h3.rta.//7.9e-25:140:100//Z64530

R-NT2RP2004124

R-NT2RP2004142//CIT-HSP-2316F21, TR CIT-HSP Homo sapiens genomic clone 2316F21, genomic survey sequence.//2.8e-83:409:98//AQ034964

R-NT2RP2004152//HS_3065_A2_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3065 Col=8 Row=G, genomic survey sequence.//2.5e-62:304:100//AQ137776

R-NT2RP2004165//Anthracidaris crassispina mRNA for dynein beta-heavy chain, complete cds.//3.4e-20:343:65//D01021

R-NT2RP2004170//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B33108: HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//2.5e-89:587:86//AC004064

R-NT2RP2004172//Dictyostelium discoideum LTR-retrotransposon Skipper, partial genomic sequence, 3' end.//0.24:440:60//AF017047

R-NT2RP2004187//RPC111-59E12, TK RPC111 Homo sapiens genomic clone R-59E12, genomic survey sequence.//3.1e-05:175:66//AQ198120

R-NT2RP2004194

R-NT2RP2004196//Fugu rubripes GSS sequence, clone 076D01bE2, genomic survey sequence.//1.6e-22:178:71//AL026601

R-NT2RP2004207//Homo sapiens BAC clone GS421103 from Xq25-q26, complete sequence.//0.19:175:64//AC005023

R-NT2RP2004226//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//6.1e-17:445:64//AL023808

R-NT2RP2004232//M. musculus (Balb/c) mRNA for serine/threonine protein kinase.//3.2e-25:326:71//Z34524

R-NT2RP2004239//Homo sapiens lok mRNA for protein kinase, complete cds.//8.7e-108:563:94//AB015718

R-NT2RP2004240//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, complete cds.//1.1e-101:530:93//AF039687

R-NT2RP2004242

R-NT2RP2004245//Homo sapiens DNA sequence from PAC 455H14 on chromosome Xq21.3-22.3. Contains genomic marker DXS1203 with a CA repeat polymorphism, STSs and GSSs, complete sequence.//5.1e-08:238:65//AL023280

R-NT2RP2004270//Lycopersicon esculentum ldh2 gene.//0.98:259:61//Y10603

R-NT2RP2004300//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1068F16, WORKING DRAFT SEQUENCE.//5.0e-14:396:65//AL023913

R-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds.//1.5e-108:544:96//AF000416

R-NT2RP2004321//Caenorhabditis elegans cosmid F47B8, complete sequence.//0.0078:333:61//Z77662

R-NT2RP2004339//Homo sapiens PAC clone DJ1136G13 from 7q35-q36, complete sequence.//1.4e-75:306:86//AC005229

R-NT2RP2004347//RPC111-90N11, TJ RPC111 Homo sapiens genomic clone R-90N11, genomic survey sequence.//2.9e-87:494:92//AQ284548

R-NT2RP2004364//Human DNA sequence from clone 422F24 on chromosome 6q24.1-25.2. Contains a novel gene similar to C. elegans C02C2.5. Contains ESTs, STSs and GSSs, complete sequence.//4.2e-10:161:76//AL031010

R-NT2RP2004365//Plasmodium falciparum chromosome 2, section 70 of 73 of the complete sequence.//3.6e-08:483:57//AE001433

R-NT2RP2004366//F. rubripes GSS sequence, clone 013B16aF3, genomic survey sequence.//2.1e-05:128:67//AL000528

R-NT2RP2004373//Homo sapiens 12q24.2 BAC RPC111-407A16 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//0.81:205:62//AC006065

R-NT2RP2004389//HS_2183_B2_H04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=8 Row=P, genomic survey sequence.//3.9e-06:82:84//AQ063969

【0811】

【表511】

R-NT2RP2004392//Ceratovacuna sp. mitochondrial cytochrome oxidase I (3' end), cytochrome oxidase II (complete cds) and transfer RNA-Leu gene.//2.7e-06:495:58//L39993	R-NT2RP2004861//Plasmodium falciparum MAL3P5, complete sequence.//0.19:189:66//AL034556
R-NT2RP2004396//Homo sapiens BAC clone RG135C18 from Tq21, complete sequence.//6.4e-11:572:96//AC005164	R-NT2RP2004897//Human Chromosome X clone bWID187, complete sequence.//1.1e-08:330:61//AC004383
R-NT2RP2004399//Arabidopsis thaliana chromosome I BAC F11M15 genomic sequence, complete sequence.//0.13:253:64//AC006085	R-NT2RP2004936//CIT-HSP-2374L4.TF CIT-HSP Homo sapiens genomic clone 2374L4, genomic survey sequence.//0.99:129:65//AQ110571
R-NT2RP2004400//HS_3238_A2_H11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3238 Col=22 Row=0, genomic survey sequence.//5.1e-23:162:89//AQ211412	R-NT2RP2004959//Plasmodium falciparum MAL3P6, complete sequence.//0.014:402:61//Z98551
R-NT2RP2004412//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COX1) gene, complete cds.//2.6e-09:458:60//M97514	R-NT2RP2004961//RPC111-45P2.TK RPC111 Homo sapiens genomic clone R-45P2, genomic survey sequence.//9.3e-90:453:97//AQ202282
R-NT2RP2004425//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acid Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DDC4 LIKE gene. Contains ESTs and GSSs, complete sequence.//0.99:481:56//AL022718	R-NT2RP2004962//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y40H4, WORKING DRAFT SEQUENCE.//0.017:291:61//AL022573
R-NT2RP2004476//Rattus norvegicus activity and neurotransmitter-induced early gene 6 (ania-6) mRNA, 3' UTR.//5.3e-99:600:90//AF030091	R-NT2RP2004967//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.6e-52:496:77//AC005077
R-NT2RP2004490//Homo sapiens chromosome 16, P1 clone 94-10H (LANL), complete sequence.//3.9e-115:575:97//AC005591	R-NT2RP2004978//Homo sapiens chromosome 19, cosmid F23269, complete sequence.//0.088:322:63//AC005614
R-NT2RP2004512//Plasmodium falciparum MAL3P3, complete sequence.//0.00034:517:58//Z98547	R-NT2RP2004982//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//0.025:339:61//AC003071
R-NT2RP2004523//Homo sapiens clone DJ0800G07, complete sequence.//1.8e-115:571:97//AC004890	R-NT2RP2004985//T3H24TF TAMU Arabidopsis thaliana genomic clone T3H24, genomic survey sequence.//0.40:111:70//B78148
R-NT2RP2004538//Homo sapiens BAC clone RG18C11 from Tpl4-p15, complete sequence.//1.7e-47:322:87//AC005091	R-NT2RP2004999//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUENCE, 30 unordered pieces.//0.23:157:68//AC005682
R-NT2RP2004551//Homo sapiens Xp22 bins 45-47 BAC GSHB-665M22 (Genome Systems Human BAC Library) complete sequence.//0.035:511:58//AC005184	R-NT2RP2005000
R-NT2RP2004568//T7C20-Sp6 TAMU Arabidopsis thaliana genomic clone T7C20, genomic survey sequence.//0.70:446:54//B08766	R-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//3.0e-111:577:95//AB014515
R-NT2RP2004580//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 136B1, WORKING DRAFT SEQUENCE.//2.2e-53:397:74//AL031768	R-NT2RP2005003//Homo sapiens Xp22-132-134 BAC GSHB-590J15 (Genome Systems Human BAC Library) complete sequence.//2.4e-21:246:77//AC004673
R-NT2RP2004587//CIT-HSP-2376P22.TF CIT-HSP Homo sapiens genomic clone 2376P22, genomic survey sequence.//0.70:446:54//AQ108976	R-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds.//9.5e-115:568:97//AF100141
R-NT2RP2004594//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-24 Bf7, complete sequence.//5.3e-10:493:62//AC004605	R-NT2RP2005018//HS_3108_B1_E09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3108 Col=17 Row=J, genomic survey sequence.//1.9e-31:222:89//AQ104050
R-NT2RP2004600//Homo sapiens full length insert cDNA clone ZE04E06.//2.1e-70:343:99//AF086522	R-NT2RP2005020//Rattus norvegicus cationic amino acid transporter-1 (CAT-1) mRNA, complete cds.//5.6e-41:566:73//U70476
R-NT2RP2004602//Homo sapiens full length insert cDNA clone YW26E09.//2.0e-96:528:93//AF086033	R-NT2RP2005031//CIT-HSP-516A2.TV CIT-HSP Homo sapiens genomic clone 516A2, genomic survey sequence.//4.1e-31:357:75//B49897
R-NT2RP2004614	R-NT2RP2005037
R-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//7.3e-117:587:96//AJ006291	R-NT2RP2005038//Sequence 5 from patent US 5552281.//2.2e-32:178:98//Z25644
R-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cds.//1.8e-105:520:96//AB007929	R-NT2RP2005108//Mus musculus orphan nuclear hormone receptor (CAR) gene, complete sequence.//3.7e-23:475:67//AF009326
R-NT2RP2004675//Human elastin (ELN) gene, partial cds, and LIM-kinase (LIMK1) gene, complete cds.//3.4e-22:197:79//U63721	R-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds.//8.4e-104:518:97//AB014564
R-NT2RP2004681//Rat notch 2 mRNA.//8.0e-30:276:78//M93661	R-NT2RP2005126//H. sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//1.4e-67:464:85//X98743
R-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cds.//1.6e-118:600:96//AB014525	R-NT2RP2005139
R-NT2RP2004709//Homo sapiens full length insert cDNA clone ZD42A08.//3.5e-14:139:86//AF086259	R-NT2RP2005140//Leishmania mexicana amazonensis kinetoplast (clone 29) maxicircle A+T-rich repetitive DNA sequence.//7.9e-08:460:60//U00101
R-NT2RP2004710//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 126A5, WORKING DRAFT SEQUENCE.//6.9e-117:592:96//AL031447	R-NT2RP2005144//Homo sapiens chromosome 12p13.3 clone RPC111-37284, WORKING DRAFT SEQUENCE, 129 ordered pieces.//2.5e-103:519:96//AC005911
R-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete cds.//4.2e-117:594:96//AB007947	R-NT2RP2005147//Homo sapiens clone DJ1125K23, WORKING DRAFT SEQUENCE, 21 unordered pieces.//0.068:100:75//AC004971
R-NT2RP2004743//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.53:403:59//AC005505	R-NT2RP2005159//CITB1-E1-2506A8.TF CITB1-E1 Homo sapiens genomic clone 2506A8, genomic survey sequence.//0.90:113:71//AQ262104
R-NT2RP2004767//Human DNA sequence from PAC 491M17 on chromosome 1 p36.2-p36.3.//2.0e-81:568:84//Z97988	R-NT2RP2005162//Homo sapiens chromosome 17, clone HC1T307A16, complete sequence.//5.0e-14:183:75//AC003041
R-NT2RP2004775//Anopheles quadrimaculatus NADH dehydrogenase subunit 1 (1-4, 4L, 5-6); cytochrome oxidase subunits (1-3); adenosine triphosphatase subunits (6, 8); cytochrome b; transfer RNA; ribosomal RNA (large and small subunits).//4.0e-08:365:62//L04272	R-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein.//7.5e-100:513:95//AJ007509
R-NT2RP2004791//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H192), complete sequence.//7.8e-111:541:98//AC005216	R-NT2RP2005204
R-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//2.5e-114:564:96//AF058953	R-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from Tpl2-p14, complete sequence.//7.2e-119:583:97//AC005189
R-NT2RP2004802	R-NT2RP2005239//Homo sapiens mRNA for putative tRNA splicing protein, partial.//8.4e-62:312:98//AJ010952
R-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds.//2.7e-118:584:97//AF054179	R-NT2RP2005254//Homo sapiens DNA sequence from PAC 262D12 on chromosome 1q23.3-24.3. Contains a Tenascin (Hexabrachion, Cytotactin, Neurectin, Myotendinous antigen)-LIKE gene and a mitochondrial/chloroplast 30S ribosomal protein S14-LIKE gene preceded by a CpG island. Contains ESTs, genomic marker D1S2691 and STSs.//5.7e-09:328:62//Z99297
R-NT2RP2004841//Human BAC clone RG308B22 from Tq22-q31, complete sequence.//4.0e-46:447:72//AC002089	R-NT2RP2005270//Plasmodium falciparum MAL3P8, complete sequence.//2.3e-05:355:61//AL034560
	R-NT2RP2005276//Genomic sequence for Arabidopsis thaliana BAC F17F8, complete sequence.//0.0014:541:58//AC000107
	R-NT2RP2005287//Cavia porcellus zinc finger protein (zfoC1) mRNA, complete cds.//4.4e-69:459:86//L26335
	R-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA

【0812】

【表512】

A, complete cds.//7.4e-124:594:98//AF060219
 R-NT2RP2005289//Homo sapiens mRNA for XRP2 protein.//1.5e-110:545:96//AJ007590
 R-NT2RP2005293//Leishmania mexicana amazonensis kinetoplast (clone 29) maxicircle A+T-rich repetitive DNA sequence.//1.1e-12:554:61//U00101
 R-NT2RP2005315//Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, ES T, GSS, STS, CpG island, complete sequence.//9.5e-15:218:77//AL022069
 R-NT2RP2005325//Rattus norvegicus LIM homeodomain protein (LH-2) mRNA sequence.//2.0e-72:478:88//L06804
 R-NT2RP2005336//ALU WARNING: Human Alu-J subfamily consensus sequence.//7.3e-33:139:82//U14567
 R-NT2RP2005344//Human DNA sequence from PAC 128N22 on chromosome X q25-q26.3. contains STS.//0.094:451:60//Z97629
 R-NT2RP2005354//Homo sapiens mRNA for putative thioredoxin-like protein.//1.3e-11:89:96//AJ010841
 R-NT2RP2005360//Homo sapiens clone RC023115, WORKING DRAFT SEQUENCE, 1 unordered pieces.//0.046:266:60//AC005049
 R-NT2RP2005393//Homo sapiens chromosome 17, clone hRPX.85_B_7, complete sequence.//6.0e-41:226:86//AC005695
 R-NT2RP2005407
 R-NT2RP2005436//Polistes annularis (clone pan117AAT) tandem repeat region.//0.039:169:63//L10835
 R-NT2RP2005441//CIT-HSP-2338P5, TR CIT-HSP Homo sapiens genomic clone 2338P5, genomic survey sequence.//3.0e-38:263:88//AQ055548
 R-NT2RP2005453//CIT-HSP-2367N1, TR CIT-HSP Homo sapiens genomic clone 2367N1, genomic survey sequence.//0.67:409:59//AQ079845
 R-NT2RP2005457//Homo sapiens partial XPG gene, exon 2.//2.0e-42:315:82//X71342
 R-NT2RP2005464//CIT-HSP-2359C16, TF CIT-HSP Homo sapiens genomic clone 2359C16, genomic survey sequence.//1.0:251:60//AQ075816
 R-NT2RP2005465//Drosophila melanogaster, chromosome 2R, region 4D1-4AD2, P1 clone DS08616, complete sequence.//0.25:288:62//AC005457
 R-NT2RP2005472//Chlorarachnion COMP621 small subunit ribosomal RNA, 5.8S ribosomal RNA, large subunit ribosomal RNA, U6 small nuclear RNA, small subunit ribosomal protein S13 (RPS13), pre-mRNA splicing factor PRP 6 homolog, small subunit ribosomal protein 4 (RPS4), small nucleolar ribonucleoprotein E homolog (snRNPE), ATP-dependent clip protease proteolytic subunit homolog (CLPP), putative RNA polymerase II subunit (RNA POLII), and RNA helicase homolog (RNA HEL) genes, complete cds.//1.0:356:59//U58510
 R-NT2RP2005476//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MALIP3, WORKING DRAFT SEQUENCE.//0.00092:421:60//AL031746
 R-NT2RP2005490//Homo sapiens clone NH0001P09, WORKING DRAFT SEQUENCE, 1 unordered pieces.//6.2e-71:187:100//AC006030
 R-NT2RP2005491//paramecium species 5, 311 mt dna dimer: replication init. region.//1.6e-10:403:62//K00917
 R-NT2RP2005495//Homo sapiens clone RG037F03, WORKING DRAFT SEQUENCE, 12 unordered pieces.//1.3e-25:208:82//AC005051
 R-NT2RP2005496//Human DNA sequence from clone 354N19 on chromosome 6q22. Contains the 3' part of the gene for Mannosyl-Oligosaccharide Alpha-1,2-Mannosidase (Man9)-alpha-mannosidase, EC 3.2.1.113), a Cytochrome C Oxidase Polypeptide I (EC 1.9.3.1) pseudogene and a pseudogene similar to 60S Ribosomal Protein L13A. Contains genomic markers D6S287 and D6S1696, ESTs, STSs, GSSs and two CA repeat polymorphisms, complete sequence.//1.5e-22:196:84//AL022722
 R-NT2RP2005498
 R-NT2RP2005501//Homo sapiens chromosome 17, clone hRPX.269_G_24, complete sequence.//1.7e-29:252:76//AC005828
 R-NT2RP2005509//CIT-HSP-2060J6, TR CIT-HSP Homo sapiens genomic clone 2060J6, genomic survey sequence.//3.1e-53:402:84//B69979
 R-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//9.9e-109:570:94//AF092563
 R-NT2RP2005525//Human clone JKA2 mRNA induced upon T-cell activation, 3' end.//5.1e-32:175:98//U38432
 R-NT2RP2005531//Homo sapiens PAC clone DJ0870F17 from 7q33-q36, complete sequence.//0.94:288:61//AC004911
 R-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP).//2.7e-106:560:94//AJ012449
 R-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//5.3e-114:583:96//AB007963
 R-NT2RP2005549//Homo sapiens *** SEQUENCING IN PROGRESS ***, WORKING DRAFT SEQUENCE.//0.91:287:58//AJ011929
 R-NT2RP2005555//Homo sapiens 12p13.3 PAC RPC15-927J10 (Roswell Park Cancer Institute Human PAC library) complete sequence.//3.6e-05:222:66//AC004804
 R-NT2RP2005557//Homo sapiens PAC clone DJ1200123 from 7p15, complete sequence.//8.2e-22:236:76//AC004996
 R-NT2RP2005581//Homo sapiens clone DJ0693M11, WORKING DRAFT SEQUENCE, 7 unordered pieces.//7.2e-45:286:85//AC006146
 R-NT2RP2005600//Human polymorphic microsatellite DNA.//0.043:304:58//M99148
 R-NT2RP2005605//Human Cosmid g1572c190, complete sequence.//2.4e-17:163:77//AC000126
 R-NT2RP2005620
 R-NT2RP2005622//jd432 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 1187, genomic survey sequence.//0.010:308:58//B13538
 R-NT2RP2005637//Homo sapiens PAC clone DJ0555L14 from 7q34-q36, complete sequence.//2.5e-26:322:72//AC005996
 R-NT2RP2005640//Mus musculus squamous cell carcinoma antigen 2 (Sc ca2) gene, complete cds.//0.030:370:60//AF063937
 R-NT2RP2005645//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//3.2e-08:355:62//AE001398
 R-NT2RP2005651
 R-NT2RP2005654//Leishmania major Friedlin cosmid L5769, complete sequence.//0.96:216:66//AL031908
 R-NT2RP2005669//Homo sapiens nitrilase homolog 1 (NIT1) gene, alternatively spliced product, complete cds.//6.7e-117:594:95//AF069984
 R-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//1.8e-89:434:98//AF089814
 R-NT2RP2005683//jd432 Trypanosome Shotgun M13 genomic Trypanosoma brucei brucei genomic clone 1187, genomic survey sequence.//0.037:283:58//B13538
 R-NT2RP2005690//Homo sapiens clone DJ0425102, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.5e-38:295:83//AC005478
 R-NT2RP2005694//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-106, complete sequence.//0.0026:414:57//AL010210
 R-NT2RP2005701
 R-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//4.1e-104:503:98//AB018342
 R-NT2RP2005719//Caenorhabditis elegans cosmid LLC1, complete sequence.//0.83:275:61//Z82277
 R-NT2RP2005722//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 228H13, WORKING DRAFT SEQUENCE.//1.2e-21:199:75//AL031985
 R-NT2RP2005723
 R-NT2RP2005726//Homo sapiens clone DJ0609N19, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.6e-64:503:82//AC004842
 R-NT2RP2005741//Human Chromosome 11 pac pDJ393o15, WORKING DRAFT SEQUENCE, 8 unordered pieces.//2.5e-09:261:64//AC000384
 R-NT2RP2005748//RPC111-64K11, TK RPC111 Homo sapiens genomic clone 64K11, genomic survey sequence.//0.00039:215:66//AQ239313
 R-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//1.3e-40:223:96//AF068868
 R-NT2RP2005753//Homo sapiens l-1 receptor candidate protein mRNA, complete cds.//3.7e-103:494:98//AF082516
 R-NT2RP2005763//Homo sapiens DNA sequence from PAC 510L9 on chromosome 6p24.1-p25.3.//9.7e-34:172:86//AL022098
 R-NT2RP2005767//Human clone H3 mRNA.//2.5e-21:179:87//U03672
 R-NT2RP2005773//HS_2168_B1.G12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2168 Col=23 Row=N, genomic survey sequence.//0.99:212:63//AQ086414
 R-NT2RP2005775//Rabbit mRNA for endopeptidase, complete cds.//4.8e-98:591:88//D13310
 R-NT2RP2005781//Streptomyces sp. genomic DNA for sarcosine oxidase.//0.019:384:59//D10623
 R-NT2RP2005784//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185N5, WORKING DRAFT SEQUENCE.//1.8e-102:490:99//AL034423
 R-NT2RP2005804//Homo sapiens chromosome 17, clone hRPX.147_L_13, complete sequence.//6.3e-16:481:63//AC005332
 R-NT2RP2005812//Caenorhabditis elegans cosmid F15810.//0.81:147:63//AF036696
 R-NT2RP2005815
 R-NT2RP2005835
 R-NT2RP2005841//Human DNA sequence from cosmid U209G1 on chromosome X.//1.5e-26:512:64//Z68873
 R-NT2RP2005853//Human DNA sequence from clone 1156N12 on chromosome X. Contains an STS and GSSs, complete sequence.//3.7e-16:340:64//AL009047
 R-NT2RP2005857//Human DNA sequence from cosmid U246D9 on chromosome X. Contains a histone H2B like pseudogene.//1.3e-09:331:65//AL021308

【0813】

【表513】

R-NT2RP2005859//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-83, complete sequence.//0.0097:363:59//AL010152

R-NT2RP2005868//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-18, complete sequence.//1.1e-07:508:60//AL008971

R-NT2RP2005890//Mouse oncogene (ect2) mRNA, complete cds.//2.7e-31:500:67//L11316

R-NT2RP2005901//Homo sapiens T-cell receptor alpha delta locus from bases 752679 to 1000555 (section 4 of 5) of the Complete Nucleotide Sequence.//0.89:276:60//AE000661

R-NT2RP2005908

R-NT2RP2005933//Rattus norvegicus nucleoporin p54 mRNA, complete cds.//1.2e-40:285:80//U63840

R-NT2RP2005942//Homo sapiens DNA sequence from PAC 142L7 on chromosome 6q21. Contains a Laminin Alpha 4 (LAMA4) LIKE gene coding for two alternatively spliced transcripts, a Tubulin Beta LIKE pseudo gene, a Connective tissue growth factor (NOV, GIG) LIKE gene, A predicted CpG island, ESTs, STSs and genomic marker D6S416, complete sequence.//0.0011:480:58//Z99289

R-NT2RP2005980//Homo sapiens Xp22 BAC GSHB-536K7 (Genome Systems Human BAC library) complete sequence.//8.9e-21:136:78//AC004616

R-NT2RP2006023//HS_2176_B1_C10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2176 Col=19 Row=F, genomic survey sequence.//2.5e-66:369:95//AQ023148

R-NT2RP2006038//Plasmodium falciparum chromosome 2, section 6 of 73 of the complete sequence.//0.00029:408:58//AE001369

R-NT2RP2006043//Polistes annularis (clone pan117AAT) tandem repeat region.//0.032:195:62//L10835

R-NT2RP2006052//Plasmodium falciparum 3D7 chromosome 12 PFYACB-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.11:263:61//AC005140

R-NT2RP2006069

R-NT2RP2006071//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.0044:333:61//AC004709

R-NT2RP2006098//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-77, complete sequence.//4.1e-09:393:62//AL010151

R-NT2RP2006100//HS_2020_A2_H02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2020 Col=4 Row=0, genomic survey sequence.//8.3e-53:304:92//AQ228761

R-NT2RP2006103//Rat sodium-hydrogen exchange protein-isoform 3 (NHE-3) mRNA, complete cds.//1.5e-16:199:79//M85300

R-NT2RP2006141

R-NT2RP2006166//Human Chromosome 16 BAC clone CIT987SK-A-589H1, complete sequence.//8.2e-48:329:76//AC002045

R-NT2RP2006184//RPC111-6016.TP RPC1-11 Homo sapiens genomic clone RPC1-11-6016, genomic survey sequence.//0.52:273:61//B49539

R-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds.//1.9e-108:553:95//AB014554

R-NT2RP2006196//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-57, complete sequence.//4.2e-05:420:59//AL008981

R-NT2RP2006200//Homo sapiens chromosome 12p13.3 clone RPC11-96H9, WORKING DRAFT SEQUENCE, 66 unordered pieces.//2.1e-100:409:96//AC006057

R-NT2RP2006219//H.sapiens mRNA for DGC6 protein.//3.8e-93:532:90//X96484

R-NT2RP2006237//P.falciparum PK1 gene.//2.9e-08:481:59//X83707

R-NT2RP2006238//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//3.5e-79:405:89//U91318

R-NT2RP2006258//Human PAC clone DJ0899821 from 7p15-p21, complete sequence.//2.2e-08:283:63//AC004008

R-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase EMK.//6.2e-13:234:58//X97630

R-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.0e-108:542:97//AF032622

R-NT2RP2006320//347J16.TVB CIT978SKA1 Homo sapiens genomic clone A-347J16, genomic survey sequence.//1.2e-27:215:65//B17768

R-NT2RP2006321//Human karyopherin beta 3 mRNA, complete cds.//1.7e-48:298:90//U72761

R-NT2RP2006323//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 702J19, WORKING DRAFT SEQUENCE.//2.8e-104:524:96//AL033531

R-NT2RP2006333//Homo sapiens PAC clone DJ0808A01 from 7q21.1-q31.1, complete sequence.//3.9e-33:298:78//AC004893

R-NT2RP2006334

R-NT2RP2006365//RPC111-72115.TK RPC111 Homo sapiens genomic clone R-72115, genomic survey sequence.//2.6e-35:217:92//AQ267043

R-NT2RP2006393//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B13E4: HTGS phase 1, WORKING DRAFT SEQUENCE, 10 unordered pieces.//8.0e-40:317:81//AC004046

R-NT2RP2006436//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//3.2e-42:184:86//AL022345

R-NT2RP2006441//Plasmodium falciparum microsatellite TA80 sequence.//0.00021:188:68//AF010568

R-NT2RP2006454//Plasmodium falciparum chromosome 2, section 60 of 73 of the complete sequence.//0.30:265:60//AE001423

R-NT2RP2006456//Homo sapiens clone 23566 mRNA sequence.//2.5e-104:532:96//AF052098

R-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//6.6e-108:524:97//AJ006266

R-NT2RP2006467//Sequence 50 from patent US 5691147.//8.3e-22:235:74//I76222

R-NT2RP2006472//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1172A22, WORKING DRAFT SEQUENCE.//5.4e-12:407:62//AL034386

R-NT2RP2006534//Dictyostelium discoideum actin 8 gene, 3' UTR.//0.44:111:65//M25216

R-NT2RP2006554//Plasmodium falciparum chromosome 2, section 7 of 73 of the complete sequence.//0.19:392:58//AE001370

R-NT2RP2006565//Sus scrofa SCAMPI gene, exon 9.//1.5e-13:292:68//AJ23742

R-NT2RP2006571//Homo sapiens chromosome 19, cosmid F17972, complete sequence.//0.0024:409:58//AC004660

R-NT2RP2006573//Human BRCA2 region, mRNA sequence CG005.//3.3e-16:334:64//U50532

R-NT2RP2006598//Mus musculus retinoid X receptor interacting protein (RIP110) mRNA, partial cds.//1.6e-19:448:64//U22015

R-NT2RP3000002//Human DNA sequence from cosmid M104C7 on chromosome 22, complete sequence.//4.4e-14:501:63//Z82246

R-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21).//5.9e-115:560:97//AJ011972

R-NT2RP3000046//Homo sapiens clone DJ0042M02, WORKING DRAFT SEQUENCE, 20 unordered pieces.//3.9e-57:402:83//AC005995

R-NT2RP3000047//Homo sapiens chromosome 17, clone hRPK.138_P_22, complete sequence.//1.0:158:66//AC005697

R-NT2RP3000050//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 451B21, WORKING DRAFT SEQUENCE.//2.7e-32:411:69//AL033522

R-NT2RP3000055//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1000N6, WORKING DRAFT SEQUENCE.//7.9e-17:309:69//AL034378

R-NT2RP3000072//Brassica rapa DNA for S-locus glycoprotein, complete cds.//2.9e-07:516:60//D88192

R-NT2RP3000080//Homo sapiens clone DJ1129D05, complete sequence.//1.7e-27:186:90//AC005630

R-NT2RP3000085//Arabidopsis thaliana acetyl-CoA carboxylase biotin-containing subunit mRNA, nuclear gene encoding chloroplast protein, complete cds.//0.0051:289:59//U23155

R-NT2RP3000109//HS_3065_A2_D04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3065 Col=8 Row=G, genomic survey sequence.//2.5e-62:304:100//AQ137776

R-NT2RP3000134//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MALIP3, WORKING DRAFT SEQUENCE.//0.027:414:57//AL031746

R-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//3.8e-115:578:96//AB011164

R-NT2RP3000149//Homo sapiens chromosome 17, clone hRPK.332_H_18, complete sequence.//1.3e-67:354:95//AC005746

R-NT2RP3000186

R-NT2RP3000197//Human DNA sequence from PAC 181M1 on chromosome X contains ESTs, STS polymorphic CA repeats.//2.5e-31:295:78//Z82899

R-NT2RP3000207//Homo sapiens chromosome 16 BAC clone CIT987SK-A-954B10, complete sequence.//0.016:305:61//AC004514

R-NT2RP3000220//RPC111-6307.TJ RPC111 Homo sapiens genomic clone R-6307, genomic survey sequence.//0.25:118:66//AQ201832

R-NT2RP3000233//Plasmodium falciparum mRNA for major merozoite surface antigen gp195.//3.2e-11:440:59//X15063

R-NT2RP3000235//Mus musculus chromosome 6 clone TB6 subclone TB6pD1.//0.81:114:64//U19530

R-NT2RP3000247//Homo sapiens DNA sequence from clone 326L12 on chromosome Xq27.1-27.3. Contains the cancer/testis antigen CT7 (melanoma-associated antigen MAGE-C1) gene, two MAGE family pseudogenes, STSs and a CA repeat polymorphism, complete sequence.//4.8e-73:362:86//AL023279

R-NT2RP3000251//Homo sapiens chromosome 17, clone hRPK.192_H_23, complete sequence.//0.025:131:66//AC005726

【0814】

【表514】

R-NT2RP3000252
R-NT2RP3000255//HS-1025-B2-F08-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 804 Col=16 Row=L, genomic survey sequence.//0.67:119:66//B34879
R-NT2RP3000267
R-NT2RP3000299//Rattus norvegicus mRNA for Crk-associated substrate, p130, complete cds.//1.2e-23:424:69//D29766
R-NT2RP3000312//Plasmodium falciparum MAL3P4, complete sequence.//0.55:414:59//AL008970
R-NT2RP3000320//HS_3056_A1_C03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3056 Col=5 Row=E, genomic survey sequence.//4.1e-32:214:89//AQ134064
R-NT2RP3000324//Rattus norvegicus potassium channel regulator 1 mRNA, complete cds.//1.5e-22:265:75//U78090
R-NT2RP3000333//Plasmodium falciparum MAL3P6, complete sequence.//0.68:460:57//Z98551
R-NT2RP3000341//H.sapiens mRNA for TIM17 preprotein translocase.//1.4e-19:137:90//X97544
R-NT2RP3000348//CITB1-E1-2513C11.TF CITB1-E1 Homo sapiens genomic clone 2513C11, genomic survey sequence.//0.0014:118:72//AQ278177
R-NT2RP3000350
R-NT2RP3000359//Homo sapiens clone NH0319F03, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.8e-55:320:75//AC006039
R-NT2RP3000361//Homo sapiens mRNA for KIAA0552 protein, complete cds.//0.18:275:61//AB011124
R-NT2RP3000366//CIT-HSP-2317H13.TF CIT-HSP Homo sapiens genomic clone 2317H13, genomic survey sequence.//6.7e-42:214:100//AQ041634
R-NT2RP3000397//HS-1012-B1-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 787 Col=1 Row=L, genomic survey sequence.//0.015:184:63//B31814
R-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//1.3e-109:529:98//AF071185
R-NT2RP3000418//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 510821, WORKING DRAFT SEQUENCE.//6.2e-15:445:65//AL031885
R-NT2RP3000433
R-NT2RP3000439
R-NT2RP3000441
R-NT2RP3000449//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018012, WORKING DRAFT SEQUENCE.//1.6e-43:300:76//AL031650
R-NT2RP3000451//3'untranslated region of human mRNA for a K+ channel protein.//0.71:101:66//E13519
R-NT2RP3000456//Human Xq28 cosmid U126G1, U142F2, U69B6, U145C10, U169A5, U84H1, U24012, U80A7, U153E6, L354B5, and R7-163A8 containing iduronate 2-sulfatase gene and pseudogene, complete sequence.//5.2e-16:376:65//AF011889
R-NT2RP3000484//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 120G22, WORKING DRAFT SEQUENCE.//0.61:326:58//AL031847
R-NT2RP3000487//Sequence 32 from patent US 5476781.//8.6e-08:409:61//I16692
R-NT2RP3000512//RPC111-60F15.TK RPC111 Homo sapiens genomic clone R-60F15, genomic survey sequence.//2.2e-68:379:93//AQ201516
R-NT2RP3000526//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 377F16, WORKING DRAFT SEQUENCE.//4.1e-07:224:65//Z93783
R-NT2RP3000527//HS_3228_A1_H07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3228 Col=13 Row=0, genomic survey sequence.//4.5e-30:184:93//AQ209131
R-NT2RP3000531//T6M24-Sp6 TAMU Arabidopsis thaliana genomic clone T6M24, genomic survey sequence.//0.67:88:58//AQ248538
R-NT2RP3000542//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 12684, WORKING DRAFT SEQUENCE.//2.0e-24:145:82//AL022316
R-NT2RP3000561//Homo sapiens PAC clone DJ0942116 from Tq11, complete sequence.//6.1e-107:548:95//AC006012
R-NT2RP3000562//HS_2041_B1_E08_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2041 Col=15 Row=J, genomic survey sequence.//9.6e-55:279:98//AQ230207
R-NT2RP3000578//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-105, complete sequence.//0.00060:356:58//AL010212
R-NT2RP3000582//Homo sapiens chromosome 17, clone hCIT.468_F_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//4.2e-29:282:67//AC004666
R-NT2RP3000584//Human PAC clone DJ222H05 from Xq25-q26, complete sequence.//7.4e-44:245:78//AC002377
R-NT2RP3000590//Arabidopsis thaliana chromosome II BAC T31E10 genomic sequence, complete sequence.//0.66:341:59//AC004077
R-NT2RP3000592//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.02
2:491:56//AC005505
R-NT2RP3000596//HS_3025_A1_D11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3025 Col=21 Row=G, genomic survey sequence.//2.6e-21:161:88//AQ101452
R-NT2RP3000599//Plasmodium falciparum MAL3P8, complete sequence.//1.3e-09:543:58//AL034560
R-NT2RP3000605//Homo sapiens chromosome 19, cosmid F20900, complete sequence.//5.6e-115:554:98//AC006128
R-NT2RP3000622//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 27 unordered pieces.//0.15:233:63//AC005414
R-NT2RP3000624//CIT-HSP-2022D4.TR CIT-HSP Homo sapiens genomic clone 2022D4, genomic survey sequence.//1.0:166:66//B64262
R-NT2RP3000628//Human BAC clone GS188P18, complete sequence.//5.3e-56:384:83//AC000115
R-NT2RP3000632//Human cyclin-selective ubiquitin carrier protein mRNA, complete cds.//4.0e-61:438:85//U73379
R-NT2RP3000644//Homo sapiens DNA from chromosome 19p13.2 cosmid R31240, R30272 and R28549 containing the EKLF, GCDH, CRTG, and RAD23A genes, genomic sequence.//1.0e-43:408:77//AD000092
R-NT2RP3000661//F.rubripes GSS sequence, clone 148D22bB9, genomic survey sequence.//2.7e-17:234:69//AL005927
R-NT2RP3000665//Human chromosome 11 46b2 cosmid, complete sequence.//2.1e-42:526:72//U73645
R-NT2RP3000685//HS_3007_A2_F02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=4 Row=X, genomic survey sequence.//1.6e-101:506:97//AQ118425
R-NT2RP3000690//Plasmodium falciparum MAL3P6, complete sequence.//1.3e-13:411:61//Z98551
R-NT2RP3000736
R-NT2RP3000742//Rattus norvegicus phospholipase C delta-4 mRNA, complete cds.//0.0071:231:65//U16655
R-NT2RP3000753//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence.//0.88:366:56//AL021368
R-NT2RP3000759//HS_2055_A2_D09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=18 Row=G, genomic survey sequence.//0.45:251:60//AQ234828
R-NT2RP3000815//Homo sapiens chromosome 17, clone hRPK.209_J_20, complete sequence.//2.0e-20:293:72//AC005822
R-NT2RP3000825//Plasmodium falciparum MAL3P6, complete sequence.//0.0044:325:62//Z98551
R-NT2RP3000826//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 117715, WORKING DRAFT SEQUENCE.//5.3e-25:375:72//AL022315
R-NT2RP3000836//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y214H10, WORKING DRAFT SEQUENCE.//1.3e-19:181:81//AL022344
R-NT2RP3000841//Homo sapiens, clone hRPK.1_A_1, complete sequence.//0.20:226:61//AC006196
R-NT2RP3000845//Homo sapiens chromosome 19, cosmid R33632, complete sequence.//6.8e-91:512:92//AC005781
R-NT2RP3000847//***ALU WARNING: Human Alu-Sp subfamily consensus sequence.//7.9e-38:179:86//U14572
R-NT2RP3000850//Homo sapiens BAC clone GS166A23 from 7p21, complete sequence.//4.4e-48:505:76//AC005014
R-NT2RP3000852//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE.//2.9e-82:311:98//AL031297
R-NT2RP3000859
R-NT2RP3000865//Human DNA sequence from clone 23K20 on chromosome Xq25-26.2 Contains EST, STS, GSS, complete sequence.//1.2e-15:482:63//AL022153
R-NT2RP3000868//Fruitfly strain g20 mitochondrial DNA, A+T-rich region, partial sequence.//0.00045:260:59//AB003097
R-NT2RP3000869//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 330012, WORKING DRAFT SEQUENCE.//0.0058:172:64//AL031731
R-NT2RP3000875//H.sapiens/Hepatitis B virus fusion mRNA for mevalonate kinase.//1.4e-99:531:93//X75311
R-NT2RP3000901
R-NT2RP3000904//Genomic sequence for Arabidopsis thaliana BAC T7N9, complete sequence.//0.32:261:57//AC000348
R-NT2RP3000917//Plasmodium falciparum MAL3P7, complete sequence.//0.00092:456:58//AL034559
R-NT2RP3000919
R-NT2RP3000968//H.sapiens mRNA for ribosomal protein S15a.//4.5e-2

【0815】

【表515】

- 4.375:71//X84407
 R-NT2RP3000980//Homo sapiens chromosome 17, clone hRPK.855_D_21, complete sequence.//0.36:186:62//AC006079
 R-NT2RP3000994//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-42 0 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.00052:413:60//AC005140
 R-NT2RP3001004//Saccharomyces cerevisiae VAR1 gene, mitochondrial gene encoding mitochondrial protein, 3' processing site, partial sequence.//1.1e-07:330:64//U32857
 R-NT2RP3001007//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-82, complete sequence.//0.045:286:61//AL010255
 R-NT2RP3001055//Human DNA sequence from PAC 27K14 on chromosome Xp11.3-Xp11.4. Contains monamine oxidase B (MAOB), ESTs and polymorphic CA repeats.//2.3e-56:348:91//Z95125
 R-NT2RP3001057//H. sapiens HZF4 mRNA for zinc finger protein.//8.2e-84:531:86//X78927
 R-NT2RP3001081//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P3, WORKING DRAFT SEQUENCE.//1.1e-08:537:60//AL031746
 R-NT2RP3001084
 R-NT2RP3001096
 R-NT2RP3001107
 R-NT2RP3001109//Human Chromosome 15q26.1 PAC clone pDJ10k5 containing human DNA polymerase gamma (polg) gene, complete sequence.//7.4e-62:272:73//AC005316
 R-NT2RP3001111
 R-NT2RP3001113
 R-NT2RP3001115//Homo sapiens PAC clone DJ0905J08 from 7p12-p14, complete sequence.//7.2e-112:550:97//AC005189
 R-NT2RP3001116//CIT-HSP-2282K23.TR CIT-HSP Homo sapiens genomic clone 2282K23, genomic survey sequence.//0.00013:160:69//AQ002011
 R-NT2RP3001119//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYN11). ESTs, STS, GSS, CpG island, complete sequence.//5.9e-99:497:96//AL031864
 R-NT2RP3001120
 R-NT2RP3001126//Plasmodium falciparum MAL3P7, complete sequence.//0.035:266:56//AL034559
 R-NT2RP3001133
 R-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//8.1e-114:549:97//AB018305
 R-NT2RP3001147//Homo sapiens chromosome 17, clone HCIT187M2, complete sequence.//0.69:198:63//AC004448
 R-NT2RP3001150//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//2.4e-108:542:97//AL034379
 R-NT2RP3001155//Homo sapiens mRNA for AMD-1 protein.//2.9e-116:563:98//AJ006266
 R-NT2RP3001176//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.44:227:62//AC004688
 R-NT2RP3001214//Borrelia burgdorferi plasmid lp25, complete plasmid sequence.//0.0023:381:61//AE000785
 R-NT2RP3001216//RPC111-18C15.TPC RPC1-11 Homo sapiens genomic clone RPC1-11-18C15, genomic survey sequence.//7.0e-29:167:97//B88077
 R-NT2RP3001221//Homo sapiens clone 14503, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.020:211:63//AC005827
 R-NT2RP3001232//Homo sapiens DNA sequence from PAC 124C6 on chromosome 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS with a CA repeat polymorphism, complete sequence.//2.7e-08:390:62//AL021326
 R-NT2RP3001236//RPC111-25C17.TKBR RPC1-11 Homo sapiens genomic clone RPC1-11-25C17, genomic survey sequence.//9.5e-41:217:88//AQ014003
 R-NT2RP3001239//Human microtubule-associated protein 18 (MAP1B) gene, complete cds.//2.9e-21:438:63//L06237
 R-NT2RP3001245//Homo sapiens DNA sequence from PAC 964D12 on chromosome 1q24-q25. Contains EST, GSS.//0.00026:439:59//AL021398
 R-NT2RP3001253//HS_3002_A2_H12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=24 Row=0, genomic survey sequence.//0.98:190:63//AQ251982
 R-NT2RP3001260
 R-NT2RP3001268//Homo sapiens clone DJ0959C21, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.012:509:57//AC004936
 R-NT2RP3001272//Homo sapiens BAC clone NHD161H12 from 7p14-p15, complete sequence.//2.2e-22:134:87//AC005589
 R-NT2RP3001274//Sequence 11 from Patent WO9517522.//0.0058:133:66//A45341
 R-NT2RP3001281//Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.//4.4e-55:558:76//Z96811
 R-NT2RP3001307//HS_2058_A1_C06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=11 Row=E, genomic survey sequence.//7.2e-33:260:86//AQ305868
 R-NT2RP3001318//Homo sapiens PAC clone DJ0649P17 from 7q11.23-q21, complete sequence.//0.27:210:65//AC004848
 R-NT2RP3001325
 R-NT2RP3001338//Rat tropoelastin gene, intron 17 (partial).//1.0:184:64//M86367
 R-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds.//1.2e-112:566:96//AB007920
 R-NT2RP3001340//Homo sapiens HMG box factor SOX-13 mRNA, complete cds.//3.2e-86:450:95//AF083105
 R-NT2RP3001355
 R-NT2RP3001374//HS_2184_A2_C04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2184 Col=8 Row=M, genomic survey sequence.//3.7e-10:101:84//AQ024647
 R-NT2RP3001383//Plasmodium falciparum chromosome 2, section 34 of 73 of the complete sequence.//7.4e-07:279:63//AE001397
 R-NT2RP3001384//Homo sapiens chromosome 19, cosmid R33907, complete sequence.//4.4e-75:382:97//AC005785
 R-NT2RP3001392//HS_3078_B2_D05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3078 Col=10 Row=H, genomic survey sequence.//1.0:164:64//AQ140587
 R-NT2RP3001396//RPC111-63N18.TJ RPC111 Homo sapiens genomic clone R-63N18, genomic survey sequence.//0.14:242:61//AQ238544
 R-NT2RP3001398//Mus musculus zinc finger protein (Zfp64) mRNA, complete cds.//1.8e-10:193:72//U49046
 R-NT2RP3001399
 R-NT2RP3001407//Caenorhabditis elegans cosmid D1046, complete sequence.//0.0011:392:60//Z68160
 R-NT2RP3001420//Human BAC clone GS165104 from 7q21, complete sequence.//3.7e-29:412:74//AC002379
 R-NT2RP3001426//Homo sapiens clone 24616 mRNA sequence.//1.1e-104:550:94//AF052158
 R-NT2RP3001427//Caenorhabditis elegans cosmid K1105.//0.39:174:64//U53152
 R-NT2RP3001428//Human nuclear pore complex-associated protein TPR (tptr) mRNA, complete cds.//1.4e-94:533:91//U69668
 R-NT2RP3001432//Homo sapiens DNA sequence from PAC 164C20 on chromosome 6q16.1-22.1. Contains ESTs and GSSs (BAC end sequences), complete sequence.//2.5e-12:415:61//AL009029
 R-NT2RP3001447//Homo sapiens PAC clone DJ0828B12 from 7q11.23-q21.1, complete sequence.//5.6e-36:358:77//AC004903
 R-NT2RP3001449//Homo sapiens clone 24497 mRNA sequence.//1.5e-100:499:97//AF070630
 R-NT2RP3001453//Homo sapiens clone DJ0852024, WORKING DRAFT SEQUENCE, 2 unordered pieces.//4.0e-47:295:86//AC004906
 R-NT2RP3001457
 R-NT2RP3001459
 R-NT2RP3001472//Crithidia fasciculata kinetoplast apocytochrome b mRNA-mRNA chimera, clone:24.//0.33:150:66//D13030
 R-NT2RP3001490//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-103, complete sequence.//2.3e-08:483:60//AL010208
 R-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//4.4e-60:338:93//U13395
 R-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRC8 (TRC8) mRNA, complete cds.//2.1e-110:549:97//AF064801
 R-NT2RP3001527//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1125A11, WORKING DRAFT SEQUENCE.//5.3e-32:310:78//AL034549
 R-NT2RP3001529//Human Chromosome X, complete sequence.//5.5e-67:280:93//AC002420
 R-NT2RP3001538
 R-NT2RP3001554//Human microtubule-associated protein 1a (MAP1A) mRNA, complete cds.//7.8e-16:391:62//U38292
 R-NT2RP3001580//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.00026:456:58//AC004688
 R-NT2RP3001587//Homo sapiens HRIHFB2115 mRNA, partial cds.//5.6e-08:86:88//AB015337
 R-NT2RP3001589//Homo sapiens chromosome 17, clone hRPK.1096_G_20, complete sequence.//0.066:360:60//AC005410
 R-NT2RP3001607//CIT-HSP-201QMB.TR CIT-HSP Homo sapiens genomic clone 201QMB, genomic survey sequence.//0.041:194:67//B53480
 R-NT2RP3001608//Human DNA sequence from PAC 296K21 on chromosome X contains cytochrome oxidase, delta-aminolevulinic acid synthase (erythroid): 5-aminolevulinic acid synthase (EC 2.3.1.37), 6-phosphofructo-2-kinase/fructose-2,6-bisphosphatase (EC 2.7.1.105, EC 3.1.3.46

【0816】

【表516】

<p>), ESTs and STS. //0.69:151:64//Z83821 R-NT2RP3001621//Human DNA sequence from clone 24o18 on chromosome 6p21.31-22.2 Contains zinc finger protein pseudogene, VMO-type olfactory receptor pseudogene, nuclear envelope pore membrane protein, EST, STS, complete sequence. //1.4e-46:354:83//AL021808 R-NT2RP3001629//H.sapiens simple DNA sequence region clone wgl10. //0.99:137:63//X76572 R-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds. //8.5e-108:541:96//AF099149 R-NT2RP3001642 R-NT2RP3001646//HS_3218_A2_A01_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=2 Row=A, genomic survey sequence. //2.6e-32:215:91//AQ303003 R-NT2RP3001671//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-88, complete sequence. //0.018:262:61//AL010157 R-NT2RP3001672 R-NT2RP3001676//Homo sapiens cosmid Q95D4, chromosome 21 5' of IFNAR2. //2.1e-48:413:77//AF039905 R-NT2RP3001678//RPC111-50C17.TK RPC111 Homo sapiens genomic clone R-50C17, genomic survey sequence. //0.15:232:62//AQ116359 R-NT2RP3001679//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11. //7.8e-104:549:95//AB020860 R-NT2RP3001688//Homo sapiens PAC clone DJ1048B16 from 7q34-q36, complete sequence. //6.6e-41:291:86//AC006019 R-NT2RP3001690//Plasmodium falciparum chromosome 2, section 52 of 73 of the complete sequence. //3.1e-07:433:59//AE001415 R-NT2RP3001708//Homo sapiens allele 14 fragile site locus (FRA108) minisatellite sequence. //6.0e-06:237:64//AF053523 R-NT2RP3001712//CITB1-E1-2516N9.TF CITB1-E1 Homo sapiens genomic clone 2516N9, genomic survey sequence. //1.5e-95:456:99//AQ279562 R-NT2RP3001716//Homo sapiens chromosome Y, clone 264.M.20, complete sequence. //0.0012:346:58//AC004617 R-NT2RP3001724//Human HepG2 3' region Mbol cDNA, clone hmd6a06m3. //1.3e-27:163:95//D17273 R-NT2RP3001730//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 111822, WORKING DRAFT SEQUENCE. //7.6e-43:409:76//Z98200 R-NT2RP3001739 R-NT2RP3001752//Human clone 23774 mRNA sequence. //1.9e-08:104:84//U79279 R-NT2RP3001753//CIT-HSP-2379P21.TF CIT-HSP Homo sapiens genomic clone 2379P21, genomic survey sequence. //8.8e-06:102:78//AQ113378 R-NT2RP3001764 R-NT2RP3001777//Human mRNA for heparan sulfate proteoglycan (glypican). //0.99:166:66//X54232 R-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds. //1.3e-111:549:97//AB007928 R-NT2RP3001792//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds. //1.6e-32:266:83//U13262 R-NT2RP3001799//H.sapiens mRNA for OX40 homologue. //8.5e-44:374:79//X75962 R-NT2RP3001819 R-NT2RP3001844//Caenorhabditis elegans cosmid C54G7. //0.0042:231:63//U40410 R-NT2RP3001854//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), O1 (o1), O3 (o3), O2 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds. //1.0:40:4:59//AF030694 R-NT2RP3001855 R-NT2RP3001896//CIT978SK-A-636F10.TV CIT978SK Homo sapiens genomic clone A-636F10, genomic survey sequence. //0.0012:68:82//AQ116409 R-NT2RP3001898//Homo sapiens Chromosome 11p15.5 PAC clone pDJ754h15 containing cdk-inhibitor p57/KIP2 (CDKN1C) gene, complete sequence. //0.37:266:65//AC005950 R-NT2RP3001915//Human BAC clone RG367017 from 7p15-p21, complete sequence. //0.018:144:66//AC002486 R-NT2RP3001926//Human polyadenylate binding protein (TIA-1) mRNA, complete cds. //2.4e-10:77:100//M77142 R-NT2RP3001929 R-NT2RP3001931//Homo sapiens full length insert cDNA clone YU73B1. //1.0e-110:562:96//AF087969 R-NT2RP3001938//Human DNA sequence from PAC 447B16 on chromosome X q13.1-q13.3. //0.38:386:56//Z95328 R-NT2RP3001943//Homo sapiens chromosome 5, PI clone 1076B9 (LBNL H14), complete sequence. //0.87:298:61//AC004500 R-NT2RP3001944//Bos taurus clone CSSM056 satellite DNA sequence. //0.0095:76:78//U03836 R-NT2RP3001969//Homo sapiens chromosome 12p13.3 clone RPC111-350L</p>	<p>7, WORKING DRAFT SEQUENCE, 72 unordered pieces. //7.0e-109:552:96//AC005844 R-NT2RP3001989//Caenorhabditis elegans cosmid C01A2, complete sequence. //0.15:111:68//Z81029 R-NT2RP3002002//Plasmodium falciparum 14-3-3 protein gene, partial cds. //0.016:286:60//AF065987 R-NT2RP3002004//H.sapiens mRNA for FAST kinase. //5.1e-41:335:82//X86779 R-NT2RP3002007 R-NT2RP3002014//Human DNA sequence from clone Z28A9 on chromosome 22q12.3-13.32 Contains 85 KDA CALCIUM-INDEPENDENT PHOSPHOLIPASE A2, EST, GSS, CpG island, complete sequence. //6.6e-41:297:86//AL022322 R-NT2RP3002033 R-NT2RP3002045//Drosophila melanogaster fat protein (fat) gene, complete cds. //0.77:320:60//M80537 R-NT2RP3002054//Caenorhabditis elegans cosmid Y69H2, complete sequence. //0.82:362:57//Z98877 R-NT2RP3002056//F.rubripes GSS sequence, clone 020E22bF7, genomic survey sequence. //0.010:185:63//Z87006 R-NT2RP3002057 R-NT2RP3002062//Human BAC clone RG356F09 from 7p21, complete sequence. //1.7e-17:164:81//AC004002 R-NT2RP3002063 R-NT2RP3002081//HS_3082_A1_G09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3082 Col=17 Row=M, genomic survey sequence. //4.2e-25:344:73//AQ122260 R-NT2RP3002097//Homo sapiens Xp22-150 BAC GSHB-309P15 (Genome Systems Human BAC Library) complete sequence. //2.6e-23:212:86//AC006210 R-NT2RP3002102//Homo sapiens BAC clone RG290G13 from 7q21, complete sequence. //0.43:168:64//AC004746 R-NT2RP3002108//CIT-HSP-2346P16.TF CIT-HSP Homo sapiens genomic clone 2346P16, genomic survey sequence. //3.5e-08:110:78//AQ059071 R-NT2RP3002146//Streptococcus gordonii competence factor (comC) and histidine protein kinase (comD) genes, complete cds, and response regulator (comE) gene, partial cds. //0.11:534:55//U80077 R-NT2RP3002147//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 329F2, WORKING DRAFT SEQUENCE. //4.1e-108:551:86//AL031710 R-NT2RP3002151//Mus musculus mRNA for Guanine Nucleotide Regulator y Protein, complete cds. //6.8e-62:347:80//AB003503 R-NT2RP3002163//Anolis pulchellus vitellogenin mRNA, partial cds. //0.77:281:63//U46857 R-NT2RP3002165 R-NT2RP3002166//D.sargus satellite DNA (clone PSE3). //0.81:124:62//Z48711 R-NT2RP3002173 R-NT2RP3002181//HS-1042-A2-F01-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 824 Col=2 Row=K, genomic survey sequence. //1.3e-35:305:81//B36980 R-NT2RP3002244//Caenorhabditis elegans cosmid R11E3. //0.0024:393:61//AF100669 R-NT2RP3002248//Human DNA sequence from PAC 170A21 on chromosome 2 2q12-qter contains ESTs. //0.30:217:63//Z82189 R-NT2RP3002255 R-NT2RP3002273//Homo sapiens BAC clone 393122 from 8q21, complete sequence. //0.84:463:57//AF070717 R-NT2RP3002276//HS_2260_A1_MF_E07 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2260 Col=13 Row=I, genomic survey sequence. //0.0017:198:63//AQ292491 R-NT2RP3002303//Human HMG-17 gene for non-histone chromosomal protein HMG-17. //7.4e-93:510:93//X13546 R-NT2RP3002304//Human BAC clone GS188P18, complete sequence. //6.3e-09:477:59//AC000115 R-NT2RP3002330//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces. //0.087:388:58//AC004688 R-NT2RP3002343 R-NT2RP3002351//Homo sapiens chromosome Y, clone 264.M.20, complete sequence. //0.20:489:56//AC004617 R-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxorf5 (7-17A) gene. //2.4e-104:516:94//Y15164 R-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds. //4.7e-102:524:95//AB014578 R-NT2RP3002484 R-NT2RP3002501//Human DNA sequence from PAC 92M18, BRCA2 gene region on chromosome 13q12-13 contains BRCA2 exons 25, 26 and 27 ESTs and STS. //5.2e-17:232:75//Z73359 R-NT2RP3002512</p>
--	---

【0817】

【表517】

R-NT2RP3002529//CIT-HSP-2340H2. TR CIT-HSP Homo sapiens genomic clone 2340H2, genomic survey sequence.//0.81:266:58//AQ057387

R-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds.//3.3e-82:438:94//AB018272

R-NT2RP3002549//Medicago truncatula ENBPI gene, exons 1 to 12.//0.95:381:56//AJ002479

R-NT2RP3002566//HS_2036_A1_D08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2036 Col=15 Row=G, genomic survey sequence.//0.18:162:64//AQ230627

R-NT2RP3002587//Homo sapiens clone DJ1090E20, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.1e-15:213:73//AC004956

R-NT2RP3002590//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MXK3, complete sequence.//0.00010:431:59//AB019236

R-NT2RP3002602//Mus musculus stannin gene, complete cds.//1.6e-20:339:70//AF030522

R-NT2RP3002603

R-NT2RP3002631//Homo sapiens chromosome 21 PAC RPC1P704A9190Q2.//1.0:241:59//AJ006997

R-NT2RP3002659//Rat sodium-hydrogen exchange protein-isoform 3 (NH E-3) mRNA, complete cds.//6.8e-24:331:76//M85300

R-NT2RP3002660//H. sapiens partial gene for progesterone receptor and Alu element DNA.//9.8e-43:273:82//Z49816

R-NT2RP3002663//Lymnaea stagnalis 16S ribosomal RNA gene, mitochondrial gene encoding ribosomal RNA, partial sequence.//0.60:300:59//U82072

R-NT2RP3002671//S. pombe chromosome III cosmid c553.//1.2e-20:399:66//AL023704

R-NT2RP3002682//RPC111-44K6.TJ RPC111 Homo sapiens genomic clone R-44K6, genomic survey sequence.//4.7e-09:122:77//AQ202481

R-NT2RP3002687//P. falciparum complete gene map of plastid-like DNA (IR-B).//1.1e-07:494:59//X95276

R-NT2RP3002688//Human TSL RNA sequence.//2.7e-32:290:79//X01037

R-NT2RP3002701

R-NT2RP3002713//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167A19, WORKING DRAFT SEQUENCE.//0.95:334:59//AL031427

R-NT2RP3002763//***ALU WARNING: Human Alu-J subfamily consensus sequence.//3.9e-40:288:85//U14567

R-NT2RP3002770//R. prowazekii genomic DNA fragment (clone A615F).//0.21:174:63//Z82710

R-NT2RP3002785//Homo sapiens PAC clone DJ0170D19 from Xq23, complete sequence.//0.78:354:59//AC004822

R-NT2RP3002799//Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions.//1.1e-20:161:77//AF003528

R-NT2RP3002810//Caenorhabditis elegans cosmid F10D2.//0.28:441:56//AF022972

R-NT2RP3002818//HS_3053_A2_A08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3053 Col=16 Row=A, genomic survey sequence.//0.19:220:60//AQ135025

R-NT2RP3002861//P. falciparum complete gene map of plastid-like DNA (IR-B).//9.3e-05:414:60//X95276

R-NT2RP3002869//Homo sapiens chromosome 19, cosmid F21967, complete sequence.//0.14:165:64//AC005256

R-NT2RP3002876//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 50024, WORKING DRAFT SEQUENCE.//2.6e-59:311:96//AL034380

R-NT2RP3002877//Homo sapiens Xp22 bins 87-93 PAC RPC11-122K4 (Rowell Park Cancer Institute Human PAC Library) complete sequence.//4.6e-24:422:63//AC003035

R-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds.//4.7e-109:570:95//AB018314

R-NT2RP3002911//Homo sapiens BAC clone GS166A23 from Tp21, complete sequence.//3.1e-16:471:64//AC005014

R-NT2RP3002948//, complete sequence.//4.5e-94:516:93//AC005500

R-NT2RP3002953//Homo sapiens chromosome 5, BAC clone 34j15 (LBML H 169), complete sequence.//3.4e-111:566:96//AC005754

R-NT2RP3002955//Plasmodium falciparum chromosome 2, section 28 of 73 of the complete sequence.//0.19:424:58//AE001391

R-NT2RP3002969//Rat mRNA for brain acyl-CoA synthetase II, complete cds.//1.1e-89:562:88//D30666

R-NT2RP3002972//Stealth virus 5 clone C1311 T7 genomic sequence.//1.0:122:67//AF067482

R-NT2RP3002978//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 455J7, WORKING DRAFT SEQUENCE.//4.8e-05:249:63//AL031733

R-NT2RP3002988//Human DNA sequence from PAC 106HB on chromosome 1q24. Contains PHOSPHATIDYLINOSITOL-GLYCAN class C (PIG-C) and DYNAMIN-3 genes. Contains ESTs and STSs and a CpG island.//0.0097:246:67//Z97195

R-NT2RP3003008//Mus musculus major histocompatibility locus class III regions Hsc70t gene, partial cds: smRNP, G7A, NG23, MutS homolog, CLCP, NG24, NG25, and NG26 genes, complete cds: and unknown genes.//1.9e-24:188:78//AF109905

R-NT2RP3003032//Arabidopsis thaliana (clone DW1) DNA retrotransposon on Tall-1 integration site.//5.3e-07:376:63//L47211

R-NT2RP3003059//Homo sapiens chromosome 3, clone hRPK.165_1_16, complete sequence.//1.4e-13:323:66//AC005669

R-NT2RP3003061//Homo sapiens mRNA from HIV associated non-Hodgkin's lymphoma (clone h11-10).//3.8e-42:265:91//Y16708

R-NT2RP3003068//HS_3214_B2_G09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3214 Col=18 Row=N, genomic survey sequence.//0.025:207:64//AQ181894

R-NT2RP3003071//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 510D11, WORKING DRAFT SEQUENCE.//0.00014:329:60//Z98044

R-NT2RP3003078//T26A1TF TAMU Arabidopsis thaliana genomic clone T2 6A1, genomic survey sequence.//0.95:219:63//B27013

R-NT2RP3003101//Plasmodium falciparum 3D7 chromosome 12 PFYACB12 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.4e-05:285:62//AC004153

R-NT2RP3003121//Homo sapiens full length insert cDNA clone ZD62010.//2.1e-47:242:98//AF086348

R-NT2RP3003133//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Z28H13, WORKING DRAFT SEQUENCE.//1.4e-21:199:75//AL031985

R-NT2RP3003138//Mouse kif4 mRNA for microtubule-based motor protein KIF4, complete cds.//5.1e-14:287:68//D12646

R-NT2RP3003139//Rattus norvegicus kappa opioid receptor gene, exon 4 and complete cds.//1.5e-13:122:80//U17995

R-NT2RP3003150

R-NT2RP3003157//Homo sapiens 12q15 BAC GSHB-410F4 (Genome Systems Human BAC Library) complete sequence.//5.5e-42:289:74//AC005294

R-NT2RP3003185//HS_2058_A1_H03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2058 Col=5 Row=O, genomic survey sequence.//0.025:52:94//AQ231298

R-NT2RP3003193//Homo sapiens chromosome 17, clone hRPK.62B_E_12, complete sequence.//4.8e-40:349:79//AC005701

R-NT2RP3003197//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 36411, WORKING DRAFT SEQUENCE.//5.2e-10:180:71//AL031319

R-NT2RP3003203//Mus musculus IFN alpha-treated embryonic fibroblast mRNA.//1.8e-11:148:77//U51904

R-NT2RP3003204//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 892F13, WORKING DRAFT SEQUENCE.//6.6e-41:282:86//AL009183

R-NT2RP3003212//Homo sapiens full length insert cDNA clone ZB91B11.//1.7e-68:363:95//AF086173

R-NT2RP3003230//Caenorhabditis elegans cosmid T12B5.//0.0018:279:64//AF100307

R-NT2RP3003242//Homo sapiens chromosome 7 clone UWGC:q3586a160 from Tpl4-15, complete sequence.//1.0:346:57//AC005272

R-NT2RP3003251//Homo sapiens BAC clone RC60N22 from 7q21, complete sequence.//2.5e-10:436:62//AC003083

R-NT2RP3003264//CIT-HSP-2296M7. TR CIT-HSP Homo sapiens genomic clone 2296M7, genomic survey sequence.//5.8e-05:308:61//AQ005862

R-NT2RP3003278//Human HepG2 partial cDNA, clone hmd3blm5.//9.4e-47:302:89//D17022

R-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds.//7.4e-101:550:93//L36983

R-NT2RP3003290//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460J8, WORKING DRAFT SEQUENCE.//3.0e-22:228:78//AL031662

R-NT2RP3003301

R-NT2RP3003302//CIT-HSP-2319H19. TF CIT-HSP Homo sapiens genomic clone 2319H19, genomic survey sequence.//1.5e-69:367:95//AQ034950

R-NT2RP3003311//Plasmodium falciparum 3D7 chromosome 12 PFYACB12 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//5.1e-08:398:64//AC005505

R-NT2RP3003313//Caenorhabditis elegans cosmid F39B1, complete sequence.//0.00022:436:58//Z69660

R-NT2RP3003327//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-237H1 complete genomic sequence, complete sequence.//1.5e-16:334:70//AC002287

R-NT2RP3003330//Homo sapiens full length insert cDNA Y124C02.//4.4e-96:458:99//AF075015

R-NT2RP3003344//HS_3235_B2_H09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=18 Row=P, genomic survey sequence.//4.1e-18:197:80//AQ303203

R-NT2RP3003346

R-NT2RP3003353//CITBI-E1-2523B18. TR CITBI-E1 Homo sapiens genomic clone 2523B18, genomic survey sequence.//8.3e-06:130:73//AQ278834

【0818】

【表518】

R-NT2RP3003377//Homo sapiens clone DJ0919J22, WORKING DRAFT SEQUEN
CE, 34 unordered pieces.//1.9e-97:481:94//AC005519
R-NT2RP3003384//Homo sapiens clone DJ0038110, WORKING DRAFT SEQUEN
CE, 5 unordered pieces.//2.3e-10:226:71//AC004820
R-NT2RP3003385
R-NT2RP3003403//Human DNA sequence from clone 227L5 on chromosome
Xp11.22-11.3. Contains a Keratin, Type I Cytoskeletal 18 (KRT18, C
YK18, K18, CK18) pseudogene and an STS, complete sequence.//2.8e-4
0:496:72//AL031585
R-NT2RP3003409//Rat POU domain factor (Brn-5) mRNA.//1.5e-20:375:6
8//L23204
R-NT2RP3003411//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 438L4, WORKING DRAFT SEQUENCE.//1.0:180:61//Z97635
R-NT2RP3003427//RPC111-45J23.TJ RPC111 Homo sapiens genomic clone
R-45J23, genomic survey sequence.//0.82:162:69//AQ195566
R-NT2RP3003433//Homo sapiens BAC clone NH0044G14 from Tq11.23-21.
1, complete sequence.//1.1e-10:379:61//AC006031
R-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, comp
lete cds.//1.1e-95:479:96//AF004828
R-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cd
s.//1.3e-100:527:93//AB018268
R-NT2RP3003491//Plasmodium falciparum chromosome 2, section 35 of
73 of the complete sequence.//4.0e-08:495:59//AE001398
R-NT2RP3003500//W. suaveolens mitochondrial ATP9 gene.//0.0074:514:
59//X77238
R-NT2RP3003543//Human clone A9A2BRB7 (CAC)n/(GTG)n repeat-containi
ng mRNA.//1.3e-31:217:88//U00952
R-NT2RP3003552
R-NT2RP3003555//Dictyostelium discoideum interaptin (abpD) gene, c
omplete cds.//0.98:321:61//AF057019
R-NT2RP3003564
R-NT2RP3003572//Human DNA sequence from BAC 992D9 on chromosome 22
q12.1 contains STS.//0.0015:507:59//AL008638
R-NT2RP3003578//Human Chromosome 16 BAC clone CIT987SK-A-61E3, com
plete sequence.//1.2e-39:359:79//AC003007
R-NT2RP3003585//Plasmodium falciparum MAL3P8, complete sequence.//
0.014:539:58//AL034560
R-NT2RP3003625//Human DNA sequence from clone 1042K10 on chromosom
e 22q13.1-13.2. Contains the ADSL gene for Adenylosuccinate lyase
(EC 4.3.2.2, Adenylosuccinase, ASL) and 4 novel genes (one with pr
obable rabGAP domains and Src homology domain 3). Contains ESTs, 5
TSs, GSSs and a putative CpG island, complete sequence.//1.8e-44:4:
48:77//AL022238
R-NT2RP3003656//Homo sapiens chromosome 17, clone hRPK.401_0_9, co
mplete sequence.//0.34:257:62//AC005291
R-NT2RP3003659//O. fuscipennis 16S rRNA gene, partial.//0.021:145:6
5//Z93701
R-NT2RP3003665//HS_3078_B2_C09_MR CIT Approved Human Genomic Sperm
Library D Homo sapiens genomic clone Plate=3078 Col=18 Row=F, gen
omic survey sequence.//1.3e-75:397:95//AQ140580
R-NT2RP3003672
R-NT2RP3003686
R-NT2RP3003701//Human BAC clone GS310A05 from Tq21-q22, complete s
equence.//6.4e-17:464:62//AC002452
R-NT2RP3003716//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 774G10, WORKING DRAFT SEQUENCE.//0.00072:425:62//AL0344
10
R-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete c
ds.//1.7e-101:492:97//AB018300
R-NT2RP3003746//Homo sapiens Chromosome 16 BAC clone CIT987-SK502C
10, complete sequence.//3.7e-07:217:66//AC003009
R-NT2RP3003795//Human DNA sequence from clone 505B13 on chromosome
1p36.2-36.3 Contains CA repeat and GSSs, complete sequence.//8.1
e-26:456:68//Z98052
R-NT2RP3003799//cSRL-138g10-u cSRL flow sorted Chromosome 11 speci
fic cosmid Homo sapiens genomic clone cSRL-138g10, genomic survey
sequence.//4.9e-09:117:77//B01736
R-NT2RP3003800//Homo sapiens tyrosine kinase pp60c-src (SRC) gene,
exon 12 and partial cds.//2.8e-106:551:95//AF077754
R-NT2RP3003805
R-NT2RP3003809//Homo sapiens full length insert cDNA clone Y295A0
1.//3.6e-106:533:97//AF086107
R-NT2RP3003819//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 34606, WORKING DRAFT SEQUENCE.//6.0e-44:288:81//Z84487
R-NT2RP3003825//Mus domestica interleukin 1 receptor antagonist
(IL-1RA) mRNA.//0.0014:410:58//M64404
R-NT2RP3003828
R-NT2RP3003831//***ALU WARNING: Human Alu-J subfamily consensus se
quence.//2.3e-41:289:85//U14567
R-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence.
//1.6e-108:541:97//AF070611
R-NT2RP3003842//Homo sapiens Xp22 BAC 620F15 (Genome Systems BAC l
ibrary) complete sequence.//1.5e-46:457:74//AC002980
R-NT2RP3003846//Plasmodium falciparum MAL3P3, complete sequence.//
3.5e-06:356:62//Z98547
R-NT2RP3003870//Homo sapiens full length insert cDNA clone ZD75H1
1.//8.2e-09:68:98//AF086402
R-NT2RP3003876//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 101B012, WORKING DRAFT SEQUENCE.//0.0027:180:66//AL0316
50
R-NT2RP3003914//Dictyostelium discoideum DNA for transposable elem
ent Tdd-3 tandem array.//0.029:234:62//X53439
R-NT2RP3003918
R-NT2RP3003932//Mus musculus MRC OX-2 antigen homolog gene, exons
2-5, and complete cds.//0.00087:164:67//AF029215
R-NT2RP3003989
R-NT2RP3003992//Sequence 1 from patent US 5591825.//0.56:235:59//I
33465
R-NT2RP3004013//HS_3018_A1_G09_MR CIT Approved Human Genomic Sperm
Library D Homo sapiens genomic clone Plate=3018 Col=17 Row=W, gen
omic survey sequence.//0.00026:421:60//AQ119904
R-NT2RP3004016//Drosophila melanogaster DNA sequence (P1s OS03465
(D149) and OS08544 (D187)), complete sequence.//4.8e-12:308:62//AC
004532
R-NT2RP3004041//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 598F2, WORKING DRAFT SEQUENCE.//0.42:190:64//AL021579
R-NT2RP3004051//Homo sapiens chromosome 19, BAC CIT-B-19In6, compl
ete sequence.//3.6e-21:332:69//AC006130
R-NT2RP3004070//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 g
enomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.0
e-05:476:57//AC005308
R-NT2RP3004078//Homo sapiens chromosome 19, cosmid R30335, complet
e sequence.//2.0e-86:486:93//AC005784
R-NT2RP3004093//Human PAC clone 257C22A from 13q12-q13, complete s
equence.//5.3e-11:230:69//AC002525
R-NT2RP3004095//Homo sapiens clone NH0486122, WORKING DRAFT SEQUEN
CE, 5 unordered pieces.//7.5e-93:551:92//AC005038
R-NT2RP3004110//Homo sapiens 12p13.3 PAC RPC15-940J5 (Roswell Park
Cancer Institute Human PAC Library) complete sequence.//1.6e-104:
317:100//AC006064
R-NT2RP3004125//Pongo pygmaeus CT microsatellite, clone #3, from t
he tandemly repeated genes encoding U2 small nuclear RNA (RNU2 loc
us).//0.73:168:60//U36532
R-NT2RP3004145//Homo sapiens full length insert cDNA clone ZE09H0
3.//2.3e-89:427:99//AF086542
R-NT2RP3004148//Arabidopsis thaliana chromosome 11 BAC T1B8 genom
ic sequence, complete sequence.//0.013:134:70//U78721
R-NT2RP3004155//Homo sapiens PAC clone DJ0320J15 from Xq23, comple
te sequence.//3.8e-10:101:87//AC004081
R-NT2RP3004206//Homo sapiens clone DJ0794K21, complete sequence.//
1.5e-06:442:57//AC005533
R-NT2RP3004207//Mouse mRNA for seizure-related gene product 6.//1.
7e-07:220:69//D29763
R-NT2RP3004209//Human cosmid Q7A10 (D21S246) insert DNA, complete
sequence.//7.3e-89:504:92//D42052
R-NT2RP3004215//Caenorhabditis elegans cosmid F11A6, complete sequ
ence.//0.018:353:59//Z81498
R-NT2RP3004242//Plasmodium falciparum chromosome 2, section 52 of
73 of the complete sequence.//4.5e-06:407:60//AE001415
R-NT2RP3004246//Homo sapiens chromosome 10 clone CIT987SK-1010K1 m
ap 10q25, complete sequence.//2.8e-105:534:97//AC005385
R-NT2RP3004253//RPC111-78J12.TJ RPC111 Homo sapiens genomic clone
R-78J12, genomic survey sequence.//4.0e-64:382:90//AQ281324
R-NT2RP3004258//Rattus norvegicus Zis mRNA, complete cds.//7.0e-6
0:417:84//AF013967
R-NT2RP3004262//Mus musculus heat shock protein hsp40-3 gene, comp
lete cds.//2.7e-43:528:73//AF092536
R-NT2RP3004334//Homo sapiens chromosome 17, clone hRPK.1110_E_20,
complete sequence.//1.4e-06:435:62//AC004231
R-NT2RP3004341//CITB1-E1-2503F11.TR CITB1-E1 Homo sapiens genomic
clone 2503F11, genomic survey sequence.//0.0018:210:65//AQ263365
R-NT2RP3004348//Homo sapiens chromosome 17, clone hRPK.85_8_7, co
mplete sequence.//7.1e-46:340:83//AC005695
R-NT2RP3004349//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 11703, WORKING DRAFT SEQUENCE.//9.4e-29:263:79//AL02099
5
R-NT2RP3004378//Human DNA sequence from PAC 27K14 on chromosome Xp
11.3-p11.4. Contains monoamine oxidase B (MAOB), ESTs and polymor
phic CA repeats.//2.0e-67:422:90//Z95125
R-NT2RP3004399//HS_3046_A1_E02_MR CIT Approved Human Genomic Sperm

【表519】

Library D Homo sapiens genomic clone Plate=3046 Col=3 Row=1, genomic survey sequence.//0.00014:186:67//AQ137619
 R-NT2RP3004424//RPC111-59114.TJ RPC111 Homo sapiens genomic clone R-59114, genomic survey sequence.//7.4e-71:370:95//AQ201461
 R-NT2RP3004428//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y66A7, WORKING DRAFT SEQUENCE.//0.096:205:64//AL022282
 R-NT2RP3004451//Arabidopsis thaliana chromosome 11 BAC F15K20 genomic sequence, complete sequence.//0.0029:396:60//AC005824
 R-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds.//2.9e-106:526:98//AB007917
 R-NT2RP3004466
 R-NT2RP3004470//Homo sapiens chromosome 5, Bac clone 5m9 (LBWL H22 O), complete sequence.//8.3e-06:229:64//AC005895
 R-NT2RP3004472//Plasmodium falciparum 3D7 chromosome 12 PFYAC1383 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.87:442:59//AC005504
 R-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds.//1.6e-105:521:97//AB007925
 R-NT2RP3004480//Mus musculus maternal-embryonic 3 (New3) mRNA, complete cds.//3.9e-38:322:81//U47024
 R-NT2RP3004490//Homo sapiens PAC clone 166H1 from 12q, complete sequence.//4.2e-96:527:92//AC003982
 R-NT2RP3004498//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//2.3e-43:342:82//AC006023
 R-NT2RP3004503//Human cosmid g1572c101, complete sequence.//2.3e-25:392:68//AC000357
 R-NT2RP3004504//M. musculus mRNA for CPEB protein.//1.8e-28:387:70//Y08260
 R-NT2RP3004507
 R-NT2RP3004527//Homo sapiens chromosome 14, BAC C1TB-135H17 containing the RAD51L1 gene, complete sequence.//0.68:244:62//AC004518
 R-NT2RP3004534//Mouse oncogene (ect2) mRNA, complete cds.//2.6e-79:525:84//L11316
 R-NT2RP3004544
 R-NT2RP3004566
 R-NT2RP3004569//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.96:296:58//AC004709
 R-NT2RP3004572//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence.//8.2e-12:457:63//AC005083
 R-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//2.4e-97:488:96//AB007946
 R-NT2RP3004594//Homo sapiens BAC clone NH0436H22 from 2, complete sequence.//1.7e-10:368:61//AC005234
 R-NT2RP3004617
 R-NT2RP3004618//F2H16TF 1GF Arabidopsis thaliana genomic clone F2H16, genomic survey sequence.//0.96:212:64//B26414
 R-NT2RP3004670//Homo sapiens GMS5T mRNA for N-acetylglucosamine-6-O-sulfotransferase 6 (GlcNAc6ST), complete cds.//2.2e-55:291:95//AB014679
 R-NT2RP4000008//H. sapiens polyA site DNA sequence.//2.5e-25:202:85//Z24749
 R-NT2RP4000023//CIT-HSP-2372A9, TF CIT-HSP Homo sapiens genomic clone 2372A9, genomic survey sequence.//3.6e-51:313:89//AQ112388
 R-NT2RP4000035//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//4.3e-69:536:81//AC005015
 R-NT2RP4000049//Homo sapiens TRAIL receptor 2 mRNA, complete cds.//2.1e-58:289:82//AF016266
 R-NT2RP4000051//Homo sapiens Chromosome 22q11.2 Cosmid Clone 20b1 n DGCR Region, complete sequence.//0.56:462:58//AC000074
 R-NT2RP4000078//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.0021:460:60//AC005506
 R-NT2RP4000102//Homo sapiens chromosome 5, PAC clone 17e19 (LBWL H148), complete sequence.//1.6e-08:518:58//AC004848
 R-NT2RP4000109//Homo sapiens mRNA for MECF5, partial cds.//3.5e-106:536:96//AB011538
 R-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds.//1.1e-110:554:97//AB007952
 R-NT2RP4000147
 R-NT2RP4000150//Rat proto-oncogene (Ets-1) mRNA, complete cds.//3.5e-46:395:83//L20681
 R-NT2RP4000151
 R-NT2RP4000159//Caenorhabditis elegans cosmid R02F11.//0.00011:261:63//AF016439
 R-NT2RP4000167//RPC111-59L8.TK RPC111 Homo sapiens genomic clone R-59L8, genomic survey sequence.//6.2e-26:163:93//AQ200049
 R-NT2RP4000185
 R-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//4.6e-99:505:96//AB014600
 R-NT2RP4000212//, complete sequence.//1.0e-106:538:96//AC005300
 R-NT2RP4000214//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.2e-39:272:88//AC005261
 R-NT2RP4000218//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//1.6e-09:457:60//AC004081
 R-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//9.0e-69:354:96//AJ006470
 R-NT2RP4000246//Mus musculus mRNA for NDPP-1 protein, complete cds.//2.0e-27:344:73//D10727
 R-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence.//9.7e-78:381:99//AF091092
 R-NT2RP4000263//CIT-HSP-2336N24, TF CIT-HSP Homo sapiens genomic clone 2336N24, genomic survey sequence.//0.26:124:69//AQ043515
 R-NT2RP4000290//ORF 5' of ECLF2...ECRF3=G protein-coupled receptor homolog [herpesvirus saimiri] HVS, host-squirrel monkey, Genomic, 4 genes, 3720 nt.//0.12:326:61//S76368
 R-NT2RP4000312//Human DNA sequence from clone 523E19 on chromosome 6p11.2-12.3 Contains ESTs STS and GSSs, complete sequence.//2.2e-111:538:98//AL033384
 R-NT2RP4000321//Homo sapiens clone 24453 mRNA sequence.//1.4e-108:515:99//AF070524
 R-NT2RP4000323//S. cerevisiae telomeric sequence DNA, clone YLP108C A-2-1.//0.048:107:69//M34311
 R-NT2RP4000355//Homo sapiens clone DJ1136A10, WORKING DRAFT SEQUENCE, 4 unordered pieces.//4.3e-39:350:79//AC004972
 R-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//2.4e-109:520:99//AB018281
 R-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//8.7e-109:527:98//AF044195
 R-NT2RP4000370//Homo sapiens PAC clone DJ0777023 from 7p14-p15, complete sequence.//9.9e-25:348:72//AC005154
 R-NT2RP4000376//Rattus norvegicus phospholipase A-2-activating protein (nap) mRNA, complete cds.//2.2e-69:391:89//U17901
 R-NT2RP4000381//Homo sapiens chromosome 17, clone hRPK.394_K_10, complete sequence.//0.066:197:63//AC005080
 R-NT2RP4000415//345F19.TV CIT978SKA1 Homo sapiens genomic clone A-345F19, genomic survey sequence.//0.10:79:75//B15527
 R-NT2RP4000417//Homo sapiens full length insert cDNA clone ZDS281 O.//9.6e-96:468:97//AF086313
 R-NT2RP4000424//Homo sapiens DNA sequence from PAC 127D3 on chromosome 1q23-25. Contains FMO2 and FMO3 genes for Flavin-containing Monooxygenase 2 and Flavin-containing Monooxygenase 3 (Dimethylaniline Monooxygenase (N-Oxide 3, EC1.14.13.8, Dimethylaniline Oxidase 3, FMO 11, FMO 3), and a gene for another, unknown, Flavin-containing Monooxygenase family protein. Contains ESTs and GSSs, complete sequence.//1.8e-08:489:59//AL021026
 R-NT2RP4000448//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.3e-07:510:60//AC005505
 R-NT2RP4000449//HS_2037_B2_A09_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2037 Col=18 Row=B, genomic survey sequence.//1.3e-58:375:88//AQ243047
 R-NT2RP4000455//Phocine herpesvirus type 1 glycoprotein D (gD) gene, partial cds.//0.62:133:63//U92271
 R-NT2RP4000457
 R-NT2RP4000480//cSRL-54b11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-54b11, genomic survey sequence.//2.1e-19:145:88//B05082
 R-NT2RP4000481
 R-NT2RP4000500
 R-NT2RP4000515//Plasmodium falciparum 3D7 chromosome 12 PFYAC88-42 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//1.4e-05:411:59//AC005140
 R-NT2RP4000517//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//2.7e-21:230:77//AC003007
 R-NT2RP4000518//Homo sapiens DNA sequence from PAC 206D15 on chromosome 1q24. Contains a Reduced Folate Carrier protein (RFC) LIKE gene, a mitochondrial ATP Synthetase protein 8 (ATP8, MTATP8) LIKE pseudogene, an unknown gene and the last exon of the JEM1 gene coding for the Basic-Leucine Zipper nuclear factor JEM-1. Contains ESTs, an STS and a BAC end sequence (GSS), complete sequence.//0.0080:461:59//AL021068
 R-NT2RP4000519
 R-NT2RP4000524
 R-NT2RP4000528//Homo sapiens chromosome 17, clone hRPK.138_P_22, complete sequence.//0.99:158:66//AC005697
 R-NT2RP4000541//Homo sapiens Chromosome 22q11.2 Cosmid Clone 33e n DGCR Region, complete sequence.//1.0:309:59//AC000078
 R-NT2RP4000556//Rattus norvegicus cell cycle protein p55CDC gene.

【0820】

【表520】

complete cds.//0.0031:126:72//AF052695
R-NT2RP4000588//Homo sapiens BAC clone RG20K23 from 7q31, complete sequence.//1.0:186:64//AC004161
R-NT2RP4000614//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS SS *** from contig 3-62, complete sequence.//1.4e-06:526:58//AL009013
R-NT2RP4000638//Homo sapiens chromosome 17, clone hCIT.468.F_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//6.9e-48:497:75//AC004666
R-NT2RP4000648//CIT-HSP-230017.TR CIT-HSP Homo sapiens genomic clone 230017, genomic survey sequence.//0.22:110:68//AQ012747
R-NT2RP4000657//Lycodichthys dearborni type III antifreeze peptide gene, clone 5' LD-1/NotI-EcoRI subclone SphI-XbaI, partial cds.//0.0065:189:63//U20443
R-NT2RP4000704//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 409J21, WORKING DRAFT SEQUENCE.//0.22:334:60//Z83824
R-NT2RP4000724//Homo sapiens Chromosome 22q11.2 Cosmid Clone 56c1 n DCR Region, complete sequence.//2.2e-70:448:88//AC000080
R-NT2RP4000728//CIT-HSP-2310K14.TF CIT-HSP Homo sapiens genomic clone 2310K14, genomic survey sequence.//0.00013:289:61//AQ019669
R-NT2RP4000739//Homo sapiens chromosome 12p13.3, WORKING DRAFT SEQUENCE, 21 unordered pieces.//0.53:254:61//AC004765
R-NT2RP4000781//P. cepacia fusaric acid-resistance genes encoding 5 proteins, complete cds.//1.0:392:59//D12503
R-NT2RP4000817//Homo sapiens Xp22 BAC GSHB 526D21 (Genome Systems Human BAC library) complete sequence.//0.59:378:58//AC003037
R-NT2RP4000831//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//3.4e-53:307:85//AL023808
R-NT2RP4000837//Homo sapiens T-cell receptor alpha delta locus from bases 501613 to 752736 (section 3 of 5) of the Complete Nucleotide Sequence.//7.0e-50:367:77//AE000660
R-NT2RP4000855
R-NT2RP4000865//Homo sapiens chromosome 17, clone HRC905N1, complete sequence.//1.5e-78:479:88//AC003098
R-NT2RP4000878//Mus musculus mRNA for myeloid associated differentiation protein.//4.5e-09:186:69//AJ001616
R-NT2RP4000879//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//7.8e-08:364:60//AC004153
R-NT2RP4000888//Human S-adenosylmethionine decarboxylase (AMD1) gene, exons 5-9.//3.5e-90:459:96//M88006
R-NT2RP4000898//H. sapiens ung gene for uracil DNA-glycosylase.//7.6e-09:392:61//X89398
R-NT2RP4000925//Rattus norvegicus Shal-related potassium channel K v4.3 mRNA, complete cds.//5.8e-45:264:92//U42975
R-NT2RP4000927//epstein-barr virus simple repeat array (ir3).//0.0012:367:61//J02079
R-NT2RP4000928//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MCL19, complete sequence.//1.0:138:68//AB006698
R-NT2RP4000929//Human DNA sequence from PAC 293L6 on chromosome 2, complete sequence.//0.45:288:62//Z82197
R-NT2RP4000955//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 633019, WORKING DRAFT SEQUENCE.//1.1e-09:322:62//AL022302
R-NT2RP4000973//Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions.//2.3e-06:326:62//AF003528
R-NT2RP4000975
R-NT2RP4000979//HS_3009_B1_F08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=15 Row=L, genomic survey sequence.//2.3e-14:117:89//AQ090957
R-NT2RP4000984//Human immunodeficiency virus type 1 envelope glycoprotein (env) gene, C2-V3 region, isolate HIV194UG011INT.01_d1PD, partial cds.//0.11:219:62//U44882
R-NT2RP4000989//Sequence 30 from patent US 5552281.//3.5e-25:154:97//125669
R-NT2RP4000996//Plasmodium falciparum strain Dd2 heat shock protein 86 (HSP86), 01 (o1), 03 (o3), 02 (o2), CG8 (cg8), CG4 (cg4), CG3 (cg3), CG9 (cg9), CG1 (cg1), CG6 (cg6), chloroquine resistance candidate protein (cg2), and CG7 (cg7) genes, complete cds.//3.8e-07:421:59//AF030694
R-NT2RP4000997//Homo sapiens chromosome 17, clone 104H12, complete sequence.//4.2e-37:499:72//AC000003
R-NT2RP4001004//HS_3163_A2_H02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3163 Col=4 Row=O, genomic survey sequence.//2.8e-38:241:90//AQ168515
R-NT2RP4001006//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//7.1e-55:372:73//AC006023
R-NT2RP4001010//Homo sapiens full length insert cDNA clone ZD38E1
2.//3.3e-09:153:74//AF086247
R-NT2RP4001029//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//2.1e-34:361:78//U20086
R-NT2RP4001041//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H 192), complete sequence.//9.9e-84:435:96//AC005216
R-NT2RP4001057//Homo sapiens KIAA0399 mRNA, partial cds.//6.2e-50:282:94//AB007859
R-NT2RP4001064//H. sapiens NOS2 gene, exon 15.//0.71:183:61//X85771
R-NT2RP4001078//Human D-site binding protein gene, exon 4 and complete cds.//1.9e-114:569:97//U48213
R-NT2RP4001079//Homo sapiens mRNA for putative Ca2+-transporting ATPase, partial.//2.4e-118:574:98//AJ010953
R-NT2RP4001080//Plasmodium falciparum chromosome 2, section 66 of 73 of the complete sequence.//0.013:430:58//AE001429
R-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds.//1.8e-119:548:95//AB011164
R-NT2RP4001095//Homo sapiens cosmids IM0525, LC1233, Qc3C1, LB143 9, Qc12C11 and 220B3 from Xq28, complete sequence.//2.8e-39:312:81//AF003626
R-NT2RP4001100//Human DNA sequence from cosmid U85A3, between markers DXS366 and DXS87 on chromosome X contains rad21 and T-cell cyclophorin pseudogenes: STS.//8.7e-41:389:78//Z78021
R-NT2RP4001117//Canis familiaris sec61 homologue mRNA, complete cds.//2.8e-12:292:68//M96629
R-NT2RP4001122//Caenorhabditis elegans cosmid F44D12, complete sequence.//0.97:129:66//Z68298
R-NT2RP4001126//HS_3146_A1_B05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3146 Col=9 Row=C, genomic survey sequence.//0.013:268:63//AQ141093
R-NT2RP4001138
R-NT2RP4001143//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 64K7, WORKING DRAFT SEQUENCE.//1.8e-31:380:68//AL031668
R-NT2RP4001148//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//1.2e-83:325:92//AC005095
R-NT2RP4001149//Mouse mRNA for thymic epithelial cell surface antigen, complete cds.//8.1e-32:553:67//D67067
R-NT2RP4001150//AK011 Genomic DNA Hordeum vulgare genomic clone to 144a similar to barley TAS, genomic survey sequence.//0.91:132:63//AQ248412
R-NT2RP4001159//Cloning vector pAP3neo DNA, complete sequence.//4.0e-118:437:97//AB003468
R-NT2RP4001174//Homo sapiens 12q24 BAC RPC111-162P23 (Roswell Park Cancer Institute Human BAC library) complete sequence.//1.7e-33:289:82//AC002996
R-NT2RP4001206//P. falciparum mRNA for AARP2 protein.//0.93:187:64//Y08924
R-NT2RP4001207
R-NT2RP4001210//CIT-HSP-2042D13.TF CIT-HSP Homo sapiens genomic clone 2042D13, genomic survey sequence.//3.8e-06:268:63//B74772
R-NT2RP4001213//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//4.7e-16:371:66//M99593
R-NT2RP4001219//HS_2190_A1_A06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2190 Col=11 Row=A, genomic survey sequence.//2.4e-06:288:61//AQ216635
R-NT2RP4001228//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS SS *** from MAL1P2, WORKING DRAFT SEQUENCE.//0.024:357:58//AL031745
R-NT2RP4001235//HS_3047_A1_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3047 Col=13 Row=L, genomic survey sequence.//0.0033:301:63//AQ126918
R-NT2RP4001256//HS_3007_A2_B06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3007 Col=12 Row=C, genomic survey sequence.//1.5e-11:140:80//AQ118389
R-NT2RP4001260//Plasmodium falciparum chromosome 2, section 63 of 73 of the complete sequence.//0.0013:486:59//AE001426
R-NT2RP4001274//RPC111-24021.TKBF RPC1-11 Homo sapiens genomic clone RPC1-11-24021, genomic survey sequence.//3.9e-25:142:99//AQ013887
R-NT2RP4001276//Homo sapiens full length insert cDNA clone ZD55D1 0.//1.2e-10:90:92//AF086334
R-NT2RP4001313//Mus musculus orphan nuclear hormone receptor (CAR) gene, complete sequence.//7.7e-23:466:66//AF009326
R-NT2RP4001315//CIT-HSP-2312C6.TR CIT-HSP Homo sapiens genomic clone 2312C6, genomic survey sequence.//0.98:305:62//AQ018036
R-NT2RP4001339
R-NT2RP4001345
R-NT2RP4001351//Fruitfly strain g20 mitochondrial DNA, A+T-rich region, partial sequence.//0.00082:260:59//AB003097
R-NT2RP4001353//RPC111-55N17.TJ RPC111 Homo sapiens genomic clone 55N17, genomic survey sequence.//0.74:106:66//AQ081821

【0821】

【表521】

R-NT2RP4001372	R-NT2RP4001696//Human chromosome 8 BAC clone CIT987SK-2A8 complete sequence.//4.5e-115:583:96//U96629
R-NT2RP4001373//Homo sapiens chromosome 17, clone hRPK.394_K_10, c complete sequence.//1.5e-09:473:60//AC006080	R-NT2RP4001725//Human Chromosome 3 pac pDJ070111, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.98:301:60//AC000380
R-NT2RP4001375	R-NT2RP4001730//Caenorhabditis elegans cosmid F48E3.//2.2e-17:328:64//U28735
R-NT2RP4001379//CIT-HSP-2335A10, TF CIT-HSP Homo sapiens genomic clone 2335A10, genomic survey sequence.//9.4e-41:441:75//AQ040083	R-NT2RP4001739//RPC111-74E7.TJ RPC111 Homo sapiens genomic clone R-74E7, genomic survey sequence.//1.1e-08:141:65//AQ268408
R-NT2RP4001389//Homo sapiens PAC clone DJ0740002 from Tpl4-p15, complete sequence.//2.4e-22:276:73//AC004691	R-NT2RP4001753//H. sapiens HZF3 mRNA for zinc finger protein.//1.7e-111:552:96//X78926
R-NT2RP4001407//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-42 0 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.49:254:61//AC005140	R-NT2RP4001760//Mouse oncogene (ect2) mRNA, complete cds.//9.3e-27:358:72//L11316
R-NT2RP4001414	R-NT2RP4001790//Homo sapiens clone GS259H13, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.7e-99:484:98//AC005020
R-NT2RP4001433//Human prohibitin (PHB) gene, exons 1-7.//6.6e-66:357:90//L14272	R-NT2RP4001803//HS_308T_B2_805_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=308T Col=10 Row=D, genomic survey sequence.//2.7e-96:471:97//AQ121405
R-NT2RP4001442//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.11:307:59//AC005308	R-NT2RP4001822
R-NT2RP4001447//cSRL-58d2-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-58d2, genomic survey sequence.//0.0039:112:71//B05220	R-NT2RP4001823
R-NT2RP4001474	R-NT2RP4001828//Human DNA sequence from PAC 179115, BRCA2 gene region chromosome 13q12-q13 contains Klotho ESTs and CpG island.//4.1e-14:136:83//Z92540
R-NT2RP4001483	R-NT2RP4001838//Plasmodium falciparum chromosome 2, section 9 of 7 3 of the complete sequence.//2.5e-06:418:60//AE001372
R-NT2RP4001498//Plasmodium falciparum (clone Dd2) heat shock protein 86 gene, complete cds.//1.2e-07:339:61//L34027	R-NT2RP4001849//P. falciparum serine rich protein (SERP 1) gene.//0.64:135:67//J03983
R-NT2RP4001502//HS_218T_B1_C10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=218T Col=19 Row=F, genomic survey sequence.//1.3e-20:183:81//AQ214108	R-NT2RP4001889//Homo sapiens PAC clone DJ1182N03 from Tq11.23-q21.1, complete sequence.//4.3e-26:212:82//AC004548
R-NT2RP4001507//Arabidopsis thaliana chromosome 1 BAC T17H3 sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.15:333:62//AC005916	R-NT2RP4001893//Homo sapiens BAC clone GS166A23 from Tp21, complete sequence.//1.8e-111:570:96//AC005014
R-NT2RP4001524//Genomic sequence from Human 13, complete sequence.//0.96:159:65//AC001226	R-NT2RP4001896
R-NT2RP4001529//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//9.5e-34:337:80//U20086	R-NT2RP4001901
R-NT2RP4001547//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00027:336:63//AC004710	R-NT2RP4001927//Borrelia burgdorferi (section 32 of 70) of the complete genome.//1.0:242:60//AE001146
R-NT2RP4001551//Arabidopsis thaliana BAC T12H20.//1.5e-11:517:60//AF080119	R-NT2RP4001938//Human aminopeptidase N gene, exon 1.//3.3e-42:195:85//M55523
R-NT2RP4001555//Human DNA sequence from PAC 481A17 on chromosome X contains ESTs.//0.0069:305:62//Z82212	R-NT2RP4001946//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.97:371:57//AC004157
R-NT2RP4001567//RPC111-61A2.TJ RPC111 Homo sapiens genomic clone R-61A2, genomic survey sequence.//0.0072:180:60//AQ200771	R-NT2RP4001950//RPC111-69C18.TJ RPC111 Homo sapiens genomic clone R-69C18, genomic survey sequence.//4.7e-91:552:89//AQ236641
R-NT2RP4001568	R-NT2RP4001953//Homo sapiens DNA sequence from PAC 958B3 on chromosome Xp22.11-Xp22.22. Contains ESTs STS and CpG island.//6.6e-70:325:84//Z93023
R-NT2RP4001571//Trypanoplasma borreli kinetoplast ribosomal protein S12 (RPS12), putative cryptogene (GR11), 12S ribosomal RNA, and apocytochrome b (Cytb) genes, primary transcripts, and cytochrome c oxidase subunit III (COIII) gene, complete cds.//1.6e-09:555:58//U14181	R-NT2RP4001966//Rat mRNA for growth potentiating factor, complete cds.//5.5e-37:141:86//D42148
R-NT2RP4001574//HS_224T_B1_805_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=224T Col=9 Row=D, genomic survey sequence.//1.1e-41:254:90//AQ182345	R-NT2RP4001975//Human Newcastle disease virus inducible protein mRNA, partial 3' UTR region.//1.0e-46:242:98//U25276
R-NT2RP4001575//Human DNA sequence from clone 1033B10 on chromosome 6p21.2-21.31. Contains the BING5 gene, exons 11 to 15 of the BIN C4 gene, the gene for GalT3 (beta3-Galactosyltransferase), the RPS18 (40S ribosomal protein S18) gene, the SACM2L (suppressor of act in mutation 2, yeast, homolog) gene, a pseudogene similar to TAT-S F1, a Pseudogene similar to zinc finger genes, the RING1 gene, the gene for HKE6 (RING2), the gene for HKE4 (RINGS), the RXRB (Retinoid X receptor beta) gene, the COL11A2 (collagen, type XI, alpha 2) gene, the HLA-DPB2 pseudogene and part of the HLA-DPA3 pseudogene. Contains predicted CpG islands, ESTs, STSs, and GSSs, complete sequence.//1.1e-118:567:98//AL031228	R-NT2RP4002018//RPC111-76123.TV RPC111 Homo sapiens genomic clone R-76123, genomic survey sequence.//7.9e-89:438:97//AQ268536
R-NT2RP4001592//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018D12, WORKING DRAFT SEQUENCE.//2.5e-09:370:61//AL031650	R-NT2RP4002047//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE.//4.1e-07:325:62//AL031297
R-NT2RP4001610//Homo sapiens Xp22 Cosmids U15E4, U115H5, U132E12; U115B9 (Lawrence Livermore human cosmid library) complete sequence.//0.99:73:75//AC002364	R-NT2RP4002052//Human DNA sequence from clone 352E11 on chromosome 22q13.1-13.31. Contains GSSs, complete sequence.//0.31:452:57//AL022353
R-NT2RP4001614	R-NT2RP4002058//RPC111-6901.TJ RPC111 Homo sapiens genomic clone R-6901, genomic survey sequence.//0.23:163:64//AQ268418
R-NT2RP4001634//Homo sapiens full length insert cDNA clone YU73B1 1.//5.8e-101:526:94//AF087969	R-NT2RP4002071//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1172A22, WORKING DRAFT SEQUENCE.//1.1e-11:407:62//AL034386
R-NT2RP4001638//Homo sapiens clone 23967 unknown mRNA, partial cds.//5.4e-115:559:91//AF007151	R-NT2RP4002075//Human DNA sequence from clone 21F7 on chromosome 6 q16.1-21. Contains part of an exon of a putative new gene and STSs and GSSs, complete sequence.//0.085:350:61//AL033375
R-NT2RP4001644//M. musculus mRNA for map kinase interacting kinase, Mnk2.//6.8e-33:286:79//Y11092	R-NT2RP4002078//RPC111-79116.TV RPC111 Homo sapiens genomic clone R-79116, genomic survey sequence.//3.3e-87:452:95//AQ283131
R-NT2RP4001656//Human Chromosome 11 pac pDJ393015, WORKING DRAFT SEQUENCE, 8 unordered pieces.//2.2e-109:515:99//AC000384	R-NT2RP4002081
R-NT2RP4001677//Genomic sequence from Human 9q34, complete sequence.//0.19:504:58//AC000397	R-NT2RP4002083//Homo sapiens mineralocorticoid receptor (MLR), exon 5.//0.50:256:61//AF068619
	R-NT2RP4002408//CIT-HSP-2376023, TF CIT-HSP Homo sapiens genomic clone 2376023, genomic survey sequence.//6.8e-62:320:96//AQ111163
	R-NT2RP4002791//Human PAC clone DJ318C15 from Xq23, complete sequence.//0.022:435:61//AC002476
	R-NT2RP4002888//Homo sapiens BAC clone RG067E13 from Tq21, complete sequence.//6.0e-56:660:71//AC002383
	R-NT2RP4002905//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-20, complete sequence.//0.0017:533:57//AL008972
	R-QVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cds.//8.7e-114:605:94//AB007934

【0822】

【表522】

R-OVARC1000004/Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//2.1e-43:326:74//AC005510
 R-OVARC1000006/Hs_2253_B1_F01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=1 Row=L, genomic survey sequence.//3.7e-35:191:98//AQ069124
 R-OVARC1000013/Hs_2212_A2_G06_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2212 Col=12 Row=M, genomic survey sequence.//0.14:212:63//AQ210584
 R-OVARC1000014/Human DNA sequence from PAC 463A9, on chromosome X q25 contains STS.//0.0053:356:62//Z80232
 R-OVARC1000017
 R-OVARC1000035/RP111-65E1.TJ RPC111 Homo sapiens genomic clone R-65E1, genomic survey sequence.//3.3e-05:236:63//AQ237194
 R-OVARC1000058/Homo sapiens DNA sequence from BAC 390C10 on chromosome 22q11.21-12.1. Contains an immunoglobulin LIKE gene and a pseudogene similar to Beta Crystallin. Contains ESTs, STSs, GSSs and tags and tat repeat polymorphisms, complete sequence.//2.7e-48:325:82//AL008721
 R-OVARC1000060/Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 27K12, WORKING DRAFT SEQUENCE.//5.0e-21:297:70//AL033397
 R-OVARC1000068/P. falciparum complete gene map of plastid-like DNA (IR-8).//0.0038:553:58//X95276
 R-OVARC1000071/Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 596C15, WORKING DRAFT SEQUENCE.//5.1e-110:599:93//AL031387
 R-OVARC1000085/DNA encoding component HCS of human proteasome.//2.7e-65:366:92//E03413
 R-OVARC1000087/CIT-HSP-2172N17.TF CIT-HSP Homo sapiens genomic clone 2172N17, genomic survey sequence.//0.80:285:59//B94391
 R-OVARC1000091
 R-OVARC1000092/CIT-HSP-2373J20.TR CIT-HSP Homo sapiens genomic clone 2373J20, genomic survey sequence.//1.4e-17:141:85//AQ111520
 R-OVARC1000106
 R-OVARC1000113/Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//2.6e-100:495:97//AF069250
 R-OVARC1000114/Homo sapiens partial XPC gene, exon 2.//9.5e-49:392:80//X71342
 R-OVARC1000133/Human Chromosome 16 BAC clone CIT987SK-A-362G6, complete sequence.//0.00020:243:65//U95740
 R-OVARC1000145/Homo sapiens chromosome 10 clone CIT987SK-1010K1 map 10q25, complete sequence.//1.8e-16:370:67//AC005385
 R-OVARC1000148/CIT-HSP-2386P14.TF.1 CIT-HSP Homo sapiens genomic clone 2386P14, genomic survey sequence.//1.1e-05:55:98//AQ240492
 R-OVARC1000151/M. musculus GEG-154 mRNA.//9.8e-21:192:81//X71642
 R-OVARC1000168/CIT-HSP-2336F6.TR CIT-HSP Homo sapiens genomic clone 2336F6, genomic survey sequence.//0.050:176:62//AQ042932
 R-OVARC1000191/Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.7e-08:534:58//AC005506
 R-OVARC1000198/Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.//6.2e-38:193:82//AC005670
 R-OVARC1000209/H. sapiens sp. 16S ribosomal RNA gene, partial sequence.//0.55:165:67//AF060350
 R-OVARC1000212/Mouse DNA for beta-casein.//0.56:225:63//X13484
 R-OVARC1000240/Homo sapiens chromosome 17, clone hRPK.63_A_1, complete sequence.//6.2e-38:193:82//AC005670
 R-OVARC1000241/Mus musculus hypoxia inducible factor three alpha mRNA, complete cds.//1.1e-25:312:73//AF060194
 R-OVARC1000288/Human HepG2 3' region Mbol cDNA, clone hmd1d01m3.//5.4e-07:128:70//D17131
 R-OVARC1000302/Homo sapiens chromosome 17, clone hRPK.651_L_9, complete sequence.//1.7e-10:100:88//AC005971
 R-OVARC1000304/Mouse mRNA from Mov10 locus.//7.9e-66:379:81//X52574
 R-OVARC1000309
 R-OVARC1000321/Homo sapiens clone MH0479C13, WORKING DRAFT SEQUENCE, 12 unordered pieces.//6.5e-83:453:94//AC005236
 R-OVARC1000326/Rattus norvegicus lamina-associated polypeptide 1C (LAP1C) mRNA, complete cds.//5.0e-58:455:81//U19614
 R-OVARC1000335/Homo sapiens chromosome 17, clone hRPK.651_L_9, complete sequence.//1.7e-10:100:88//AC005971
 R-OVARC1000347/Mus musculus HRS gene, complete cds.//4.6e-06:339:61//AF020308
 R-OVARC1000384/D. discoideum glycoprotein 24 A and B (GP24A and GP24B) genes, complete cds.//0.48:296:62//M27588
 R-OVARC1000408/Homo sapiens DNA from chromosome 19-cosmid R27740 containing MEF2B and RSRFR2 genes, genomic sequence.//9.4e-39:286:87//AD000812
 R-OVARC1000411/CIT-HSP-2303H10.TF CIT-HSP Homo sapiens genomic clone 2303H10, genomic survey sequence.//1.5e-07:94:84//AQ016720
 R-OVARC1000414/Homo sapiens genomic DNA, 21q region, clone: 149C3 X10, genomic survey sequence.//1.8e-32:296:75//AC002388
 R-OVARC1000420/Homo sapiens clone DJ1137M13, complete sequence.//2.0e-48:354:77//AC005378
 R-OVARC1000427/D. discoideum vegetative specific gene V18 gene for ribosomal protein.//2.5e-09:370:59//X15382
 R-OVARC1000431/Hs_2199_A2_E02_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2199 Col=4 Row=L, genomic survey sequence.//1.3e-34:186:98//AQ093722
 R-OVARC1000437/Gallus gallus tensin mRNA, 3' end.//1.3e-15:160:80//L06662
 R-OVARC1000440/Homo sapiens BAC clone MH0538D15 from 7q11.23-q21.1, complete sequence.//0.0054:337:61//AC006043
 R-OVARC1000442/CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.0e-45:322:86//AQ037381
 R-OVARC1000443/Homo sapiens mRNA for KIAA0683 protein, complete cds.//1.1e-77:418:94//AB014583
 R-OVARC1000461/Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 215D11, WORKING DRAFT SEQUENCE.//0.62:333:59//AL034417
 R-OVARC1000465/Bos taurus guanine nucleotide-exchange protein (ARF-GEPI) mRNA, complete cds.//1.1e-81:489:91//AF023451
 R-OVARC1000466/Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//0.0088:98:72//AC004526
 R-OVARC1000473/Homo sapiens full length insert cDNA clone Y153C1.0.//3.2e-92:317:100//AF058581
 R-OVARC1000479/Rattus norvegicus mRNA for TIP120, complete cds.//2.7e-70:502:84//D87671
 R-OVARC1000486/Dictyostelium discoideum FusC (fusC) gene, partial cds.//0.52:411:58//AF019984
 R-OVARC1000496
 R-OVARC1000520/Homo sapiens PAC clone DJ412A9 from Z2, complete sequence.//3.8e-17:294:71//AC005005
 R-OVARC1000526/Homo sapiens clone GS438P06, WORKING DRAFT SEQUENCE, 17 unordered pieces.//4.5e-109:547:96//AC005024
 R-OVARC1000533/Homo sapiens chromosome 19, cosmid R30385, complete sequence.//3.0e-46:264:93//AC004510
 R-OVARC1000543/Caenorhabditis elegans cosmid F10C1.//0.00063:417:59//U49831
 R-OVARC1000556/Homo sapiens DNA sequence from PAC 168L15 on chromosome 6q26-27. Contains RSK3 gene, ribosomal protein S6 kinase, ES T, GSS, STS, CpG island, complete sequence.//1.5e-39:144:92//AL022069
 R-OVARC1000557/Homo sapiens chromosome 19, cosmid R32469, complete sequence.//1.5e-81:429:96//AC005197
 R-OVARC1000564/Homo sapiens chromosome 17, clone HRPK837J1, complete sequence.//0.83:301:58//AC004223
 R-OVARC1000573/Homo sapiens Xq28 genomic DNA in the region of the ALD locus containing the genes for creatine transporter (SLC6A8), CDM, adrenoleukodystrophy (ALD), Na+-isocitrate dehydrogenase gamma subunit (IDH), and translocin-associated protein delta (TRAP) genes, complete cds, plexin related protein (PLEXR) and serine kinase (SK) genes, partial cds, Iq28lul gene and cytochrome C (CCp) pseudogene.//2.4e-44:300:88//U52111
 R-OVARC1000578/Human Chromosome 16 BAC clone CIT987SK-A-270G1, complete sequence.//6.4e-48:436:78//AF001549
 R-OVARC1000588/Homo sapiens chromosome 19, cosmid F19847, complete sequence.//2.7e-32:313:78//AC005952
 R-OVARC1000605
 R-OVARC1000622/Homo sapiens PAC clone DJ0942116 from 7q11, complete sequence.//6.2e-43:328:83//AC006012
 R-OVARC1000640/High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.9e-47:514:73//AC005840
 R-OVARC1000661/Homo sapiens mRNA for KIAA0590 protein, complete cds.//1.1e-29:162:100//AB011162
 R-OVARC1000678/Plasmodium falciparum 3D7 chromosome 12 PFYACB8-42 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.50:270:60//AC005140
 R-OVARC1000679/Rattus norvegicus mRNA for myosin-RhoGAP protein Myr 7.//1.4e-83:549:86//AJ001713
 R-OVARC1000681/Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 257E24, WORKING DRAFT SEQUENCE.//3.2e-13:160:76//AL034424
 R-OVARC1000689/Schistosoma americanus Antennapedia homeotic protein (Antp) mRNA, complete cds.//0.90:210:61//U32943
 R-OVARC1000700/Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//5.1e-15:133:85//AC005754

【0823】

【表523】

R-OVARC1000703//Homo sapiens chromosome 22, clone hRPC.130_H_16, c complete sequence.//6.9e-48:525:73//AC005585
R-OVARC1000730//HS_3018_B1_H10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=19 Row=P, genomic survey sequence.//0.00019:198:63//AQ093513
R-OVARC1000746//P. falciparum complete gene map of plastid-like DNA (IR-B).//0.98:154:65//X95276
R-OVARC1000769//Human coagulation factor XI gene, intron 2, partial, clone pT218R.//2.0e-30:187:78//M21185
R-OVARC1000771
R-OVARC1000781//Sequence 5 from Patent WO9722695.//8.4e-47:401:77//A63552
R-OVARC1000787//Homo sapiens PAC clone DJ430ND8 from 22q12.1-qter, complete sequence.//7.8e-111:567:96//AC004542
R-OVARC1000800//Homo sapiens mitochondrial HSP75 mRNA, complete cds.//1.3e-17:119:95//L15189
R-OVARC1000802//Homo sapiens chromosome 5, BAC clone 120c13 (LBML H171), complete sequence.//2.3e-51:482:78//AC005574
R-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CA LC.//3.6e-105:536:95//Y17111
R-OVARC1000846//Homo sapiens chromosome 16, cosmid clone 390H2 (LA ML), complete sequence.//2.7e-107:538:96//AC004494
R-OVARC1000850//Homo sapiens PB39 mRNA, complete cds.//3.6e-114:579:96//AF045584
R-OVARC1000862//M. musculus F1t mRNA.//2.3e-20:346:73//X71978
R-OVARC1000876//Plasmodium falciparum chromosome 2, section 53 of 73 of the complete sequence.//9.1e-08:427:58//AE001416
R-OVARC1000883//Mus domesticus nuclear binding factor NF2d9 mRNA, complete cds.//5.6e-34:357:78//U20086
R-OVARC1000885//Lycopodium obscurum alcohol dehydrogenase homolog (GAD3) mRNA, partial cds.//0.47:305:60//U21801
R-OVARC1000886
R-OVARC1000891//HS_3082_A2_F04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3082 Col=8 Row=K, genomic survey sequence.//1.1e-16:187:79//AQ122500
R-OVARC1000897//Human DNA sequence from clone 192P9 on chromosome Xp11.23-11.4. Contains a pseudogene similar to rat Plasmalogen, ESTs and GSSs, complete sequence.//7.2e-07:476:60//AL020989
R-OVARC1000912
R-OVARC1000915//Homo sapiens chromosome 17, clone hRPC.971_F_3, WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.4e-70:509:86//AC004150
R-OVARC1000924//Homo sapiens Chromosome 22q11.2 Cosmid Clone cosk In NF1 Region, complete sequence.//1.6e-77:465:90//AC002471
R-OVARC1000936//HS_2195_A2_C12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2195 Col=24 Row=E, genomic survey sequence.//2.4e-76:463:90//AQ191108
R-OVARC1000937//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 250D10, WORKING DRAFT SEQUENCE.//0.0028:161:65//Z99716
R-OVARC1000945//Rattus norvegicus mRNA for atypical PKC specific binding protein, complete cds.//3.5e-62:526:78//AB005549
R-OVARC1000948//Hypocistis postica NADH dehydrogenase subunit 1 (ND1) gene, partial cds, tRNA-Leu gene, complete sequence, and 16S ribosomal gene, partial sequence, mitochondrial genes encoding mitochondrial products.//0.018:212:61//U61169
R-OVARC1000959//CIT-HSP-2371K16, TR CIT-HSP Homo sapiens genomic clone 2371K16, genomic survey sequence.//1.1e-45:303:87//AQ111323
R-OVARC1000960//Homo sapiens BAC clone GS293CD5 from 7q21-q22, complete sequence.//7.5e-44:353:81//AC005021
R-OVARC1000971//H. sapiens DNA for repeat unit locus D185S1 (285 bp).//2.2e-07:223:70//X91255
R-OVARC1000984
R-OVARC1000996//Human DNA sequence from clone 272L16 on chromosome 1q32.1-32.3. Contains the 3' end of the LAMB3 gene for Laminin, B eta 3 (Niecein, Kalinin, BM600) and a novel Rat Ca2+/Calmodulin dependent Protein Kinase LIKE gene. Contains ESTs, STSs, GSSs, genomic marker D1S491 and a ca repeat polymorphism, complete sequence.//1.3e-06:179:70//AL023754
R-OVARC1000999//Homo sapiens chromosome 17, clone hCIT.457_L_16, complete sequence.//5.8e-71:332:87//AC003957
R-OVARC1001000//HS_3032_B1_G11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3032 Col=21 Row=N, genomic survey sequence.//5.1e-51:257:99//AQ096695
R-OVARC1001004//Homo sapiens from UNGC:y18c282 from 6p21, complete sequence.//5.6e-92:473:96//AC004190
R-OVARC1001010//RPC111-10P1, TV RPC1-11 Homo sapiens genomic clone RPC1-11-10P1, genomic survey sequence.//4.1e-05:201:65//B71813
R-OVARC1001011//Homo sapiens clone DJ1021120, WORKING DRAFT SEQUENCE, 6 unordered pieces.//7.9e-18:219:69//AC005520
R-OVARC1001032//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y738F9, WORKING DRAFT SEQUENCE.//2.7e-89:464:86//AL022345
R-OVARC1001034//Homo sapiens chromosome 20, BAC clone 99 (LBML H8 D), complete sequence.//1.4e-18:451:64//AC005220
R-OVARC1001038//Homo sapiens TRIAD1 type I mRNA, complete cds.//1.3e-99:501:96//AF099149
R-OVARC1001040//Homo sapiens chromosome 17, clone hRPK.1096_G_20, complete sequence.//9.7e-17:180:78//AC005410
R-OVARC1001044
R-OVARC1001051//H. sapiens mRNA for homologue to yeast ribosomal protein L41.//3.7e-15:124:88//Z12962
R-OVARC1001055//Homo sapiens, clone hRPK.15_A_1, complete sequence.//2.0e-30:292:76//AC006213
R-OVARC1001062//Sequence 65 from patent US 5691147.//2.6e-54:312:92//I76237
R-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds.//2.3e-95:463:98//AF082657
R-OVARC1001072//Gallus gallus chicken brain factor-2 (CBF-2) mRNA, complete cds.//0.92:272:59//U47276
R-OVARC1001074//HS_2205_A1_D07_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2205 Col=13 Row=C, genomic survey sequence.//1.3e-35:205:94//AQ184530
R-OVARC1001085
R-OVARC1001092//Homo sapiens mRNA for JMS protein, complete CDS (clone IMAGE 53337, LLNLc110F185707 (RZPD Berlin) and LLNLc110G0913Q7 (RZPD Berlin)).//4.5e-95:325:98//AJ005897
R-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds.//1.0e-73:386:95//AF051782
R-OVARC1001117//Homo sapiens chromosome 7 clone UNGC:g3586a160 from 7p14-15, complete sequence.//6.1e-37:314:81//AC005272
R-OVARC1001118//Homo sapiens chromosome 5, P1 clone 1195e2 (LBML H73), complete sequence.//1.5e-44:390:77//AC005372
R-OVARC1001129//Rickettsia prowazekii strain Madrid E, complete genome: segment 1/4.//0.81:461:57//AJ235270
R-OVARC1001161//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 850H21, WORKING DRAFT SEQUENCE.//4.6e-08:342:64//AL031680
R-OVARC1001162//CIT-HSP-2171J2, TR CIT-HSP Homo sapiens genomic clone 2171J2, genomic survey sequence.//5.9e-48:347:85//B89781
R-OVARC1001167//Homo sapiens clone DJ1102A12, WORKING DRAFT SEQUENCE, 15 unordered pieces.//1.3e-28:427:70//AC004963
R-OVARC1001169//RPC111-36P6, TV RPC1-11 Homo sapiens genomic clone RPC1-11-36P6, genomic survey sequence.//0.56:113:72//AQ045859
R-OVARC1001170//Homo sapiens Xp22 BAC GS-377014 (Genome Systems Human BAC library) complete sequence.//8.8e-39:301:85//AC002549
R-OVARC1001173//Human clone HS2.30 Alu-Ya5 sequence.//2.4e-35:183:83//U67213
R-OVARC1001180//Homo sapiens 12q24.1 NOVETOR P443K8 () complete sequence.//9.1e-41:516:72//AC005907
R-OVARC1001188//Homo sapiens Chromosome 11p14.3 PAC clone pDJ1034g4, complete sequence.//1.2e-14:134:85//AC004796
R-OVARC1001200//ALS-85 kDa insulin-like growth factor binding protein-3 complex acid-labile subunit [baboons, liver, mRNA Partial, 1818 nt].//0.12:345:60//S83462
R-OVARC1001237//Bovine tyrosine hydroxylase mRNA, complete cds.//0.66:257:59//M36794
R-OVARC1001240//Homo sapiens chromosome 17, clone hCIT.124_H_2, complete sequence.//1.4e-41:284:87//AC006071
R-OVARC1001243//HS_2055_B2_C01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2055 Col=2 Row=F, genomic survey sequence.//0.59:83:75//AQ243142
R-OVARC1001261//Crocodylus porosus mRNA for transthyretin.//0.93:121:66//AJ223148
R-OVARC1001268
R-OVARC1001270//Plasmodium falciparum MAL3P6, complete sequence.//0.0031:295:62//Z98551
R-OVARC1001271//Homo sapiens chromosome 16, cosmid clone 390H2 (LA ML), complete sequence.//1.6e-107:544:97//AC004494
R-OVARC1001282//Homo sapiens Xp22-39-47 PAC RPC11-199J3 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.025:402:59//AC006062
R-OVARC1001296//Homo sapiens echinoderm microtubule-associated protein homolog HuEMAP mRNA, complete cds.//1.1e-05:319:62//U97018
R-OVARC1001306//Sequence 13 from patent US 5624818.//5.4e-85:577:84//I41142
R-OVARC1001329//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30G7, WORKING DRAFT SEQUENCE.//4.2e-71:282:88//AL034402
R-OVARC1001330//Homo sapiens PAC clone DJ0697H17 from 7q11.23-q21.1, complete sequence.//0.19:256:59//AC004862
R-OVARC1001339//Homo sapiens 12q13 PAC RPC11-316M24 (Roswell Park Cancer Institute Human PAC library) complete sequence.//2.5e-49:35

【表524】

6:83//AC004242
 R-OVARC1001341//Human DNA sequence *** SEQUENCING IN PROGRESS ***
 from clone 695020, WORKING DRAFT SEQUENCE.//4.8e-26:447:69//AL032818
 R-OVARC1001342//Homo sapiens chromosome 10 clone CIT987SK-1175G20 map 10q25.2-10q25.3, complete sequence.//5.5e-86:569:86//AC005874
 R-OVARC1001344//Homo sapiens chromosome 5, BAC clone 261j17 (LBML H190), complete sequence.//2.8e-46:424:78//AC005350
 R-OVARC1001357//Sequence 1 from patent US 5597707.//3.0e-42:250:93//134297
 R-OVARC1001360//Homo sapiens chromosome 17, clone hRPK.785_0_4, complete sequence.//0.20:335:60//AC005863
 R-OVARC1001369
 R-OVARC1001372//S. scrofa DNA for myogenin 3' flanking region (285 bp).//6.9e-29:249:83//X89210
 R-OVARC1001376//Homo sapiens BAC clone RG139P11 from Tq11-q21, complete sequence.//2.1e-50:491:73//AC004491
 R-OVARC1001381//Homo sapiens chromosome 17, clone hRPK.156_L14, complete sequence.//9.3e-20:422:60//AC005821
 R-OVARC1001391
 R-OVARC1001399
 R-OVARC1001417//Homo sapiens EXLMI mRNA, complete cds.//9.9e-110:561:95//AB006651
 R-OVARC1001419//CIT-HSP-2362F16, TR CIT-HSP Homo sapiens genomic clone 2362F16, genomic survey sequence.//7.6e-47:242:98//AQ074668
 R-OVARC1001425//Homo sapiens PAC clone DJ1108A12 from 14q24.3, complete sequence.//2.3e-20:211:66//AC005157
 R-OVARC1001436//Human DNA flanking 3' end of transposon L1.1.//0.18:148:66//M80341
 R-OVARC1001442
 R-OVARC1001453//Human PAC clone DJ525N14 from Xq23, complete sequence.//2.3e-19:181:81//AC002086
 R-OVARC1001476//CITBI-E1-251786, TR CITBI-E1 Homo sapiens genomic clone 251786, genomic survey sequence.//0.24:308:59//AQ278655
 R-OVARC1001480//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 753D4, WORKING DRAFT SEQUENCE.//0.99:294:62//AL031676
 R-OVARC1001489//E. caballus microsatellite DNA marker (clone ASB32).//0.87:81:71//X93546
 R-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds.//9.3e-116:585:96//AF016507
 R-OVARC1001506//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-13 F4 complete genomic sequence, complete sequence.//2.6e-40:285:86//AC002039
 R-OVARC1001525//Homo sapiens clone RH0215P16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.0:320:59//AC006036
 R-OVARC1001542//Homo sapiens hTb mRNA, complete cds.//5.0e-110:566:95//AB016488
 R-OVARC1001547
 R-OVARC1001577//Homo sapiens SRP46 splicing factor transcribed retropseudogene.//5.9e-33:216:92//AF031165
 R-OVARC1001600//Human Chromosome X, complete sequence.//3.0e-22:157:89//AC002418
 R-OVARC1001610//HS_3070_A2_A06_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3070 Col=12 Row=A, genomic survey sequence.//0.47:107:66//AQ103523
 R-OVARC1001611//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1185M5, WORKING DRAFT SEQUENCE.//0.17:236:63//AL034423
 R-OVARC1001615//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 310013, WORKING DRAFT SEQUENCE.//1.3e-19:248:70//AL031658
 R-OVARC1001668//HS_3228_A2_E12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3228 Col=24 Row=I, genomic survey sequence.//4.6e-13:156:76//AQ188379
 R-OVARC1001702//CITBI-E1-2501P16, TR 1 CITBI-E1 Homo sapiens genomic clone 2501P16, genomic survey sequence.//1.6e-41:217:99//AQ241965
 R-OVARC1001703
 R-OVARC1001711//CITBI-E1-2502N10, TF CITBI-E1 Homo sapiens genomic clone 2502N10, genomic survey sequence.//2.0e-14:220:72//AQ266194
 R-OVARC1001726//CIT-HSP-232D01, TF CIT-HSP Homo sapiens genomic clone 232D01, genomic survey sequence.//0.021:170:62//AQ038145
 R-OVARC1001731//Human mRNA for fibroblast tropomyosin TM30 (p1).//2.5e-72:422:90//X05276
 R-OVARC1001745//Human DNA sequence from clone 796111 on chromosome 20q12. Contains ESTs, an STS and GSSs, complete sequence.//7.6e-44:314:84//AL031257
 R-OVARC1001762//S. cerevisiae N-acetyltransferase (AAA1) mRNA, complete cds.//1.6e-08:396:60//M23166
 R-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds.//3.5e-108:567:94//U97670
 R-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds.//6.3e-108:529:97//AB014575
 R-OVARC1001768//Caenorhabditis elegans cosmid Y57G11A, complete sequence.//0.24:205:64//Z99279
 R-OVARC1001791//Homo sapiens BAC clone RG118P15 from 8q21, complete sequence.//4.6e-58:558:76//AC005066
 R-OVARC1001795
 R-OVARC1001802//Human HLA class III region containing CAMP response element binding protein-related protein (CREB-RP) and tenascin X (tenascin-X) genes, complete cds, complete sequence.//1.1e-37:346:78//J89337
 R-OVARC1001805//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence.//3.0e-112:581:95//AL023694
 R-OVARC1001812//Human DNA sequence from clone 227L5 on chromosome Xp11.22-11.3. Contains a Keratin, Type 1 Cytoskeletal 18 (KRT18, CK18, K18, CK18) pseudogene and an STS, complete sequence.//6.6e-41:345:81//AL031585
 R-OVARC1001813//CITBI-E1-2508J18, TR CITBI-E1 Homo sapiens genomic clone 2508J18, genomic survey sequence.//1.6e-72:386:95//AQ263046
 R-OVARC1001820//Human PAC clone DJ525N14 from Xq23, complete sequence.//4.8e-41:320:83//AC002086
 R-OVARC1001828//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//3.4e-08:527:58//AC004688
 R-OVARC1001846//CIT-HSP-2014F15, TR CIT-HSP Homo sapiens genomic clone 2014F15, genomic survey sequence.//0.0045:165:67//B58905
 R-OVARC1001861//M. musculus mRNA for pMEM2 protein.//9.5e-28:405:68//X95350
 R-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence.//5.9e-104:571:91//AF070611
 R-OVARC1001879//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein n, first coding exon of dynamin 2 (DYNI1). ESTs, STS, GSS, CpG island, complete sequence.//9.1e-20:206:80//AL031864
 R-OVARC1001880//RPC111-42115, TJ RPC111 Homo sapiens genomic clone 42115, genomic survey sequence.//3.9e-50:287:88//AQ052700
 R-OVARC1001883//Homo sapiens chromosome 17, clone hCIT.123_J14, complete sequence.//6.1e-13:457:63//AC003950
 R-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//2.5e-86:346:90//AF061749
 R-OVARC1001901//Homo sapiens testis specific methyl-CpG binding protein MBD2 (MBD2) mRNA, partial cds.//7.2e-89:421:100//AF072246
 R-OVARC1001911//Homo sapiens full length insert cDNA clone ZD52F10.//8.2e-106:510:98//AF086315
 R-OVARC1001916
 R-OVARC1001928
 R-OVARC1001942//S. cerevisiae N-acetyltransferase (AAA1) mRNA, complete cds.//0.0013:231:63//M23166
 R-OVARC1001943//Human immunodeficiency virus type 1, strain FRMP329, envelope glycoprotein V3 region (env) gene, partial cds.//0.14:173:64//U58826
 R-OVARC1001949//Human zinc finger protein 20 (ZNF20) pentanucleotide repeat polymorphism.//1.3e-09:306:63//M99593
 R-OVARC1001950//Homo sapiens chromosome 17, clone hRPK.112_M10, complete sequence.//8.2e-38:385:75//AC005666
 R-OVARC1001987
 R-OVARC1001989//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y57G11, WORKING DRAFT SEQUENCE.//6.3e-08:355:60//Z92841
 R-OVARC1002044//Human DNA sequence from clone 681J21 on chromosome 1q23.2-24.3 Contains CpG island, complete sequence.//5.0e-42:298:86//AL031286
 R-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds.//1.4e-107:542:96//AB007934
 R-OVARC1002066//Arabidopsis thaliana chromosome 11 BAC F14M4 genomic sequence, complete sequence.//0.23:210:61//AC004411
 R-OVARC1002082//Homo sapiens clone OJ095K10, WORKING DRAFT SEQUENCE, 5 unordered pieces.//5.4e-99:546:92//AC006015
 R-OVARC1002107//Human DNA sequence from PAC 417G15 on chromosome X q25-q26. Contains glycan-3 precursor (intestinal protein OC1-5) (CTR2-2), pseudogene, ESTs.//4.4e-34:375:74//AL009174
 R-OVARC1002127
 R-OVARC1002138//CIT-HSP-2290018, TF CIT-HSP Homo sapiens genomic clone 2290018, genomic survey sequence.//2.4e-07:316:62//AQ003988
 R-OVARC1002143//RPC111-54M8, TJ RPC111 Homo sapiens genomic clone 54M8, genomic survey sequence.//2.3e-35:220:90//AQ083241
 R-OVARC1002156

【0825】

【表525】

R-OVARC1002158//CITBI-EI-251404.TF CITBI-EI Homo sapiens genomic clone 251404, genomic survey sequence.//1.6e-12:140:79//AQ265720
 R-OVARC1002165//CIT-HSP-2307C9.TF CIT-HSP Homo sapiens genomic clone 2307C9, genomic survey sequence.//5.0e-59:291:99//AQ20420
 R-OVARC1002182//P. falciparum SD17 gene for knob-associated histidine-rich protein.//0.74:161:65//Y00060
 R-PLACE1000004//D. discoideum gene for protein kinase.//0.00081:263:59//Z37981
 R-PLACE1000005//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-62 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//0.0082:477:58//AC005507
 R-PLACE1000007//Homo sapiens clone 24422 mRNA sequence.//1.2e-14:100:97//AF070557
 R-PLACE1000014//Homo sapiens genomic DNA, chromosome 21q22.2, p1 clone: T1212 and T1601, WORKING DRAFT SEQUENCE.//2.8e-44:405:77//D83253
 R-PLACE1000031//Homo sapiens clone UNGC:y23c049 from 6p21, complete sequence.//1.8e-24:291:73//AC006162
 R-PLACE1000040//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y105C5, WORKING DRAFT SEQUENCE.//0.00039:289:61//Z98855
 R-PLACE1000048//Human BAC clone RG210104, complete sequence.//4.7e-83:518:89//AC002462
 R-PLACE1000050//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.9e-73:76//AC005505
 R-PLACE1000061//Human ribosomal protein L37a mRNA sequence.//5.9e-21:125:98//L22154
 R-PLACE1000066
 R-PLACE1000078//Homo sapiens chromosome 11 clone CIT987SK-1012F4, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.2e-87:456:95//AC005848
 R-PLACE1000081
 R-PLACE1000094//RPC111-91K6.TV RPC111 Homo sapiens genomic clone 91K6, genomic survey sequence.//2.3e-83:409:98//AQ282619
 R-PLACE1000133//Homo sapiens chromosome 17, clone hRPK.746_E_8, complete sequence.//1.8e-06:420:57//AC005358
 R-PLACE1000142
 R-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds.//1.3e-112:594:94//AF058291
 R-PLACE1000185
 R-PLACE1000213//CIT-HSP-2308A18.TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey sequence.//8.2e-80:410:97//AQ022149
 R-PLACE1000214//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-09, complete sequence.//1.6e-05:548:59//AL008989
 R-PLACE1000236//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 695020, WORKING DRAFT SEQUENCE.//2.2e-16:118:91//AL032818
 R-PLACE1000246//X. laevis mRNA for XLCL2 protein.//6.5e-13:66:95//Z14122
 R-PLACE1000292//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 111822, WORKING DRAFT SEQUENCE.//6.6e-41:322:84//Z98200
 R-PLACE1000332//Homo sapiens chromosome 17, clone hCIT.281_F_24, complete sequence.//1.8e-16:598:62//AC004706
 R-PLACE1000347//Homo sapiens PAC clone DJ1090P18 from 7q21-q22, complete sequence.//2.3e-11:237:69//AC005326
 R-PLACE1000374//Arabidopsis thaliana chromosome 1 BAC F15K9 sequence, complete sequence.//8.7e-09:492:58//AC005278
 R-PLACE1000380//Plasmodium falciparum chromosome 2, section 1 of 73 of the complete sequence.//0.59:354:59//AE001364
 R-PLACE1000383//Mus musculus myotubularin related protein 1 (Mtar1) mRNA, complete cds.//0.55:65:84//AF073997
 R-PLACE1000401//Homo sapiens clone GS166C05, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.6e-17:152:83//AC005015
 R-PLACE1000406//Arabidopsis thaliana genomic DNA, chromosome 5, TA C clone: K21H1, complete sequence.//0.51:346:58//AB020742
 R-PLACE1000420//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 2/15, WORKING DRAFT SEQUENCE.//1.5e-25:243:79//AP000009
 R-PLACE1000421//HS_2251_B2_G12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2251 Col=24 Row=M, genomic survey sequence.//1.4e-82:430:95//AQ192807
 R-PLACE1000424//Human PAC clone DJ51SN1 from 22q11.2-q22, complete sequence.//1.8e-36:483:71//AC002073
 R-PLACE1000435//Homo sapiens chromosome 21q22.2 cosmid clone Q71A3, complete sequence.//2.6e-37:371:76//AF015724
 R-PLACE1000444//Homo sapiens chromosome 17, clone hRPK.227_G_15, complete sequence.//1.0e-54:429:81//AC005899
 R-PLACE1000453//Murine genomic DNA: partially digested Sau3A fragment, cloned into cosmid vector pEMBLcos2, complete sequence.//0.6e-103:72//AF059580
 R-PLACE1000481//Human DNA sequence from clone 960017 on chromosome Xp11.21-11.22 Contains EST, CA repeat (DXS991), STS, GSS, complete sequence.//0.019:171:66//AL022166
 R-PLACE1000492//Rat vacuolar protein sorting homolog r-vps33b mRNA A, complete cds.//3.2e-17:221:72//U35245
 R-PLACE1000540//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.0045:480:60//AC005308
 R-PLACE1000547//Homo sapiens chromosome 19, cosmid F17987, complete sequence.//9.6e-32:231:85//AC004790
 R-PLACE1000562//, complete sequence.//1.8e-45:280:92//AC005409
 R-PLACE1000564//Human chromosome 16 creatine transporter (SLC6A8) and (CDM) paralogous genes, complete cds.//0.0079:180:65//U41302
 R-PLACE1000583//Homo sapiens chromosome 17, clone hRPK.799_N_11, complete sequence.//1.5e-37:414:74//AC005323
 R-PLACE1000588//Human guanylate binding protein isoform 1 (GBP-2) mRNA, complete cds.//1.9e-77:542:82//M55542
 R-PLACE1000596//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.0019:482:59//AC005506
 R-PLACE1000599//Human germline T-cell receptor beta chain Dopamine-beta-hydroxylase-like, TRY1, TRY2, TRY3, TCRBV27S1P, TCRBV22S1A2 NIT, TCRBV9S1A1T, TCRBV7S1A1N2T, TCRBV5S1A1T, TCRBV13S3, TCRBV6S7P, TCRBV7S3A2T, TCRBV13S2A1T, TCRBV9S2A2PT, TCRBV7S2A1N4T, TCRBV13S9/13S2A1T, TCRBV6S5A1N1, TCRBV30S1P, TCRBV31S1, TCRBV13S5, TCRBV6S1A1N1, TCRBV32S1P, TCRBV5S5P, TCRBV1S1A1N1, TCRBV12S2A1T, TCRBV21S1, TCRBV8S4P, TCRBV12S3, TCRBV21S3A2N2T, TCRBV8S5P, TCRBV13S1 genes from bases 1 to 267156 (section 1 of 3).//5.6e-51:369:85//U66059
 R-PLACE1000610//HS_3071_A1_C05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=9 Row=E, genomic survey sequence.//0.051:147:65//AQ103341
 R-PLACE1000636//HS_3220_B2_E09_TT CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3220 Col=18 Row=J, genomic survey sequence.//0.010:253:64//AQ181157
 R-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//1.6e-99:506:96//AF102265
 R-PLACE1000656//Homo sapiens mRNA for JMA protein, complete CDS (clone IMAGE 546750 and LLNLc110F1857Q7 (RZPD Berlin)).//4.5e-101:559:92//AJ005896
 R-PLACE1000706//nuclear protein TIF1 [mice, mRNA, 3951 nt].//9.1e-10:331:63//S78219
 R-PLACE1000712//Homo sapiens full length insert cDNA clone ZD76G1 0.//1.0e-69:345:98//AF086408
 R-PLACE1000716//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-27 9B10, complete sequence.//1.0:174:62//AC002300
 R-PLACE1000748//Plasmodium falciparum MAL3P3, complete sequence.//1.0e-06:337:60//Z98547
 R-PLACE1000749//cSRL-15g9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-15g9, genomic survey sequence.//8.8e-26:236:80//B02791
 R-PLACE1000755//HS_2183_B1_H11_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=21 Row=P, genomic survey sequence.//0.47:151:65//AQ064202
 R-PLACE1000769//Homo sapiens clone DJ0647J21, WORKING DRAFT SEQUENCE, 10 unordered pieces.//7.0e-38:492:74//AC004847
 R-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//2.6e-101:513:96//AB014548
 R-PLACE1000786//Human putative outer mitochondrial membrane 34 kDa translocase hTOM34 mRNA, complete cds.//0.078:180:68//U58970
 R-PLACE1000793
 R-PLACE1000798//Homo sapiens cosmid D66B10, chromosome 21 5' of IF NARI.//5.1e-26:348:72//AF039904
 R-PLACE1000841//Human guanine nucleotide regulatory protein (NET1) mRNA, complete cds.//1.4e-26:110:95//U02081
 R-PLACE1000849//Homo sapiens full length insert cDNA clone Z05501 0.//1.4e-13:93:96//AF086334
 R-PLACE1000856//Anopheles quadrimaculatus NADH dehydrogenase subunits (1-4, 4L, 5-6): cytochrome oxidase subunits (1-3): adenosine triphosphatase subunits (6,8): cytochrome b: transfer RNA: ribosomal RNA (large and small subunits).//2.7e-09:484:59//L04272
 R-PLACE1000863
 R-PLACE1000909//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//3.0e-05:274:60//AC005505
 R-PLACE1000931//RPC111-66P7.TK RPC111 Homo sapiens genomic clone 66P7, genomic survey sequence.//3.4e-73:369:97//AQ237489
 R-PLACE1000948//RPC111-64K15.TK RPC111 Homo sapiens genomic clone

【0826】

【表526】

R-64K15, genomic survey sequence.//6.6e-05:258:62//AQ239337
 R-PLACE1000972//Homo sapiens chromosome 17, clone hRPK.112_J_9, complete sequence.//8.3e-20:223:76//AC005553
 R-PLACE1000977//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.00030:448:59//AC005506
 R-PLACE1000979
 R-PLACE1001000//CIT-HSP-229718.TF CIT-HSP Homo sapiens genomic clone 229718, genomic survey sequence.//7.0e-07:54:95//AQ04997
 R-PLACE1001007//Human endothelial nitric oxide synthase gene, complete cds.//0.0078:215:64//D26607
 R-PLACE1001010
 R-PLACE1001015//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 150C2, WORKING DRAFT SEQUENCE.//1.5e-16:452:63//AL022318
 R-PLACE1001024//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 417M14, WORKING DRAFT SEQUENCE.//0.99:186:63//AL024498
 R-PLACE1001036//Homo sapiens clone DJ1136G02, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.5e-15:313:68//AC005377
 R-PLACE1001062//Homo sapiens chromosome 17, clone hC1T54K19, complete sequence.//7.3e-16:119:84//AC003654
 R-PLACE1001076
 R-PLACE1001088//Human DNA sequence from cosmid 203C2, between markers DXS6791 and DXS8038 on chromosome X contains ESTs.//0.97:332:59//Z74696
 R-PLACE1001092//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.2e-07:302:62//AC005139
 R-PLACE1001104//Plasmodium falciparum chromosome 2, section 9 of 73 of the complete sequence.//0.057:280:60//AE001372
 R-PLACE1001118//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.//4.9e-06:334:60//Z84480
 R-PLACE1001136//Homo sapiens chromosome 17, clone hRPK.22_M_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//1.1e-31:331:75//AC005412
 R-PLACE1001168//HS_2036_A1_H04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2036 Col=7 Row=0, genomic survey sequence.//0.40:144:63//AQ230662
 R-PLACE1001171
 R-PLACE1001185
 R-PLACE1001238//Human coxVib gene, last exon and flanking sequence.//3.4e-36:349:76//X58139
 R-PLACE1001241//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-20, complete sequence.//0.11:258:61//AL008972
 R-PLACE1001257//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone B4P3: HTGS phase 1, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.9e-46:484:73//AC000016
 R-PLACE1001272//Homo sapiens chromosome 21q22.3 PAC 191P10, complete sequence.//0.89:119:65//AF045448
 R-PLACE1001279//Caenorhabditis elegans cosmid Y39A1C, complete sequence.//0.99:95:69//AL023839
 R-PLACE1001280//CIT-HSP-2328824.TF CIT-HSP Homo sapiens genomic clone 2328824, genomic survey sequence.//5.4e-24:147:76//AQ042129
 R-PLACE1001294//M.musculus GEG-154 mRNA.//1.3e-22:472:65//X71642
 R-PLACE1001304//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//2.2e-22:139:77//AC003682
 R-PLACE1001311//Loligo pealei repeat region.//0.84:232:64//Z18286
 R-PLACE1001323//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.//7.2e-39:308:83//Z84480
 R-PLACE1001351//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y39B6, WORKING DRAFT SEQUENCE.//0.0018:408:59//Z95399
 R-PLACE1001366//Human Na+/phosphate co-transporter gene, exon 1, partial sequence.//2.2e-46:369:82//D89927
 R-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds.//7.1e-80:431:93//AF009615
 R-PLACE1001383//Homo sapiens clone 24538 mRNA sequence.//3.6e-35:192:97//AF055030
 R-PLACE1001384//Homo sapiens mRNA for multi PDZ domain protein.//2.6e-86:456:94//AJ001319
 R-PLACE1001387
 R-PLACE1001395//Nyctalus leisleri mitochondrial D-loop, partial sequence.//0.054:148:68//U95355
 R-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22_M_12, WORKING DRAFT SEQUENCE, 2 ordered pieces.//6.7e-70:352:98//AC005412
 R-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence.//8.0e-44:242:95//AF091087
 R-PLACE1001414//Homo sapiens chromosome 9, clone hRPK.202_H_3, complete sequence.//0.12:53:84//AC006241
 R-PLACE1001440//Homo sapiens Xq28 genomic DNA in the region of the ALD locus containing the genes for creatine transporter (SLC6A8), CDM, adrenoleukodystrophy (ALD), Na+-isocitrate dehydrogenase gamma subunit (IDH), and translocan-associated protein delta (TRAP) genes, complete cds, plexin related protein (PLEXR) and serine kinase (SK) genes, partial cds, Xq28lul gene and cytochrome C (CCp) pseudogene.//1.0:250:61//U52111
 R-PLACE1001456//Borrelia burgdorferi (section 16 of 70) of the complete genome.//0.0077:173:62//AE001130
 R-PLACE1001468//HS_3050_A2_D07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3050 Col=14 Row=G, genomic survey sequence.//0.00023:202:65//AQ133920
 R-PLACE1001484//Homo sapiens Xq28 BAC PAC and cosmid clones containing FMR2 gene exons 1, 2, and 3, complete sequence.//7.2e-17:180:80//AC002368
 R-PLACE1001502//RPC111-24F2.TP RPC1-11 Homo sapiens genomic clone RPC1-11-24F2, genomic survey sequence.//0.15:203:66//B84401
 R-PLACE1001503//HS_2183_A1_B10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2183 Col=19 Row=C, genomic survey sequence.//1.3e-38:181:82//AQ022613
 R-PLACE1001517//Homo sapiens hGA1 mRNA, complete cds.//6.4e-56:339:90//AB006969
 R-PLACE1001534//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 620E11, WORKING DRAFT SEQUENCE.//8.6e-59:304:97//AL031667
 R-PLACE1001545//Homo sapiens chromosome 3, clone hRPK.165_L_16, complete sequence.//2.6e-18:171:82//AC005669
 R-PLACE1001551
 R-PLACE1001570//M.capricolum DNA for CONTIG MC188.//0.0043:305:57//Z33135
 R-PLACE1001602//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 3/11.//2.5e-82:408:98//AB020860
 R-PLACE1001603//Homo sapiens KED5 protein mRNA, complete cds.//1.5e-40:295:84//AF064605
 R-PLACE1001610//Homo sapiens clone NH0469807, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.5e-39:307:82//AC005037
 R-PLACE1001611//Homo sapiens histone macroH2A1.2 mRNA, complete cds.//4.9e-41:217:97//AF054174
 R-PLACE1001632//Human DNA binding protein (HPF2) mRNA, complete cds.//1.4e-08:178:65//M72787
 R-PLACE1001634//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone H06C16, WORKING DRAFT SEQUENCE.//0.00026:221:62//Z92791
 R-PLACE1001640//Homo sapiens chromosome 17, clone hRPK.651_L_9, complete sequence.//2.6e-83:441:95//AC005971
 R-PLACE1001672//H. sapiens flow-sorted chromosome 6 TaqI fragment, SC6pA26H8.//0.91:115:69//Z79253
 R-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (O448-18) mRNA, complete cds.//1.5e-111:545:97//AF069250
 R-PLACE1001692//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.0e-46:478:75//AC005077
 R-PLACE1001705//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 250D10, WORKING DRAFT SEQUENCE.//0.79:91:73//Z99716
 R-PLACE1001716//Homo sapiens Xp22 PAC RPC11-167A22 (from Roswell Park Cancer Center) complete sequence.//0.96:172:66//AC002349
 R-PLACE1001720
 R-PLACE1001729//Human interleukin-13 (IL-13) precursor gene, complete cds.//0.79:280:60//U31120
 R-PLACE1001739//Homo sapiens chromosome 19, CIT-HSP-444n24, complete sequence.//1.0:109:65//AC005261
 R-PLACE1001740//Homo sapiens BAC clone GS114109 from 7p14-p15, complete sequence.//5.3e-11:249:67//AC006027
 R-PLACE1001745
 R-PLACE1001746//Homo sapiens chromosome 4 clone B200N5 map 4q25, complete sequence.//6.0e-05:337:61//AC005509
 R-PLACE1001748//Homo sapiens retinol protease 1 (MP1) mRNA, complete cds.//1.3e-91:540:89//AF061243
 R-PLACE1001756//Human BAC clone RG302F04 from 7q31, complete sequence.//0.074:344:62//AC002463
 R-PLACE1001761
 R-PLACE1001771//Homo sapiens full length insert cDNA clone ZD79C1.//4.4e-57:298:96//AF086426
 R-PLACE1001781//T. thermophila micronuclear DNA containing to chromosomal breakage sequence Cbs-1, clone Tt819.//4.6e-05:282:61//M15711
 R-PLACE1001799//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 g

【0827】

【表527】

enomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.015:331:58//AC004710

R-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//4.1e-92:463:95//AF058953

R-PLACE1001821//Homo sapiens Alu-J subfamily consensus sequence.//3.6e-36:281:82//U14567

R-PLACE1001845//Mus musculus Paneth cell enhanced expression PCEE mRNA, complete cds.//9.1e-26:313:73//U37351

R-PLACE1001869

R-PLACE1001897//Mus musculus homeobox protein (Dlx5) mRNA, complete cds.//0.0043:207:64//AF033011

R-PLACE1001912//RPC111-25F23.TKBR RPC1-11 Homo sapiens genomic clone RPC1-11-25F23, genomic survey sequence.//6.3e-33:248:67//AQ013567

R-PLACE1001920//Homo sapiens TNF-induced protein CG2-1 mRNA, complete cds.//5.0e-73:363:98//AF070671

R-PLACE1001928//Homo sapiens chromosome 17, clone hRPK.642_C_21, complete sequence.//0.98:248:60//AC005245

R-PLACE1001983//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y40H7, WORKING DRAFT SEQUENCE.//0.12:157:61//AL021389

R-PLACE1001989//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D23, genomic survey sequence.//1.4e-44:376:80//AL023755

R-PLACE1002046//CITB1-E1-2520J24.TF CITB1-E1 Homo sapiens genomic clone 2520J24, genomic survey sequence.//4.5e-20:144:89//AQ280117

R-PLACE1002052//Human DNA sequence from cosmid U160A4, between markers DXS366 and DXS87 on chromosome X contains STS.//0.025:362:57//Z80900

R-PLACE1002066//Leishmania tarentolae maxicircle DNA fragment.//0.0034:197:62//X02438

R-PLACE1002072//Homo sapiens chromosome 5, P1 clone 854b11 (LBML H44), complete sequence.//9.7e-06:414:60//AC004763

R-PLACE1002073

R-PLACE1002090//Homo sapiens Chromosome 16 BAC clone CIT987-SKA-34 SG4, complete genomic sequence, complete sequence.//1.8e-06:278:63//AC002302

R-PLACE1002115//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y214H10, WORKING DRAFT SEQUENCE.//6.0e-12:327:64//AL002344

R-PLACE1002119//Mus musculus IER5 (Ier5) mRNA, complete cds.//5.1e-67:442:86//AF079527

R-PLACE1002140//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCLRL gene for Lowe Oculocerebrorenal Syndrome protein OCLRL-1. Contains ESTs, STSs and GSSs, complete sequence.//2.2e-80:403:97//AL022162

R-PLACE1002150//Human DNA sequence from PAC 145B12 on chromosome X q27-q28. Contains EST, CA repeat and STS.//0.043:455:59//AL008706

R-PLACE1002157//Human DNA sequence from Fosmid 6587 on chromosome 22q11.2-qter. Contains exons 6-12 of the SLC6A1 (SGLT1) gene for solute carrier family 5 (sodium/glucose cotransporter) member 1 (High Affinity Sodium-Glucose Cotransporter), complete sequence.//9.8e-58:384:79//Z83849

R-PLACE1002163//Canis familiaris MHC class IIA DLA-DQA (DQA 1 allele) gene, exon 2, partial cds.//0.82:96:70//U44785

R-PLACE1002171//Homo sapiens PAC clone DJ1100F23 from 7q31, complete sequence.//0.83:196:65//AC004456

R-PLACE1002205//Human DNA sequence from PAC 436M11 on chromosome X p22.11-22.2. Contains the serine threonine protein phosphatase gene PPEF1, and the first coding exon of the RSI gene for retinoschisis (X-linked, juvenile) 1 (XLRSI). Contains ESTs, an STS and GSSs, complete sequence.//0.0017:193:61//Z94056

R-PLACE1002213//Homo sapiens chromosome 19, fosmid 37308, complete sequence.//8.0e-42:330:81//AC004152

R-PLACE1002227//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//2.1e-10:126:80//AC003071

R-PLACE1002256//Homo sapiens clone DJ0853H20, WORKING DRAFT SEQUENCE, 5 unordered pieces.//2.7e-06:478:57//AC004907

R-PLACE1002259//Human DNA sequence from cosmid U75A4 on chromosome X.//6.5e-81:501:88//Z82255

R-PLACE1002319//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0023:549:58//AC005505

R-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds.//4.9e-94:501:93//AB018271

R-PLACE1002395//Homo sapiens chromosome 19, cosmid R34382, complete sequence.//1.4e-69:385:93//AC005329

R-PLACE1002399//Human HepG2 3' region cDNA, clone hmd5d06.//2.4e-71:411:92//D16939

R-PLACE1002433//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 173D1, WORKING DRAFT SEQUENCE.//0.85:176:63//AL031984

R-PLACE1002437//Human BAC clone RG114A06 from 7q31, complete sequence.//0.0040:213:63//AC002542

R-PLACE1002438//CITB1-E1-2501M20.TF.1 CITB1-E1 Homo sapiens genomic clone 2501M20, genomic survey sequence.//0.70:247:61//AQ242104

R-PLACE1002450//Homo sapiens 959 kb contig between AML1 and CBR1 on chromosome 21q22: segment 1/3.//0.00060:471:59//AJ229041

R-PLACE1002465//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//2.5e-10:98:81//AC004854

R-PLACE1002474//Mus musculus matrilin-2 precursor mRNA, complete cds.//1.7e-25:199:71//U69262

R-PLACE1002477//Human DNA sequence from PAC 50A13 on chromosome Xp 11. Contains ATP SYNTHASE LIPID BINDING PROTEIN P1 (P2, P3) precursor (ATP5G1, ATP5G2, ATP5G3) like pseudogene, ESTs and STSs. Contains polymorphic CA repeat.//1.2e-11:382:63//Z92545

R-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2 A (STAM2) mRNA, complete cds.//1.1e-53:307:91//AF042273

R-PLACE1002499//Plasmodium falciparum MAL3P6, complete sequence.//0.56:270:60//Z98551

R-PLACE1002500//CIT-HSP-2337C20.TR CIT-HSP Homo sapiens genomic clone 2337C20, genomic survey sequence.//3.2e-42:297:85//AQ037614

R-PLACE1002514//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 212A2, WORKING DRAFT SEQUENCE.//7.8e-16:221:73//Z95114

R-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//1.6e-86:582:85//AB018256

R-PLACE1002532//Homo sapiens BAC clone RG300E22 from 7q21-q31.1, complete sequence.//9.0e-91:453:97//AC004774

R-PLACE1002537//Hansenula wingei mitochondrial gene for NADH dehydrogenase subunit 5, complete cds.//0.0042:489:60//D16253

R-PLACE1002571//Apis mellifera ligustica complete mitochondrial genome.//0.034:493:55//L06178

R-PLACE1002578//Homo sapiens chromosome 5, Pac clone 9c13 (LBML HI 27), complete sequence.//2.5e-44:292:84//AC006084

R-PLACE1002583//Homo sapiens wbscr1 (WBSR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//3.1e-17:517:61//AF045555

R-PLACE1002591

R-PLACE1002598//Caenorhabditis elegans cosmid Y37D8A, complete sequence.//0.080:308:60//AL032626

R-PLACE1002604//Human cosmid LL12MC01-88A9, ETV6 gene, exons 6, 7 and 8 and partial cds.//0.0013:176:65//U63313

R-PLACE1002625//HS_2233_B2_H04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2233 Col=8 Row=P, genomic survey sequence.//5.2e-13:137:79//AQ146663

R-PLACE1002665//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//5.8e-45:272:94//AF079765

R-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//1.2e-77:390:97//AF068180

R-PLACE1002714//Mus musculus clone OST2473, genomic survey sequence.//1.3e-35:328:78//AF046656

R-PLACE1002722//Sequence 1 from patent US 5686597.//1.7e-42:276:89//I173723

R-PLACE1002768//Homo sapiens Xp22 bins 169-171 BAC G5HB-383H3 (Genome Systems Human BAC Library) complete sequence.//0.0098:197:64//AC005185

R-PLACE1002772//Homo sapiens PAC clone DJ0560014 from 7q21.1-q21.2, complete sequence.//6.7e-49:378:82//AC006145

R-PLACE1002782

R-PLACE1002794

R-PLACE1002811//CIT-HSP-2316H11.TF CIT-HSP Homo sapiens genomic clone 2316H11, genomic survey sequence.//6.0e-50:250:100//AQ034981

R-PLACE1002815//Sequence 2 from patent US 5747660.//2.7e-59:312:84//AR005279

R-PLACE1002816//Homo sapiens 12q13.1 PAC RPC15-1057120 (Roswell Park Cancer Institute Human PAC library) complete sequence.//6.3e-59:339:93//AC004466

R-PLACE1002834//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//1.4e-78:413:95//M27877

R-PLACE1002839//Homo sapiens PAC clone DJ0015123 from 22, complete sequence.//6.5e-25:301:74//AC004819

R-PLACE1002851//CIT-HSP-2317M9.TR CIT-HSP Homo sapiens genomic clone 2317M9, genomic survey sequence.//0.0011:210:61//AQ040519

R-PLACE1002853//Human interleukin 6 (IL6) gene, 3' flank.//5.8e-06:327:61//J03049

R-PLACE1002881

R-PLACE1002908//HS_3064_A1_004_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3064 Col=7 Row=C, genomic survey sequence.//1.9e-09:156:72//AQ142985

R-PLACE1002941

R-PLACE1002962

【0828】

【表528】

R-PLACE1002968//Human DNA sequence from clone 109F14 on chromosome 6p21.2-21.3. Contains the alternatively spliced gene for Transcriptional Enhancer Factor TEF-5, the 60S Ribosomal Protein RPL10A gene, a PUTATIVE ZNF127 LIKE gene, and the PPAR for Peroxisome Proliferator Activated Receptor Delta (PPAR-Delta, PPAR-Beta, Nuclear Hormone Receptor 1, NUC1, NUC1, PPARB). Contains three putative CpG islands, ESTs, STSs, GSSs and a ca repeat polymorphism, complete sequence.//1.9e-32:314:77//AL022721

R-PLACE1002991//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 968D22, WORKING DRAFT SEQUENCE.//1.6e-42:343:81//AL023755

R-PLACE1002993//Homo sapiens PAC clone DJ0899E09 from 7q11.23-q21.1, complete sequence.//0.56:88:72//AC004921

R-PLACE1002996//HS_2064_A1_A05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2064 Col=9 Row=A, genomic survey sequence.//4.9e-18:117:95//AQ243211

R-PLACE1003025//Homo sapiens PAC clone DJ0560014 from 7q21.1-q21.2, complete sequence.//0.26:428:56//AC006145

R-PLACE1003027//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence.//1.3e-95:465:98//AC005920

R-PLACE1003044

R-PLACE1003092//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-89, complete sequence.//3.6e-05:358:60//AL010266

R-PLACE1003100//HS_2244_A2_H12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2244 Col=24 Row=0, genomic survey sequence.//2.3e-42:288:86//AQ084224

R-PLACE1003108//Homo sapiens clone DJ0781A18, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.00066:233:61//AC004885

R-PLACE1003136//Plasmodium falciparum MAL3P2, complete sequence.//0.019:429:57//AL034558

R-PLACE1003145

R-PLACE1003153//Homo sapiens Xp22 BAC GSHB-S36K7 (Genome Systems Human BAC library) complete sequence.//3.2e-05:390:58//AC004616

R-PLACE1003174//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTE17, complete sequence.//2.4e-06:390:60//AB015479

R-PLACE1003176

R-PLACE1003190//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENCE, 1 unordered pieces.//4.0e-78:406:81//AC005095

R-PLACE1003200//Plasmodium falciparum MAL3P6, complete sequence.//0.016:411:57//Z98551

R-PLACE1003205//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00084:288:61//AC005139

R-PLACE1003238//Homo sapiens full length insert cDNA clone ZD79H1.1.//7.6e-114:567:96//AF086432

R-PLACE1003249//Human Chromosome X, complete sequence.//1.3e-45:317:85//AC002416

R-PLACE1003256//Homo sapiens chromosome 17, clone HClT421K24, complete sequence.//1.0e-45:328:85//AC004099

R-PLACE1003258

R-PLACE1003296//Diphtheria sp. 16S ribosomal RNA gene, mitochondrial gene encoding mitochondrial rRNA, partial sequence.//0.050:228:59//U39952

R-PLACE1003302//Figure 2. Nucleotide and translated protein sequences of HPF1, -2, and -9.//1.7e-91:458:96//M27877

R-PLACE1003334//Homo sapiens DNA sequence from BAC 217C2 on chromosome 22q13-q13.33. Contains a gene for the presumptive isolog of Rat RTP60 (nuclear pore complex protein Npap60). Contains ESTs, complete sequence.//4.3e-34:370:71//Z82243

R-PLACE1003342//CIT-HSP-2311D21.TF CIT-HSP Homo sapiens genomic clone 2311D21, genomic survey sequence.//1.0:159:68//AQ020460

R-PLACE1003343//Plasmodium falciparum 3D7 chromosome 12 PFYACB12 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//1.1e-05:330:61//AC004153

R-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//3.4e-98:469:98//U92715

R-PLACE1003361

R-PLACE1003366//Homo sapiens CAG repeated sequence.//0.018:319:61//AJ006805

R-PLACE1003369//T18H17-T7 TAMU Arabidopsis thaliana genomic clone T18H17, genomic survey sequence.//0.050:155:63//B20174

R-PLACE1003373//Homo sapiens chromosome 17, clone hRPC.1050_D_4, complete sequence.//1.2e-62:434:83//AC004771

R-PLACE1003375//Dictyostelium discoideum golvesin (gol) gene, complete cds.//0.042:263:57//U89350

R-PLACE1003383//Homo sapiens genomic DNA of 9q32 anti-oncogene of flat epithelium cancer, segment 10/10.//1.7e-83:429:96//AB020878

R-PLACE1003401//Homo sapiens chromosome 17, clone hRPK.85_B_7, complete sequence.//2.4e-13:175:76//AC005695

R-PLACE1003420//Homo sapiens PAC clone DJ0988G15 from 7q33-q35, complete sequence.//2.1e-05:340:61//AC005587

R-PLACE1003454//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-64, complete sequence.//0.47:411:58//AL009014

R-PLACE1003478//M.capricolum DNA for CONTIG MC175.//0.51:253:59//Z33125

R-PLACE1003493//Homo sapiens chromosome 17, clone hRPK.394_K_10, complete sequence.//4.6e-37:319:81//AC006080

R-PLACE1003516//CIT-HSP-2295M19.TF CIT-HSP Homo sapiens genomic clone 2295M19, genomic survey sequence.//1.0e-40:251:90//AQ007480

R-PLACE1003519//Homo sapiens chromosome 21q22.3 PAC 141B3, complete sequence, containing ribosomal protein homologue pseudogene L23a.//2.7e-29:163:89//AF064859

R-PLACE1003521//HS_3252_A2_G05_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3252 Col=10 Row=M, genomic survey sequence.//0.00017:274:60//AQ221562

R-PLACE1003528//HS_2041_B1_B07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2041 Col=13 Row=D, genomic survey sequence.//6.6e-40:219:83//AQ230483

R-PLACE1003537//Drosophila melanogaster mitochondrial cytochrome c oxidase subunits, ATPase6, 7 tRNAs (Trp, Cys, Tyr, Leu(UUR), Lys, Asp, Gly) genes, and unidentified reading frames A61. 2 and 3.//8.3e-05:300:61//J01404

R-PLACE1003553//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE.//2.7e-87:450:96//AL031297

R-PLACE1003566

R-PLACE1003575//Homo sapiens chromosome 16, cosmid clone 325D7, complete sequence.//4.7e-20:148:78//AC003965

R-PLACE1003583//Human DNA sequence from PAC 38B15 on chromosome X q21.1.//3.5e-18:287:68//Z99571

R-PLACE1003584

R-PLACE1003592//Homo sapiens cosmid 223D9 from Xq28, complete sequence.//2.5e-10:153:73//AF061032

R-PLACE1003593//Human BAC clone RG030H15 from 7q31, complete sequence.//6.9e-07:240:65//AC002066

R-PLACE1003596//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y87G2, WORKING DRAFT SEQUENCE.//0.13:393:60//AL022597

R-PLACE1003602//Homo sapiens mRNA expressed in placenta.//2.4e-95:576:88//D83200

R-PLACE1003605//Homo sapiens BAC clone RG331C24 from 7q21, complete sequence.//2.9e-19:302:71//AC002081

R-PLACE1003611

R-PLACE1003618//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 191E19, WORKING DRAFT SEQUENCE.//8.3e-57:469:80//AL034451

R-PLACE1003625//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//2.1e-05:339:62//AC004688

R-PLACE1003638//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1104E15, WORKING DRAFT SEQUENCE.//2.5e-38:279:84//AL022312

R-PLACE1003669//HS_3054_A2_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3054 Col=14 Row=1, genomic survey sequence.//0.014:265:61//AQ132713

R-PLACE1003704//HS_3213_A1_D12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3213 Col=23 Row=C, genomic survey sequence.//0.80:195:61//AQ176784

R-PLACE1003709//Human BAC clone RG126M09 from 7q21-q22, complete sequence.//0.018:152:61//AC002067

R-PLACE1003711//Human endothelial nitric oxide synthase gene, complete cds.//1.7e-61:366:89//D26607

R-PLACE1003723//Homo sapiens DNA sequence from clone 78F24 on chromosome 22q12.1-12.3. Contains one exon of an Oxysterol-binding protein (OSBP) LIKE gene. Contains GSSs and an STS, complete sequence.//2.7e-44:505:73//AL022336

R-PLACE1003738//H. sapiens DNA sequence.//0.93:185:60//Z22357

R-PLACE1003760//Human globin gene.//5.9e-97:538:91//M69023

R-PLACE1003762//Homo sapiens chromosome 17, clone HClT339C8, complete sequence.//4.6e-13:134:79//AC003070

R-PLACE1003768//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence.//5.4e-12:189:71//AC005919

R-PLACE1003771//Homo sapiens BAC clone GS164B05 from 7p21-p22, complete sequence.//1.7e-119:619:95//AC004160

R-PLACE1003783

R-PLACE1003784//Homo sapiens chromosome 19, CIT-HSP-87a17 BAC clone, complete sequence.//5.6e-15:204:74//AC004659

R-PLACE1003795//CIT-HSP-2374C8.TR CIT-HSP Homo sapiens genomic clone 2374C8, genomic survey sequence.//7.0e-37:234:89//AQ114933

【表529】

R-PLACE1003833//Homo sapiens full length insert cDNA clone ZE15C0 5.//4.4e-59:313:95//AF086558	R-PLACE1004384//CIT-HSP-2316J11.TF CIT-HSP Homo sapiens genomic cl one 2316J11, genomic survey sequence.//0.035:109:69//AQ037817
R-PLACE1003850	R-PLACE1004388//Plasmodium falciparum DNA *** SEQUENCING IN PROGRE SS *** from contig 3-82, complete sequence.//4.2e-06:381.60//AL010 149
R-PLACE1003858	R-PLACE1004405//Homo sapiens clone G5512121, WORKING DRAFT SEQUENC E, 9 unordered pieces.//0.20:270:60//AC005027
R-PLACE1003864	R-PLACE1004425//Homo sapiens PAC clone DJ0733809 from 7p14-p13, co mplete sequence.//1.3e-96:516:94//AC005532
R-PLACE1003870//Homo sapiens Chromosome 22q11.2 Cosmid Clone 15a10 in DGCR Region, complete sequence.//8.7e-33:285:81//AC000072	R-PLACE1004428//Human DNA sequence from clone 888M10 on chromosome 1p36.11-36.31 Contains part of gene KIAA0453, EST, STS, GSS, comp lete sequence.//5.8e-10:279:65//AL031296
R-PLACE1003885	R-PLACE1004437//Human NAD+ specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial prote in, complete cds.//2.9e-88:516:88//U49283
R-PLACE1003886	R-PLACE1004451//HS_2258_B2_F01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2258 Col=2 Row=L, geno mic survey sequence.//0.82:172:61//AQ221189
R-PLACE1003888//Homo sapiens chromosome 4 clone B71M12 map 4q25, c omplete sequence.//0.73:127:65//AC004069	R-PLACE1004460
R-PLACE1003900//Homo sapiens ADP/ATP carrier protein (ANT-2) gene, complete cds.//1.9e-05:239:59//L78810	R-PLACE1004467//Syrian hamster carbamoylphosphate synthetase-aspar tate transcarbamylase-dihydroorotase (CAD) gene, exons 1 and 2.// 1.2e-24:311:62//M31621
R-PLACE1003903//Homo sapiens full length insert cDNA clone ZD78D1 1.//8.1e-74:369:97//AF086422	R-PLACE1004471//Homo Sapiens Chromosome X clone bWXD75, complete s equence.//2.1e-34:333:70//AC004389
R-PLACE1003915//Mus musculus bone morphogenetic protein-6 (BMP-6) gene, exons 6 and 7 and complete cds.//0.56:247:61//U73520	R-PLACE1004473
R-PLACE1003923//Caenorhabditis elegans cosmid Y57G11C, complete se quence.//0.67:213:63//Z99281	R-PLACE1004491//Drosophila melanogaster Oregon-R mitochondrial A+T region.//1.0e-08:485:60//U11584
R-PLACE1003932//Human DNA sequence from cosmid U90B3, on chromosom e Xp11, contains ESTs.//8.7e-49:342:85//Z74022	R-PLACE1004506
R-PLACE1003936//H. sapiens gene for ventricular myosin light chain 2.//2.6e-09:394:61//Z15030	R-PLACE1004510//Plasmodium falciparum chromosome 2, section 64 of 73 of the complete sequence.//0.0094:543:56//AE001427
R-PLACE1003968//Plasmodium falciparum DNA *** SEQUENCING IN PROGRE SS *** from contig 4-62, complete sequence.//1.3e-07:245:65//AL010 247	R-PLACE1004516//Homo sapiens BAC clone BK085E05 from 22q12.1-qter, complete sequence.//0.00011:343:59//AC003071
R-PLACE1004104	R-PLACE1004518
R-PLACE1004114//Human PAC clone RG212D03, complete sequence.//5.0 e-07:336:61//AC002485	R-PLACE1004548//Homo sapiens Xp22 BAC GS-551019 (Genome Systems Hu man BAC library) and cosmids U199A7 and U209F2 (Lawrence Livermore X chromosome cosmid library) containing part of human chloride ch annel 4 gene, complete sequence.//4.9e-40:245:80//AC003666
R-PLACE1004118//HS_3092_B1_B01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3092 Col=1 Row=D, geno mic survey sequence.//0.80:207:60//AQ128151	R-PLACE1004550
R-PLACE1004128//Rattus norvegicus guanine nucleotide binding prote in beta 4 subunit mRNA, partial cds.//1.8e-06:193:66//AF022085	R-PLACE1004564//B. taurus mRNA for cleavage and polyadenylation spe cificity factor.//2.7e-82:532:86//X75931
R-PLACE1004149//HS_2253_A2_F11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2253 Col=22 Row=K, gen omic survey sequence.//2.4e-59:315:95//AQ129711	R-PLACE1004629//Homo sapiens chromosome 7 clone UWCC:g3586a230 fro m 7p14-15, complete sequence.//0.015:437:59//AC004800
R-PLACE1004156//Homo sapiens Xp22 bins 3-5 PAC RPC14-617A9 (Roswel l Park Cancer Institute Human PAC Library) containing Arylsulfatas e D and E genes, complete sequence.//8.3e-53:299:76//AC005295	R-PLACE1004645//CIT-HSP-2370D6, TR CIT-HSP Homo sapiens genomic clo ne 2370D6, genomic survey sequence.//0.033:76:75//AQ110136
R-PLACE1004161	R-PLACE1004646//Homo sapiens cosmid 120C12 from Xq28, complete seq uence.//2.0e-23:237:79//AF036876
R-PLACE1004183//Homo sapiens for TOM1-like protein.//1.3e-80:434:9 3//AJ010071	R-PLACE1004658//Homo sapiens Chromosome 12p13.3 BAC RPC111-21K20 (Roswell Park Cancer Institute Human BAC Library) complete sequenc e.//7.1e-09:94:87//AC005343
R-PLACE1004197//RPC111-69N15, TK RPC111 Homo sapiens genomic clone R-69N15, genomic survey sequence.//0.0078:170:65//AQ265515	R-PLACE1004664//RPC111-79G23, TV RPC111 Homo sapiens genomic clone R-79G23, genomic survey sequence.//2.2e-81:433:94//AQ283692
R-PLACE1004203//Homo sapiens semaphorin L (SEMA1) mRNA, complete c ds.//3.4e-105:501:98//AF030698	R-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putativ e MB604 Met protein (MB604 Met) gene, complete cds.//2.7e-24:263: 74//U07561
R-PLACE1004242//Homo sapiens DNA sequence from PAC 124C6 on chromo some 6q21. Contains genomic marker D6S1603, ESTs, GSSs and a STS w ith a CA repeat polymorphism, complete sequence.//6.1e-65:373:86// AL021326	R-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds.//1.1e-89:513:91//AF035606
R-PLACE1004256//Homo sapiens BAC clone NH0044G14 from 7q11.23-21. 1, complete sequence.//0.011:383:61//AC006031	R-PLACE1004681//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncoge ne of hepatocellular colorectal and non-small cell lung cancer, s egment 3/11.//1.3e-96:498:95//AB020860
R-PLACE1004257//Homo sapiens Xp22 BAC GSHB-433024 (Genome Systems Human BAC library) complete sequence.//3.4e-09:576:59//AC004470	R-PLACE1004686
R-PLACE1004258//HS_3034_A1_B12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3034 Col=23 Row=C, gen omic survey sequence.//1.4e-35:359:77//AQ128936	R-PLACE1004691//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncoge ne of hepatocellular colorectal and non-small cell lung cancer, s egment 2/11.//2.1e-33:290:80//AB020859
R-PLACE1004270//CITB1-E1-2504K14, TR CITB1-E1 Homo sapiens genomic clone 2504K14, genomic survey sequence.//2.7e-06:150:74//AQ261108	R-PLACE1004693//Caenorhabditis elegans cosmid Y2H9A, complete sequ ence.//1.0:195:60//AL021448
R-PLACE1004274//Homo sapiens BAC clone NH0436H22 from 2, complete sequence.//0.025:116:72//AC005234	R-PLACE1004716//CITB1-E1-2519C14, TR CITB1-E1 Homo sapiens genomic clone 2519C14, genomic survey sequence.//5.0e-43:245:93//AQ276965
R-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) m RNA, complete cds.//4.4e-106:581:91//AF084830	R-PLACE1004722//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-62 8 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.// 0.0022:360:60//AC005507
R-PLACE1004284//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 g enomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.5 9:231:60//AC005308	R-PLACE1004736
R-PLACE1004289//Homo sapiens chromosome 17, clone hRPK.700_H_6, co mplete sequence.//5.8e-31:340:75//AC005920	R-PLACE1004740
R-PLACE1004302//Homo sapiens clone RG332P12, WORKING DRAFT SEQUENC E, 1 unordered pieces.//6.4e-90:572:86//AC005095	R-PLACE1004743//Homo sapiens ubiquitin-protein ligase E3-alpha (UB R1) mRNA, partial cds.//5.4e-105:575:92//AF061556
R-PLACE1004316//H. sapiens mRNA for apoptosis specific protein.//1. 9e-113:590:94//Y11588	R-PLACE1004751//Homo sapiens Xq28 BACs 360 F12, GSHB-555C13, compl ete sequence.//9.0e-26:317:76//AC002523
R-PLACE1004336//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1013A10, WORKING DRAFT SEQUENCE.//2.3e-65:292:82//AL033 383	R-PLACE1004773//Homo sapiens invasin protein mRNA, complete cds.// 8.5e-88:437:96//AF084367
R-PLACE1004358//Homo sapiens connector enhancer of KSR-like protei n CNK1 mRNA, complete cds.//2.4e-70:379:93//AF100153	R-PLACE1004777//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//0.050:13
R-PLACE1004376//CIT-HSP-2287M8, TF CIT-HSP Homo sapiens genomic clo ne 2287M8, genomic survey sequence.//0.47:173:61//AQ000837	

【0830】

【表530】

8:65//AP000010
R-PLACE1004793//Human endogenous retrovirus HERV-K(HML6) proviral clone HML6:17 putative polymerase and envelope genes, partial cds, and 3'LTR.//5.1e-58:313:80//U60269
R-PLACE1004804//Homo sapiens mRNA for KIAA0606 protein, partial cds.//5.8e-98:580:88//AB011178
R-PLACE1004813//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-42 0 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//5.3e-09:256:64//AC005140
R-PLACE1004814//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds.//3.5e-107:358:99//AF069250
R-PLACE1004815//Human Chromosome 11q12.2 PAC clone pJ606g6, complete sequence.//3.8e-61:353:89//AC004126
R-PLACE1004824//Homo sapiens chromosome 17, clone hCIT.468_F_23, WORKING DRAFT SEQUENCE, 3 unordered pieces.//5.7e-42:364:79//AC004666
R-PLACE1004827//Homo sapiens Xp22 BAC GS-594A7 (Genome Systems Human BAC library) contains Bmx gene, complete sequence.//2.7e-14:156:79//AC003669
R-PLACE1004836//HS_2270_A2_H10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=20 Row=D, genomic survey sequence.//8.6e-51:267:96//AQ164110
R-PLACE1004838//CIT-HSP-2343E10, TR CIT-HSP Homo sapiens genomic clone 2343E10, genomic survey sequence.//0.071:168:63//AQ058544
R-PLACE1004840//Sequence 4 from patent US 5728819.//1.6e-26:150:98//192820
R-PLACE1004858//Human Chromosome X clone hWDX342, complete sequence.//0.57:344:59//AC004072
R-PLACE1004885//HS_3235_B2_E07_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3235 Col=14 Row=J, genomic survey sequence.//1.1e-38:175:78//AQ210193
R-PLACE1004900//Human DNA sequence from clone 353H6 on chromosome Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SMN2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//2.0e-44:334:84//AL022577
R-PLACE1004902
R-PLACE1004913//Human DNA sequence from clone J428A131, WORKING DRAFT SEQUENCE.//7.7e-58:377:87//Z82209
R-PLACE1004918//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-24 Bf7, complete sequence.//0.00084:373:60//AC004605
R-PLACE1004930//Homo sapiens MDC-3.13 isoform 1 mRNA, complete cds.//2.0e-100:532:93//AF099936
R-PLACE1004934//Homo sapiens clone RG062N11, WORKING DRAFT SEQUENCE, 2 unordered pieces.//0.00030:198:66//AC005683
R-PLACE1004937//Caenorhabditis elegans SEL-10 (sel-10) mRNA, complete cds.//1.3e-13:367:61//AF020788
R-PLACE1004969//Human DNA sequence from clone LUCA7 on chromosome 3, complete sequence.//0.97:116:71//Z84494
R-PLACE1004972
R-PLACE1004979//Plasmodium falciparum MAL3P4, complete sequence.//0.74:304:60//AL008970
R-PLACE1004982//Plasmodium falciparum 3D7 chromosome 12 PFYAC492 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//4.7e-05:495:57//AC005308
R-PLACE1004985//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 451B21, WORKING DRAFT SEQUENCE.//2.5e-10:410:60//AL033522
R-PLACE1005026//Homo sapiens PAC clone DJ0907C10 from 7q31-3q32, complete sequence.//2.7e-56:158:99//AC004925
R-PLACE1005027
R-PLACE1005046//Homo sapiens chromosome 19, cosmid F20237, complete sequence.//3.1e-63:438:86//AC005775
R-PLACE1005052//Homo sapiens chromosome Xp22-135-136 clone CSHB-56711, WORKING DRAFT SEQUENCE, 35 unordered pieces.//6.1e-87:301:98//AC005867
R-PLACE1005066//Human DNA sequence from clone 67K17 on chromosome 6q24.1-24.3. Contains the HIVP2 (Schnurri-2) gene for HIV type 1 Enhancer-binding Protein 2, and a possible pseudogene in an intron of this gene. Contains STSs and GSSs and an AAT repeat polymorphism, complete sequence.//1.1e-09:453:61//AL023584
R-PLACE1005077//H. sapiens genes for semenogelin I and semenogelin II.//2.6e-05:199:66//Z47556
R-PLACE1005085//Homo sapiens chromosome 17, clone hRPK.293_K_20, complete sequence.//2.1e-42:384:69//AC005495
R-PLACE1005086//RPC111-30H10, TV RPC1-11 Homo sapiens genomic clone RPC1-11-30H10, genomic survey sequence.//0.13:112:67//B87788
R-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds.//2.5e-97:531:92//L40401
R-PLACE1005102//Homo sapiens chromosome 19, cosmid R29388, complete sequence.//1.3e-91:504:92//AC004476
R-PLACE1005108//Homo sapiens BAC129, complete sequence.//4.0e-28:32:84//U85195
R-PLACE1005111//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 566H6, WORKING DRAFT SEQUENCE.//3.0e-18:174:74//AL031845
R-PLACE1005128
R-PLACE1005146
R-PLACE1005162//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-42 0 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//2.4e-07:273:61//AC005140
R-PLACE1005176//Rat alternatively spliced mRNA.//8.1e-20:185:82//M93018
R-PLACE1005181//HS_2182_B2_B05_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2182 Col=10 Row=D, genomic survey sequence.//4.9e-05:193:65//AQ030787
R-PLACE1005187//Arabidopsis thaliana chromosome 11 BAC T14A4 genomic sequence, complete sequence.//0.00073:264:60//AC006161
R-PLACE1005206//Homo sapiens full length insert cDNA YN66A06.//6.3e-64:343:93//AF075043
R-PLACE1005232//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 25J6, WORKING DRAFT SEQUENCE.//1.3e-34:286:81//Z84476
R-PLACE1005243
R-PLACE1005261//Caenorhabditis elegans cosmid ZK666, complete sequence.//0.66:180:60//Z49132
R-PLACE1005266//Homo sapiens clone RG122E10, complete sequence.//1.3e-15:166:78//AC005067
R-PLACE1005277//CITB1-E1-2514D4, TF CITB1-E1 Homo sapiens genomic clone 2514D4, genomic survey sequence.//2.5e-34:358:74//AQ265720
R-PLACE1005287//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P1, WORKING DRAFT SEQUENCE.//4.1e-07:495:60//AL031744
R-PLACE1005305//HS_3180_B2_D02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3180 Col=4 Row=H, genomic survey sequence.//1.1e-42:308:85//AQ169443
R-PLACE1005308
R-PLACE1005313//Human Chromosome 11 pac pJ227b23, WORKING DRAFT SEQUENCE, 19 unordered pieces.//0.00048:320:60//AC000383
R-PLACE1005327//chromosome 1 specific transcript KIAA0491.//5.4e-10:537:94//AB007960
R-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569, complete sequence.//2.2e-94:536:91//AC004794
R-PLACE1005335//Human Chromosome 3 pac pJ7011, WORKING DRAFT SEQUENCE, 2 unordered pieces.//5.3e-32:313:79//AC000380
R-PLACE1005373//Homo sapiens BAC129, complete sequence.//8.8e-10:29:68//U85195
R-PLACE1005374//Homo sapiens chromosome 17, clone hRPK.401_0_9, complete sequence.//3.0e-44:434:77//AC005291
R-PLACE1005409//Human BAC clone RG167B05 from 7q21, complete sequence.//8.8e-105:529:96//AC003991
R-PLACE1005453//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//4.7e-39:302:82//AC002477
R-PLACE1005467//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167P19, WORKING DRAFT SEQUENCE.//1.1e-40:328:81//Z93014
R-PLACE1005471//Human DNA sequence from clone 395P12 on chromosome 1q24-25. Contains the TXGP1 gene for tax-translationally activated glycoprotein 1 (34kD) (OX40 ligand, OX40L) and a GOT2 (Aspartate Aminotransferase, mitochondrial precursor, EC 2.6.1.1, Transaminase A, Glutamate Oxaloacetate Transaminase-2) pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//6.4e-68:409:90//AL022310
R-PLACE1005477//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 32B1, WORKING DRAFT SEQUENCE.//0.020:216:66//AL023693
R-PLACE1005480//Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338531), complete sequence.//2.8e-44:327:70//AC005392
R-PLACE1005481//Homo sapiens chromosome 17, clone hRPC.1164_0_3, complete sequence.//4.2e-23:284:74//AC004703
R-PLACE1005494//Danio rerio homeobox protein LIM-3 (lim3) gene, exon 4.//0.19:468:60//AF031631
R-PLACE1005502//Homo sapiens formin binding protein 21 mRNA, complete cds.//1.6e-55:277:98//AF071185
R-PLACE1005526//Human mRNA for alpha-1 type II collagen.//0.10:227:63//X16468
R-PLACE1005528//Homo sapiens genomic DNA, chromosome 21q11.1, segment 9/28, WORKING DRAFT SEQUENCE.//2.3e-76:395:96//AP000038
R-PLACE1005530//C. familiaris CA repeat sequence (isolate).//0.023:90:75//X86184
R-PLACE1005550//Fugu rubripes GSS sequence, clone 048A08bH1, genomic survey sequence.//2.0e-09:235:64//AL025928

【0831】

【表531】

R-PLACE1005554//Homo sapiens chromosome 17, clone hRKC.215_P_18, c
omplete sequence.//0.069:305:60//AC005969
R-PLACE1005557//Homo sapiens chromosome 17, clone hRKC.117_B_12, c
omplete sequence.//4.3e-105:587:91//AC004707
R-PLACE1005574//Human BAC 367017 from chromosome 18, complete sequ
ence.//1.5e-17:274:67//AC003971
R-PLACE1005584//Homo sapiens PAC clone DJ1186C01 from 7q21.2-q31.
1, complete sequence.//2.7e-15:191:77//AC004991
R-PLACE1005595//Human Chromosome 11q12.2 PAC clone pJ606g6, compl
ete sequence.//6.4e-90:453:96//AC004126
R-PLACE1005603//Homo sapiens cosmid clone U16902 from Xp22.1-22.2,
complete sequence.//0.69:322:61//U72788
R-PLACE1005611//Borrelia burgdorferi plasmid cpl8, OspE (ospE) gen
e, partial cds.//0.059:473:56//U42599
R-PLACE1005623//Homo sapiens full length insert cDNA clone ZD7680
3.//1.6e-113:575:95//AF086405
R-PLACE1005630//High throughput sequencing of human chromosome 12,
WORKING DRAFT SEQUENCE, 1 ordered pieces.//5.6e-79:270:94//AC0058
40
R-PLACE1005639//Human BAC clone RGD22117 from 7q21, complete sequ
ence.//8.2e-56:441:83//AC002382
R-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, co
mplete cds.//3.2e-110:585:93//AF083255
R-PLACE1005656//Homo sapiens chromosome 17, clone hRKC.628_E_12, c
omplete sequence.//8.6e-08:505:58//AC005701
R-PLACE1005666//Human DNA sequence from PAC 360E18 on chromosome X
contains EST, CpG island and polymorphic CA repeat.//3.2e-27:307:
72//Z82203
R-PLACE1005698//344822.TV C17978SKAI Homo sapiens genomic clone A-
344822, genomic survey sequence.//0.030:91:70//B15144
R-PLACE1005727//Human variable number tandem repeat (VNTR) region,
allele 17R1 3' to collagen type II (COL2A1) gene.//5.2e-10:587:59
//L10171
R-PLACE1005730//Homo sapiens ADP/ATP carrier protein (ANT-2) gene,
complete cds.//0.0039:239:58//L78810
R-PLACE1005739//Mus musculus IFN-gamma induced (Mg11) mRNA, comple
te cds.//2.2e-21:270:72//U15635
R-PLACE1005755//Caenorhabditis elegans cosmid M03F4.//6.9e-08:219:
64//U64601
R-PLACE1005763//Human mRNA for KIAA0118 gene, partial cds.//1.0e-4
5:268:87//D42087
R-PLACE1005799//Human X chromosome mRNA for CCC1 protein inv. in ce
ll proliferation.//0.030:91:78//X07024
R-PLACE1005802//Homo sapiens PAC clone DJ044L15 from Xq23, complet
e sequence.//1.4e-69:391:92//AC004827
R-PLACE1005803
R-PLACE1005804//Human BAC clone RG341D10 from 7p15-p21, complete s
equence.//1.8e-21:175:75//AC002530
R-PLACE1005828//Homo sapiens chromosome 17, clone hRKC.971_F_3, WO
RKING DRAFT SEQUENCE, 1 ordered pieces.//2.9e-56:333:91//AC004150
R-PLACE1005834//Plasmodium falciparum DNA *** SEQUENCING IN PROGRE
SS *** from MAL1P2, WORKING DRAFT SEQUENCE.//0.020:513:55//AL03174
5
R-PLACE1005845//Rabbit mRNA for protein phosphatase 2A-beta.//1.8
e-10:182:69//Y00763
R-PLACE1005850
R-PLACE1005851//Homo sapiens clone DJ0789105, WORKING DRAFT SEQUEN
CE, 2 unordered pieces.//5.5e-06:318:63//AC004887
R-PLACE1005876//B. taurus mRNA for cleavage and polyadenylation spe
cificity factor.//6.7e-28:366:72//X75931
R-PLACE1005884//Human DNA sequence from cosmid Y526F1, between mar
kers DXS366 and DXS87 on chromosome X contains STS.//1.0e-06:306:6
4//Z70281
R-PLACE1005898//Plasmodium falciparum 3D7 chromosome 12 PFYAC336 g
enomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.00
94:449:59//AC005139
R-PLACE1005921//CITBI-E1-2509N21.TF CITBI-E1 Homo sapiens genomic
clone 2509N21, genomic survey sequence.//4.8e-84:494:89//AQ261347
R-PLACE1005923//RPC111-65N9.TJ RPC111 Homo sapiens genomic clone
R-65N9, genomic survey sequence.//8.3e-97:520:93//AQ237243
R-PLACE1005925//Human DNA sequence from clone 231L4 on chromosome
Xq27.1-27.3 Contains GSS, STS, complete sequence.//5.2e-67:578:78/
//AL022719
R-PLACE1005932//Caenorhabditis elegans cosmid Y52B11A, complete se
quence.//0.0035:176:62//AL032654
R-PLACE1005934
R-PLACE1005936//Arabidopsis Thaliana BAC F6A4, Chromosome IV, near
60.5 cM, complete sequence.//0.00021:272:62//AF069716
R-PLACE1005951
R-PLACE1005953//Caenorhabditis elegans cosmid F09E5.//1.3e-07:349:
60//U37429
R-PLACE1005955//Human HepG2 3' region Mbol cDNA, clone hmd101m3./
//8.3e-08:128:70//D17131
R-PLACE1005966//Pontia protodice large subunit ribosomal RNA gene,
partial sequence: tRNA-Val gene, complete sequence: and small sub
unit ribosomal RNA gene, partial sequence, mitochondrial genes for
mitochondrial RNAs.//7.0e-09:549:59//AF044863
R-PLACE1005968//Rattus norvegicus mRNA for p47, complete cds.//1.1
e-51:394:81//AB002086
R-PLACE1005990//Homo sapiens chromosome 12p13.3 clone RPC111-407G
6, WORKING DRAFT SEQUENCE, 51 ordered pieces.//4.4e-63:369:91//AC0
05866
R-PLACE1006002//Human cosmid CRI-JC2015 at D10S289 in 10p13.//5.9
e-27:299:74//U15177
R-PLACE1006003//Mus musculus clone OST18050, genomic survey sequen
ce.//3.5e-07:164:67//AF046375
R-PLACE1006011//Mus musculus poly-(ADPriboseyl)-transferase homolog
PARP mRNA, complete cds.//1.1e-32:266:83//AF072521
R-PLACE1006017//Homo sapiens Chromosome 22q11.2 Cosmid Clone 31e 1
n DGCR Region, complete sequence.//1.8e-17:164:82//AC000077
R-PLACE1006037//Mus musculus B6D2F1 clone 2C118 mRNA.//2.0e-49:55
7:72//U01139
R-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.3e-13:
128:81//X99906
R-PLACE1006076//Homo sapiens clone DJ0781A18, WORKING DRAFT SEQUEN
CE, 3 unordered pieces.//3.3e-18:220:74//AC004885
R-PLACE1006119//Plasmodium berghei (STRAIN ANKA) gamma-GCS gene, c
omplete CDS.//0.0050:271:63//AJ005122
R-PLACE1006129//Drosophila melanogaster, chromosome 2R, region 31C
1-3106. P1 clone DS08879, complete sequence.//0.43:178:65//AC00545
4
R-PLACE1006139//Homo sapiens PAC clone DJ0659J06 from 7q33-q35, co
mplete sequence.//7.5e-13:222:68//AC004849
R-PLACE1006143//Plasmodium falciparum MAL3P6, complete sequence.//
0.00019:455:59//Z98551
R-PLACE1006157//Plasmodium falciparum DNA *** SEQUENCING IN PROGRE
SS *** from MAL4P1, WORKING DRAFT SEQUENCE.//0.00018:351:60//AL034
557
R-PLACE1006159//Homo sapiens chromosome 10 clone LA10NC01.124_D_3
map 10q25.1, WORKING DRAFT SEQUENCE, 1 ordered pieces.//1.0e-113:5
86:96//AC006103
R-PLACE1006164//Human hereditary haemochromatosis region, histone
2A-like protein gene, hereditary haemochromatosis (HLA-H) gene, Ro
Ret gene, and sodium phosphate transporter (NPT3) gene, complete c
ds.//1.0e-28:342:75//U91328
R-PLACE1006167//Homo sapiens full length insert cDNA clone ZE14E0
4.//4.6e-77:426:93//AF086555
R-PLACE1006170//Mouse mRNA for alpha-adaptin (C).//3.0e-46:188:82/
//X14972
R-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds.//1.6e-1
16:597:95//AF091433
R-PLACE1006195//Homo sapiens chromosome 19, fosmid 39554, complete
sequence.//8.8e-11:148:74//AC004410
R-PLACE1006196
R-PLACE1006205//Genomic sequence from Mouse 11, complete sequence.
//8.4e-44:332:85//AC000398
R-PLACE1006223//Human DNA sequence from cosmid U74C11, between mar
kers DXS6791 and DXS8038 on chromosome X contains ESTs.//0.041:21
5:61//Z73362
R-PLACE1006225//Caenorhabditis elegans cosmid Y59H2, complete sequ
ence.//9.7e-13:358:63//Z98877
R-PLACE1006236//Plasmodium falciparum MAL3P4, complete sequence.//
0.00019:538:58//AL008970
R-PLACE1006239//Homo sapiens BAC clone RG118D07 from 7q31, complet
e sequence.//3.1e-96:497:95//AC004142
R-PLACE1006246//Homo sapiens clone NH0144M13, WORKING DRAFT SEQUEN
CE, 1 unordered pieces.//0.029:499:56//AC006034
R-PLACE1006248//Homo sapiens mRNA for KIA0648 protein, partial cd
s.//9.2e-96:499:95//AB014548
R-PLACE1006262//Homo sapiens Xp22 CSHB-314C4 (Genome Systems Human
BAC library) complete sequence.//0.00043:160:66//AC004087
R-PLACE1006288//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 20N2, WORKING DRAFT SEQUENCE.//3.5e-120:611:96//AL03132
0
R-PLACE1006318
R-PLACE1006325//Plasmodium falciparum MAL3P8, complete sequence.//
1.0:426:57//AL034560
R-PLACE1006335//Human DNA sequence from PAC 849L7 on chromosome Xq
21.//0.96:173:66//AL008987
R-PLACE1006357//P. falciparum complete gene map of plastid-like DNA

【0832】

【表532】

(IR-B). //1.9e-07:491:58//X95276	R-PLACE1006815//HS_3028_B1_B04_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3028 Col=7 Row=D, genomic survey sequence. //1.5e-33:251:77//AQ120174
R-PLACE1006360//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence. //0.25:484:56//AE001398	R-PLACE1006819//Human DNA sequence from PAC 121G13 on chromosome 6 contains flow sorted chromosome 6 HindIII fragment ESTs, polymorphic CA repeat, CpG island, CpG island genomic fragments. //1.4e-76:544:84//Z86062
R-PLACE1006368//Caenorhabditis elegans cosmid Y38H6C, complete sequence. //1.0:240:59//AL031630	R-PLACE1006829
R-PLACE1006371//Homo sapiens chromosome 16, cosmid clone 360H6 (LA NL), complete sequence. //3.7e-101:574:91//AC004232	R-PLACE1006860
R-PLACE1006382	R-PLACE1006867//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 323M4, WORKING DRAFT SEQUENCE. //3.2e-107:549:95//AL033378
R-PLACE1006385//Mus musculus intersecin-EH binding protein lbp2 mRNA, partial cds. //1.4e-50:350:86//AF057286	R-PLACE1006878//Homo sapiens full length insert cDNA clone Z855G0 5. //1.4e-46:241:97//AF086155
R-PLACE1006412//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces. //5.1e-51:339:82//AC004854	R-PLACE1006883//Homo sapiens chromosome 16, cosmid clone 360H6 (LA NL), complete sequence. //1.3e-38:283:85//AC004232
R-PLACE1006414//Homo sapiens 12p13.3 PAC RPC15-927J10 (Roswell Park Cancer Institute Human PAC library) complete sequence. //1.6e-38:297:84//AC004804	R-PLACE1006901
R-PLACE1006438//Homo sapiens full length insert cDNA YH73H06. //7.5e-73:422:90//AF074985	R-PLACE1006904//Human DNA sequence from PAC 360E18 on chromosome X contains EST, CpG island and polymorphic CA repeat. //4.1e-15:477:62//Z82203
R-PLACE1006445//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1018K9, WORKING DRAFT SEQUENCE. //3.0e-07:376:61//AL031726	R-PLACE1006917//Homo sapiens Xp22 bins 45-47 BAC GSHB-665M22 (Genome Systems Human BAC Library) complete sequence. //1.3e-42:305:87//AC005184
R-PLACE1006469	R-PLACE1006932
R-PLACE1006470//Mouse B1 repetitive sequence DNA. //1.0:96:66//M24152	R-PLACE1006935//Human DNA sequence from PAC 117P19 on chromosome X. //0.0014:114:74//Z86061
R-PLACE1006482//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 447C4, WORKING DRAFT SEQUENCE. //3.0e-101:535:94//AL021977	R-PLACE1006958//Mouse mRNA for germ cell specific protein APC-1, complete cds. //9.5e-85:590:83//D49482
R-PLACE1006492//Homo sapiens chromosome 17, clone hRPK.180_P_8, complete sequence. //0.78:44:95//AC005972	R-PLACE1006961//Homo sapiens chromosome 17, clone hRPK.349_A_8, complete sequence. //6.7e-42:295:86//AC005544
R-PLACE1006506//R. norvegicus BSP gene. //1.0:206:60//X86100	R-PLACE1006962//Homo sapiens Xp22 PAC RPC11-167A22 (from Roswell Park Cancer Center) complete sequence. //1.1e-19:302:71//AC002349
R-PLACE1006521//RPC111-13L8.TV RPC1-11 Homo sapiens genomic clone RPC1-11-13L8, genomic survey sequence. //9.0e-17:414:61//B75158	R-PLACE1006966//HS_2219_B2_C02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2219 Col=4 Row=F, genomic survey sequence. //0.019:180:63//AQ145873
R-PLACE1006531//Plasmodium falciparum coronin gene, isolate 3D7. //0.98:186:63//AJ002197	R-PLACE1006989
R-PLACE1006534//Anopheles gambiae complete mitochondrial genome. //0.051:412:61//L20934	R-PLACE1007014
R-PLACE1006540//Homo sapiens clone UNGC:y55c025 from 6p21, complete sequence. //7.5e-41:470:70//AC004209	R-PLACE1007021//Homo sapiens chromosome 12p13.3 clone RPC13-454B2 3, WORKING DRAFT SEQUENCE, 48 unordered pieces. //1.6e-23:362:70//AC005845
R-PLACE1006552//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y47D3, WORKING DRAFT SEQUENCE. //0.57:355:57//Z98865	R-PLACE1007045//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 32B1, WORKING DRAFT SEQUENCE. //2.3e-90:584:86//AL023693
R-PLACE1006598//Plasmodium falciparum 3D7 chromosome 12 PFYAC588 genomic sequence, WORKING DRAFT SEQUENCE, 2 unordered pieces. //0.016:291:58//AC004710	R-PLACE1007053//Homo sapiens clone DJ0810E06, WORKING DRAFT SEQUENCE, 8 unordered pieces. //2.4e-108:550:96//AC004895
R-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds. //2.9e-116:590:95//U97670	R-PLACE1007097//Homo sapiens DNA sequence from BAC 55C20 on chromosome 6. Contains a Spinal Muscular Atrophy (SMA3) LIKE gene overlapping with a beta-glucuronidase LIKE pseudogene. Contains a membrane protein LIKE pseudogene, a Glyceraldehyde 3-phosphate dehydrogenase (GAPDH) LIKE pseudogene, five predicted tRNA genes. Contains ESTs, GSSs (BAC end sequences) and a CA repeat polymorphism, complete sequence. //1.8e-103:552:93//AL021368
R-PLACE1006617//Homo sapiens chromosome 4 clone B207D4 map Aq25, complete sequence. //2.2e-45:209:88//AC004050	R-PLACE1007105//Mus musculus muskulin mRNA, complete cds. //2.7e-3:2379:73//U72194
R-PLACE1006626//C. elegans cosmid X12M4. //1.2e-16:344:64//L14331	R-PLACE1007111//Plasmodium falciparum 3D7 chromosome 12 PFYAC69 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces. //0.422:57//AC004688
R-PLACE1006629//Homo sapiens chromosome 19, cosmid F20900, complete sequence. //2.8e-25:343:70//AC006128	R-PLACE1007112//Cynops cornifex cytb gene. //0.020:427:58//AJ228479
R-PLACE1006640//CIT-HSP-2169L1.TF CIT-HSP Homo sapiens genomic clone 2169L1, genomic survey sequence. //0.00020:201:62//B90038	R-PLACE1007132//Homo sapiens full length insert cDNA YH77E09. //5.7e-107:535:96//AF074987
R-PLACE1006673//Homo sapiens clone DJ076820, WORKING DRAFT SEQUENCE, 6 unordered pieces. //1.4e-42:309:84//AC004882	R-PLACE1007140//Homo sapiens clone RG030L05, WORKING DRAFT SEQUENCE, 3 unordered pieces. //0.36:408:58//AC005050
R-PLACE1006678//Homo sapiens PAC clone DJ1166G19 from 7p12-p11.2, complete sequence. //6.4e-09:454:59//AC006024	R-PLACE1007178//Homo sapiens clone HEA4 Cri-du-chat region mRNA. //0.99:63:73//AF009283
R-PLACE1006704//Human DNA sequence from clone 249C1 on chromosome Xq21.1-22.2 Contains GSS, complete sequence. //0.56:226:63//AL022154	R-PLACE1007226
R-PLACE1006731//Homo sapiens clone 23923 mRNA sequence. //6.0e-101:486:98//AF038172	R-PLACE1007238
R-PLACE1006754//Homo sapiens chromosome 19, cosmid R29124, complete sequence. //1.4e-68:381:93//AC005626	R-PLACE1007239//Homo sapiens mRNA for transcription elongation factor 5-11, hS-11-T1, complete cds. //2.0e-91:534:89//D50495
R-PLACE1006760//Homo sapiens clone 24800 mRNA sequence. //6.2e-72:397:92//AF070622	R-PLACE1007242//CITB1-E1-2512M9.TF CITB1-E1 Homo sapiens genomic clone 2512M9, genomic survey sequence. //1.3e-05:117:76//AQ279454
R-PLACE1006779//Rattus norvegicus intestinal trefoil factor gene, promoter and partial cds. //1.6e-11:420:61//U20984	R-PLACE1007243//Prototheca wickerhamii 263-11 complete mitochondrial DNA. //0.21:284:58//U02970
R-PLACE1006782//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y47D3, WORKING DRAFT SEQUENCE. //0.60:321:58//Z98865	R-PLACE1007257//Homo sapiens mRNA for dia-12c protein. //6.9e-113:607:93//Y15908
R-PLACE1006792//Homo sapiens chromosome 4 clone C0026P05 map 4P16, complete sequence. //2.9e-40:379:77//AC005599	R-PLACE1007274//Homo sapiens chromosome 17, clone hRPK.394_K_10, complete sequence. //4.4e-10:135:74//AC006080
R-PLACE1006795//Homo sapiens BAC clone RG281G05 from 7p15-p21, complete sequence. //6.2e-07:291:63//AC005083	R-PLACE1007276//Homo sapiens BAC clone 255A7 from 8q21 containing NBS1 gene, complete sequence. //1.7e-36:435:72//AF069291
R-PLACE1006800//HS_2270_B1_D02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2270 Col=3 Row=H, genomic survey sequence. //4.1e-76:367:99//AQ085793	R-PLACE1007282//B. garinii (strain T1s1) p83/100 gene (partial). //0.95:183:60//X81533
R-PLACE1006805//Plasmodium falciparum 3D7 chromosome 12 PFYAC88-62 8 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces. //0.00058:354:59//AC005507	R-PLACE1007286//RPC111-13L8.TV RPC1-11 Homo sapiens genomic clone

【0833】

【表533】

RPC1-11-13L8, genomic survey sequence.//6.1e-55:519:76//B75158
 R-PLACE1007301//Human DNA sequence from PAC 106H8 on chromosome 1q24. Contains PHOSPHATIDYLINISITOL-GLYCAN class C (PIG-C) and DYNAMIN-3 genes. Contains ESTs and STSs and a CpG island.//0.75:180:62//Z97195
 R-PLACE1007317//Drosophila dasycnemis 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence.//0.59:236:59//J94253
 R-PLACE1007342
 R-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//3.7e-65:367:91//AF096870
 R-PLACE1007367//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-62 8 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.0e-06:385:62//AC005507
 R-PLACE1007375//Plasmodium falciparum 3D7 chromosome 12 PFYAC1122 genomic sequence, WORKING DRAFT SEQUENCE, 3 unordered pieces.//0.10:309:59//AC004709
 R-PLACE1007386//Reclinomonas americana mitochondrial DNA, complete genome.//0.0012:403:58//AF007261
 R-PLACE1007402//HS_2055_A2_D03_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-2055 Col=6 Row=C, genomic survey sequence.//0.0046:88:79//AQ234824
 R-PLACE1007409//Homo sapiens mitoxanthone resistance protein 1 mRNA, partial sequence.//7.6e-112:590:94//AF093771
 R-PLACE1007416//Homo sapiens chromosome 19, cosmid R26894, complete sequence.//0.96:98:70//AC005594
 R-PLACE1007450//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54B20, WORKING DRAFT SEQUENCE.//1.7e-39:308:82//Z98304
 R-PLACE1007452//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//2.6e-59:389:82//AC004081
 R-PLACE1007460
 R-PLACE1007478//Homo sapiens 12q13.1 PAC RPC13-197B17 (Roswell Park Cancer Institute Human PAC library) complete sequence.//7.0e-08:335:60//AC004241
 R-PLACE1007484
 R-PLACE1007488//Glossina morsitans morsitans 16S ribosomal RNA gene, mitochondrial gene for mitochondrial RNA, partial sequence.//2.5e-05:421:61//AF072373
 R-PLACE1007507//Plasmodium falciparum MAL3P7, complete sequence.//2.3e-09:577:57//AL034559
 R-PLACE1007511//Homo sapiens chromosome 17, clone hRPC.1110_E_20, complete sequence.//1.2e-79:387:96//AC004231
 R-PLACE1007524//Homo sapiens chromosome 19, overlapping cosmids F18547, F11133, R27945, R28830 and R32804, complete sequence.//3.4e-09:148:73//AC003682
 R-PLACE1007525//Homo sapiens Chromosome 16 BAC clone CIT987SK-44M2, complete sequence.//4.7e-38:297:82//AC004381
 R-PLACE1007544
 R-PLACE1007547//Human laminin alpha 4 chain (LAMA4-1) mRNA, complete cds.//4.0e-17:108:97//U77706
 R-PLACE1007557//Human BAC clone RG343P13 from 7q31, complete sequence.//2.2e-45:390:77//AC004265
 R-PLACE1007583//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 54S117, WORKING DRAFT SEQUENCE.//1.0e-56:302:95//AL031665
 R-PLACE1007598//Homo sapiens clone 23939 mRNA sequence.//1.5e-102:554:93//AF038179
 R-PLACE1007618
 R-PLACE1007621//Homo sapiens clone 23859 mRNA sequence.//1.4e-103:537:94//AF038176
 R-PLACE1007632//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//3.3e-76:289:94//AC005840
 R-PLACE1007645//Homo sapiens full length insert cDNA clone ZD76G10.//0.0080:96:77//AF086408
 R-PLACE1007649//CIT-HSP-2308A18, TR CIT-HSP Homo sapiens genomic clone 2308A18, genomic survey sequence.//1.1e-82:412:97//AQ022149
 R-PLACE1007677//Plasmodium falciparum chromosome 2, section 4 of 73 of the complete sequence.//0.0041:470:57//AE001367
 R-PLACE1007688
 R-PLACE1007690//Human Chromosome 16 BAC clone CIT987SK-A-418G10, complete sequence.//1.3e-22:162:91//AC002044
 R-PLACE1007697
 R-PLACE1007705//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460J8, WORKING DRAFT SEQUENCE.//4.4e-121:624:95//AL031662
 R-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//1.8e-73:374:96//AF061243
 R-PLACE1007725//Caenorhabditis elegans cosmid F38A5.//0.070:186:60//U70854
 R-PLACE1007729//Human endogenous retrovirus HERV-K (HML6) proviral clone HML6.17 putative polymerase and envelope genes, partial cds. and 3' LTR.//3.8e-53:415:81//U60269
 R-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//2.1e-92:556:89//AB014585
 R-PLACE1007737//Homo sapiens clone Sb19.12 Alu-Yb8 sequence.//4.0e-43:302:77//AF015169
 R-PLACE1007743//Plasmodium falciparum MAL3P8, complete sequence.//1.0e-06:533:59//AL034560
 R-PLACE1007746//T. brucei mitochondrial maxicircle DNA encoding cytochrome c oxidase subunit I (COI), and NADH dehydrogenase subunits 4 and 5, complete cds.//0.28:386:58//M14820
 R-PLACE1007791//D. discoideum gene for protein kinase.//0.17:263:60//Z37981
 R-PLACE1007807//Human DNA sequence from clone 87808 on chromosome Xq21.1-21.33. Contains an EST, STSs, a GSS and genomic marker DXS472, complete sequence.//1.1e-72:324:88//AL031116
 R-PLACE1007810//Homo sapiens chromosome 7 common fragile site, complete sequence.//2.2e-14:325:67//AF017104
 R-PLACE1007829//Human BAC clone GS165104 from 7q21, complete sequence.//0.00052:455:61//AC002379
 R-PLACE1007843//P. falciparum complete gene map of plastid-like DNA (IR-A).//0.0050:447:57//X95275
 R-PLACE1007846//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 3/15, WORKING DRAFT SEQUENCE.//2.2e-11:570:95//AP000010
 R-PLACE1007852//HS_3028_B2_F04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3028 Col=8 Row=L, genomic survey sequence.//1.3e-12:209:71//AQ131021
 R-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//6.6e-110:574:94//AB018309
 R-PLACE1007866//Homo sapiens DNA sequence from PAC 454M7 on chromosome Xq25-26.3. Contains the OCRL1 gene for Lowe Oculocerebrorenal Syndrome protein OCRL-1. Contains ESTs, STSs and GSSs, complete sequence.//1.6e-43:551:70//AL022162
 R-PLACE1007877//Homo sapiens chromosome 5, BAC clone 34j15 (LBNL H169), complete sequence.//1.6e-22:222:78//AC005754
 R-PLACE1007897//HS_3113_B2_E04_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3113 Col=8 Row=J, genomic survey sequence.//2.9e-72:381:95//AQ186905
 R-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487.//8.8e-88:460:95//AB007956
 R-PLACE1007946//Human chromosome Y cosmid 54E8 genomic sequence, WORKING DRAFT SEQUENCE.//4.9e-23:172:78//AC003095
 R-PLACE1007954//Homo sapiens BAC clone NH0414C23 from Y, complete sequence.//1.7e-27:303:75//AC006157
 R-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds.//3.9e-102:513:95//AF084530
 R-PLACE1007958//Homo sapiens CAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//2.2e-87:465:93//AF079529
 R-PLACE1007969//Mus musculus myelin gene expression factor (MEF-2) mRNA, partial cds.//4.8e-72:556:81//U13262
 R-PLACE1007990//E. tenella antigen LPMC1 mRNA, partial cds.//0.043:273:63//M30933
 R-PLACE1008000//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 668J24, WORKING DRAFT SEQUENCE.//8.8e-10:453:62//AL034346
 R-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//9.0e-114:563:96//AC005628
 R-PLACE1008044//Rattus norvegicus nuclear pore complex protein NUP107 mRNA, complete cds.//2.6e-44:509:72//L31840
 R-PLACE1008045//Homo sapiens chromosome 5, BAC clone 79a6 (LBNL H172), complete sequence.//0.32:137:66//AC005592
 R-PLACE1008080//Arabidopsis thaliana chromosome 11 BAC F10A12 genomic sequence, complete sequence.//0.082:292:59//AC006232
 R-PLACE1008095//Homo sapiens BAC clone NH0364H22 from 2, complete sequence.//5.4e-27:260:76//AC005036
 R-PLACE1008111//Human variable number tandem repeat (VNTR) region, allele 12R1 3' to collagen type II (COL2A1) gene.//2.2e-07:444:59//L10157
 R-PLACE1008122//Homo sapiens chromosome 17, clone hRPC.142_H_19, complete sequence.//1.9e-11:384:63//AC005919
 R-PLACE1008129//Homo sapiens clone DJ1087M19, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.0e-10:189:66//AC004955
 R-PLACE1008132//Human HepG2 3' region cDNA, clone hnd5d06.//7.4e-47:320:86//D16939
 R-PLACE1008177//Mouse mRNA for meiosis-specific nuclear structural protein 1 (MNS1), complete cds.//2.6e-32:410:70//D14849
 R-PLACE1008181//Caenorhabditis elegans cosmid C31H2.//0.055:358:60//U41748

【0834】

【表534】

R-PLACE1008198
R-PLACE1008201//Homo sapiens mRNA for KIAA0530 protein, partial cds.//4.8e-103:551:93//AB011102
R-PLACE1008209//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1125A11, WORKING DRAFT SEQUENCE.//4.6e-16:250:71//AL034549
R-PLACE1008231//Plasmodium falciparum 3D7 chromosome 12 PFYAC59 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.13:341:60//AC004688
R-PLACE1008244//P. falciparum P.195 gene.//0.11:212:66//A04562
R-PLACE1008273//Human MEST mRNA, complete cds.//0.00013:52:100//D78611
R-PLACE1008275
R-PLACE1008280//Homo sapiens chromosome 7 clone UWGC:g3586a160 from 7p14-15, complete sequence.//1.5e-05:104:76//AC005272
R-PLACE1008309//Human alpha-rich region adjacent to alpha satellite DNA.//0.70:138:63//M80308
R-PLACE1008329//Homo sapiens chromosome 10 clone CIT-HSP-1240G16 map 10q25.1, complete sequence.//0.00061:150:68//AC005886
R-PLACE1008330//Homo sapiens chromosome 19, cosmid F21431, complete sequence.//4.8e-74:252:98//AC005176
R-PLACE1008331//Genomic sequence from Human 13, complete sequence.//1.0:176:65//AC001226
R-PLACE1008356//Homo sapiens meningioma-expressed antigen 5 (MEAS) mRNA, 3' UTR.//2.5e-98:556:90//AF036145
R-PLACE1008368//HS-1039-A1-C10-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 821 Col=19 Row=E, genomic survey sequence.//1.2e-05:375:62//B36336
R-PLACE1008369//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 4/15, WORKING DRAFT SEQUENCE.//2.8e-10:466:61//AP000011
R-PLACE1008392//Homo sapiens chromosome 17, clone hRPC.471_L_13, complete sequence.//1.0e-46:282:82//AC005244
R-PLACE1008398//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 215D11, WORKING DRAFT SEQUENCE.//4.1e-101:529:94//AL034417
R-PLACE1008401//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0366H07: HTGS phase 1, WORKING DRAFT SEQUENCE, 28 unordered pieces.//0.18:379:58//AC004604
R-PLACE1008402//Homo sapiens mRNA for p115, complete cds.//1.6e-101:521:95//D086326
R-PLACE1008405//Human cosmid CRI-JC2015 at D10S289 in 10sp13.//6.8e-22:328:71//J015177
R-PLACE1008424
R-PLACE1008426//Homo sapiens genomic DNA of 8p21.3-p22 anti-oncogene of hepatocellular colorectal and non-small cell lung cancer, segment 7/11.//7.5e-101:505:96//AB020864
R-PLACE1008429//Human DNA sequence from clone 20J23 on chromosome Xq26.2-27.2 Contains ras-related C3 botulinum toxin substrate 1 (P21-RAC1) (ras-like protein TC25) EST, CA repeat, STS, CpG island, complete sequence.//1.2e-11:118:78//AL022576
R-PLACE1008437//H. sapiens genomic DNA (PAC 838L14) from chromosome 11, WORKING DRAFT SEQUENCE.//2.2e-06:159:69//Y12335
R-PLACE1008455
R-PLACE1008457//Homo sapiens chromosome 17, Neurofibromatosis 1 locus, complete sequence.//1.2e-109:588:93//AC004526
R-PLACE1008465//CIT978SK-A-28A11.TVE CIT978SK Homo sapiens genomic clone A-28A11, genomic survey sequence.//1.1e-10:133:77//B78696
R-PLACE1008488
R-PLACE1008524//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 34821, WORKING DRAFT SEQUENCE.//7.3e-120:612:95//AL031778
R-PLACE1008531//Homo sapiens wbscr1 (WBSR1) and replication factor C subunit 2 (RFC2) genes, complete cds.//8.5e-96:510:93//AF045555
R-PLACE1008532
R-PLACE1008533
R-PLACE1008568//HS_3218_02_008_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3218 Col=16 Row=H, genomic survey sequence.//0.0042:295:62//AQ214623
R-PLACE1008584//Human PAC clone DJ0596009 from 7p15, complete sequence.//5.0e-26:254:66//AC003074
R-PLACE1008621//Homo sapiens chromosome 17, clone hRPC.346_K_10, complete sequence.//4.0e-78:498:86//AC006120
R-PLACE1008625
R-PLACE1008626//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 97P20, WORKING DRAFT SEQUENCE.//5.5e-06:228:67//AL031297
R-PLACE1008627//Cricetulus griseus mRNA for Zn finger factor.//3.4e-20:335:71//Y12836
R-PLACE1008629//Homo sapiens clone DJ0309D19, WORKING DRAFT SEQUENCE, 12 unordered pieces.//0.55:326:58//AC004826
R-PLACE1008630//Homo sapiens genomic DNA, 21q region, clone: B175P11X96, genomic survey sequence.//0.13:440:55//AG011096
R-PLACE1008643//Human BAC clone RG083J23 from 7q31, complete sequence.//1.3e-58:356:82//AC004001
R-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//2.4e-88:434:97//AF044333
R-PLACE1008693//CIT-HSP-2025M9.TR CIT-HSP Homo sapiens genomic clone 2025M9, genomic survey sequence.//1.2e-41:300:82//B64742
R-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//4.8e-31:320:75//AF038406
R-PLACE1008715//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 799N4, WORKING DRAFT SEQUENCE.//0.074:478:58//AL022147
R-PLACE1008748//CIT-HSP-2170P12.TR CIT-HSP Homo sapiens clone 2170P12, genomic survey sequence.//8.5e-42:160:86//B90841
R-PLACE1008757//Homo sapiens 12q24.2 PAC RPC14-765H13 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.99:21:1:61//AC005864
R-PLACE1008790//Rattus norvegicus clonol polymeric immunoglobulin receptor mRNA 3' untranslated region, CA rich region, and microsatellites with GGA-triplet and GAA-triplet repeats.//0.052:108:68//U00762
R-PLACE1008798//Homo sapiens full length insert cDNA clone Y286CD5.//7.7e-58:285:100//AF086088
R-PLACE1008807//CIT-HSP-2366014.TR CIT-HSP Homo sapiens genomic clone 2366014, genomic survey sequence.//3.5e-35:223:89//AQ079210
R-PLACE1008808//Homo sapiens exonuclease homolog RAD1 (RAD1) mRNA, complete cds.//2.3e-97:499:95//AF030933
R-PLACE1008813//Rattus norvegicus rsec15 mRNA, complete cds.//9.7e-45:394:78//AF032668
R-PLACE1008851//Human Chromosome 15q26.1 PAC clone pJ460g16, WORKING DRAFT SEQUENCE, 3 unordered pieces.//2.9e-28:207:87//AC004581
R-PLACE1008854//CIT-HSP-2172B3.TF CIT-HSP Homo sapiens genomic clone 2172B3, genomic survey sequence.//8.9e-30:166:97//B93289
R-PLACE1008867//Homo sapiens BAC clone RG054D04 from 7q31, complete sequence.//3.5e-76:404:95//AC005058
R-PLACE1008887//Homo sapiens clone DJ0943F02, WORKING DRAFT SEQUENCE, 3 unordered pieces.//7.7e-37:585:67//AC004932
R-PLACE1008902//Homo sapiens chromosome Y, clone hCIT.494_G_17, complete sequence.//0.0022:409:60//AC005820
R-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds.//8.2e-55:344:89//AB018308
R-PLACE1008925//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y53F4, WORKING DRAFT SEQUENCE.//0.0014:398:58//Z92860
R-PLACE1008934
R-PLACE1008941//Homo sapiens chromosome 17, clone hRPC.293_K_20, complete sequence.//9.8e-84:429:92//AC005495
R-PLACE1008947
R-PLACE1009020
R-PLACE1009027//Human DNA sequence from clone 914P14 on chromosome Xq23 Contains calpain-like protease gene, OCX (doublecortin).EST s, CA repeat, GSS, complete sequence.//1.3e-82:434:95//AL031117
R-PLACE1009039//Human DNA sequence from clone 276K20 on chromosome 6p22.1-22.3. Contains STSs, GSSs and a putative CpG island, complete sequence.//0.00010:297:58//AL031391
R-PLACE1009045//Homo sapiens chromosome 17, clone hRPC.117_B_12, complete sequence.//2.9e-06:160:70//AC004707
R-PLACE1009048//Human DNA sequence from clone 511E16 on chromosome 6p24.3-25.1. Contains the last coding exon of the gene for P18 component of aminoacyl-tRNA synthetase complex, part of an unknown gene downstream of a putative CpG island, and an STS with a CA repeat polymorphism, complete sequence.//1.3e-16:339:66//AL023694
R-PLACE1009050//Aedes aegypti gene sequence, primary transcript.//0.40:393:59//L17023
R-PLACE1009060//Mus musculus mRNA for Alix-SF (ALG-2-interacting protein X, short form, complete CDS.//0.00075:79:83//AJ005074
R-PLACE1009090//Homo sapiens chromosome 1, BAC CIT-HSP-292g8 (BC262482), complete sequence.//6.7e-13:212:73//AC004783
R-PLACE1009094//Caenorhabditis elegans cosmid C49F8, complete sequence.//0.49:221:61//Z70206
R-PLACE1009099
R-PLACE1009110//Homo sapiens Xp22 BAC GS-321G17 (Genome Systems Human BAC library) complete sequence.//5.1e-17:301:66//AC004025
R-PLACE1009111//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-42 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//1.2e-06:234:61//AC005140
R-PLACE1009130//Plasmodium falciparum MAL3P6, complete sequence.//

【0835】

【表535】

7.5e-06:426:58//Z98551
R-PLACE1009150//Homo sapiens *** SEQUENCING IN PROGRESS *** WORKING DRAFT SEQUENCE.//2.3e-118:614:95//AJ011929
R-PLACE1009155//Homo sapiens genomic DNA, chromosome 21q11.1, segment 2/28, WORKING DRAFT SEQUENCE.//1.4e-107:584:93//AF000031
R-PLACE1009158//Homo sapiens full length insert cDNA clone YP1000.3.//1.9e-105:539:95//AF085876
R-PLACE1009166//Homo sapiens chromosome 17, clone hRPK.180_P.8, complete sequence.//2.8e-44:360:71//AC005972
R-PLACE1009172//Human cosmid QLL2C9 from Xq28.//4.1e-37:401:74//Z47046
R-PLACE1009174//Homo sapiens PAC clone DJ0907C10 from 7q31-3q32, complete sequence.//2.1e-17:140:81//AC004925
R-PLACE1009183//Homo sapiens DNA sequence from PAC 418A9 on chromosome 6q21. Contains the first (5') two exons of a CDK8 (Cell Division Protein Kinase 8) LIKE gene, a Neutral Calponin LIKE pseudogene, ESTs and STSs, complete sequence.//1.9e-46:572:69//Z84480
R-PLACE1009186//Human Chromosome X, complete sequence.//0.016:322:61//AC004070
R-PLACE1009190//Plasmodium falciparum MAL3P8, complete sequence.//0.050:487:58//AL034560
R-PLACE1009200//H. sapiens mRNA for sortilin.//1.0e-31:195:92//X98248
R-PLACE1009230//Homo sapiens chromosome 19, CIT-HSP BAC 490g23 (BC338531), complete sequence.//1.8e-75:364:85//AC005392
R-PLACE1009246//Cricetulus griseus SRD-2 mutant steroid regulatory element binding protein-2 (SREBP-2) mRNA, complete cds.//6.6e-44:525:71//U22818
R-PLACE1009308
R-PLACE1009319//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.00010:132:75//AC004801
R-PLACE1009328//Homo sapiens chromosome 17, clone hRPK.346_K_10, complete sequence.//3.3e-87:576:85//AC006120
R-PLACE1009335//Borrelia burgdorferi (section 62 of 70) of the complete genome.//0.32:315:60//AE001176
R-PLACE1009338//Plasmodium falciparum 3D7 chromosome 12 PFYAC88-420 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered-pieces.//6.8e-05:411:59//AC005140
R-PLACE1009368//Homo sapiens PAC clone DJ1179J19 from 7q11.23-q21, complete sequence.//0.00040:280:61//AC004989
R-PLACE1009375//D. yakuba mitochondrial DNA for origin of replication, small ribosomal RNA, transfer RNAs tRNA-Met, tRNA-Gln, tRNA-A-Ile and tRNA-Val.//1.1e-08:444:60//X05915
R-PLACE1009388
R-PLACE1009398//Homo sapiens BAC clone GS011E15 from Sq31, complete sequence.//0.065:279:61//AC002427
R-PLACE1009404//Homo sapiens clone NH0486122, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.0e-06:253:64//AC005038
R-PLACE1009410//Homo sapiens chromosome 17, clone hRPK.142_H_19, complete sequence.//9.8e-112:561:96//AC005919
R-PLACE1009434//Human DNA sequence from clone 459L4 on chromosome 6p22.3-24.1 Contains EST, STS, GSS, complete sequence.//2.2e-21:126:79//AL031120
R-PLACE1009443//Homo sapiens nucleolar protein Nop30 and cytoplasmic protein Myp (NOP) gene, alternatively spliced products, complete cds.//4.5e-14:117:91//AF064598
R-PLACE1009444//Homo sapiens phosphatidylinositol 4-kinase mRNA, complete cds.//9.6e-85:479:90//L36151
R-PLACE1009459
R-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67A1, complete sequence.//5.6e-101:540:94//AC004531
R-PLACE1009477//Homo sapiens, clone hRPK.15_A_1, complete sequence.//3.4e-46:284:91//AC006213
R-PLACE1009493//Human Chromosome 16 BAC clone CIT987SK-A-363E6, complete sequence.//5.5e-107:581:92//U91321
R-PLACE1009524//Homo sapiens DNA sequence from PAC 63G5 on chromosome 22q12.3-13.1. Contains part of a gene for a human SEC7 homolog B2-1 (cytohesin-2, Arno, ARF exchange factor) LIKE protein, an unknown gene and a gene coding for a Leucine rich protein. Contains ESTs, STSs and GSSs, complete sequence.//0.74:301:61//Z94160
R-PLACE1009539//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167A19, WORKING DRAFT SEQUENCE.//5.7e-29:357:74//AL031427
R-PLACE1009542//CIT-HSP-2166P10, TRB CIT-HSP Homo sapiens genomic clone 2166P10, genomic survey sequence.//2.6e-10:145:75//B89614
R-PLACE1009571//RPC11-61J16, TK RPC111 Homo sapiens genomic clone R-61J16, genomic survey sequence.//0.016:68:80//AQ020146
R-PLACE1009581
R-PLACE1009595//Homo sapiens clone DJ56J10, complete sequence.//1.8e-38:365:79//AC005006
R-PLACE1009596//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 501A4, WORKING DRAFT SEQUENCE.//1.2e-29:314:76//Z98051
R-PLACE1009607//cSRL-77g9-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-77g9, genomic survey sequence.//2.1e-05:142:69//B06230
R-PLACE1009613//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 4-89, complete sequence.//3.6e-08:434:59//AL010266
R-PLACE1009621//Sequence 50 from patent US 5691147.//1.5e-20:235:73//I76222
R-PLACE1009622//CIT-HSP-2023D13, TFB CIT-HSP Homo sapiens genomic clone 2023D13, genomic survey sequence.//0.72:176:62//B81271
R-PLACE1009637//P. falciparum complete gene map of plastid-like DNA (IR-B).//0.0068:396:59//X95276
R-PLACE1009639//Arabidopsis thaliana DNA chromosome 4, BAC clone F10M6 (ESSA11 project).//0.013:521:58//AL021811
R-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds.//1.0e-107:589:92//AB011159
R-PLACE1009665//Human PAC clone DJ0658N05 from 7p21, complete sequence.//8.4e-72:487:85//AC003075
R-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//2.0e-61:310:97//AF062534
R-PLACE1009708//Homo sapiens clone DJ0935K16, complete sequence.//2.8e-103:542:94//AC006011
R-PLACE1009721//Human Cosmid g0771a222 from 7q31.3, complete sequence.//4.6e-85:518:88//AC000109
R-PLACE1009731//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2BP adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//0.0033:215:65//AL022398
R-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds.//6.2e-116:598:95//AF046024
R-PLACE1009794
R-PLACE1009798//Human DNA sequence from clone 1189824 on chromosome Xc25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, C1-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs, an STS and GSSs, complete sequence.//7.5e-88:191:96//AL030996
R-PLACE1009845//Homo sapiens DNA sequence from PAC 234H5 on chromosome 6q21. Contains an unknown gene, ESTs and STSs, complete sequence.//8.7e-19:226:69//Z98172
R-PLACE1009879//Homo sapiens genomic DNA, 21q region, clone: 149C3A68, genomic survey sequence.//2.1e-29:230:76//AC002672
R-PLACE1009886//Homo sapiens PAC clone DJ0997N05 from 7q11.23-q21.1, complete sequence.//0.99:203:61//AC004945
R-PLACE1009888//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC301323), complete sequence.//5.3e-91:577:88//AC006116
R-PLACE1009908
R-PLACE1009921//Homo sapiens cosmid clone HDAB (15149) insert DNA, complete cosmid.//4.7e-81:385:84//M63005
R-PLACE1009924//HS_3151_B1_B10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3151 Col-19 Row-D, genomic survey sequence.//5.5e-47:240:99//AQ167412
R-PLACE1009925//CIT978SK-A-931F6, TV CIT978SK Homo sapiens genomic clone A-931F6, genomic survey sequence.//0.00010:159:68//B51673
R-PLACE1009935//Plasmodium falciparum 3D7 chromosome 12 PFYAC92 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.081:238:65//AC005308
R-PLACE1009947//Homo sapiens PAC clone 248015 from 13q12-q13, complete sequence.//1.0:353:58//AC002483
R-PLACE1009971//Homo sapiens full length insert cDNA clone ZD38E1.2.//3.7e-11:152:75//AF086247
R-PLACE1009992
R-PLACE1009995//Plasmodium falciparum chromosome 2, section 4 of 73 of the complete sequence.//0.0019:305:61//AE001367
R-PLACE1009997//Homo sapiens chromosome 10 clone CIT987SK-1175G20 map 10q25.2-10q25.3, complete sequence.//1.8e-43:462:76//AC005874
R-PLACE1010023//HS_3018_B1_H10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3018 Col-19 Row-P, genomic survey sequence.//0.00013:198:63//AQ093513
R-PLACE1010031//Human DNA sequence from clone 30M3 on chromosome 6p22.1-22.3. Contains three novel genes, one similar to C. elegans Y63D3A.4 and one similar to (predicted) plant, worm, yeast and archaea bacterial genes, and the first exon of the KIAA0319 gene. Contains ESTs, GSSs and putative CpG islands, complete sequence.//7.4

【表536】

e-115:581:96//AL031775
R-PLACE1010053//M.musculus Spnr mRNA for RNA binding protein.//1.9
e-05:136:74//X84692
R-PLACE1010069//CIT-HSP-2328B12.TF CIT-HSP Homo sapiens genomic cl
one 2328B12, genomic survey sequence.//2.6e-60:324:94//AQ042094
R-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete
cds.//4.6e-87:543:88//AF065482
R-PLACE1010076//*** SEQUENCING IN PROGRESS *** Homo sapiens chromo
some 4, BAC clone C0473M13: HTGS phase 1, WORKING DRAFT SEQUENCE,
4 unordered pieces.//6.3e-08:489:58//AC005699
R-PLACE1010083
R-PLACE1010089//F19F22-Sp6 IGF Arabidopsis thaliana genomic clone
F19F22, genomic survey sequence.//0.14:400:59//B10583
R-PLACE1010096//R.norvegicus mRNA for 100 kDa protein.//4.3e-91:56
2:87//X64411
R-PLACE1010102//Apis mellifera tRNA-Leu cytochrome oxidase II inte
rgenic spacer region, mitochondrial sequence.//1.5e-08:357:60//AF0
39556
R-PLACE1010105//Plasmodium falciparum chromosome 2, section 11 of
73 of the complete sequence.//4.0e-09:510:59//AE001374
R-PLACE1010106//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 54820, WORKING DRAFT SEQUENCE.//1.4e-12:194:73//Z98304
R-PLACE1010134
R-PLACE1010148//HS_3128_A1_D09_MR CIT Approved Human Genomic Sperm
Library D Homo sapiens genomic clone Plate=3128 Col=17 Row=G, gen
omic survey sequence.//0.17:281:61//AQ140790
R-PLACE1010152//Mouse mRNA for arylhydrocarbon receptor, complete
cds.//3.1e-45:351:81//D38417
R-PLACE1010181//Homo sapiens clone DJ0914M06, WORKING DRAFT SEQUEN
CE, 1 unordered pieces.//3.6e-06:207:66//AC004928
R-PLACE1010194//HS_2232_B1_H10_MR CIT Approved Human Genomic Sperm
Library D Homo sapiens genomic clone Plate=2232 Col=19 Row=P, gen
omic survey sequence.//2.4e-08:134:74//AQ185425
R-PLACE1010202//Human DNA sequence from clone 227L5 on chromosome
Xp11.22-11.3. Contains a Keratin, Type I Cytoskeletal 18 (KRT18, C
YK18, K18, CK18) pseudogene and an STS, complete sequence.//0.0003
5:383:61//AL031585
R-PLACE1010231//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 287G14, WORKING DRAFT SEQUENCE.//1.2e-95:519:94//AL0333
77
R-PLACE1010261
R-PLACE1010270//H.sapiens CpG island DNA genomic MseI fragment, cl
one 85a6, reverse read cpg85a6.rta.//0.068:171:63//Z63482
R-PLACE1010274//S.douglasii gene for cytochrome b.//4.5e-07:276:63
//X59280
R-PLACE1010293//Homo sapiens chromosome 2 PAC RPC13-417E16 (Roswel
l Park Cancer Institute Human PAC library) complete sequence.//4.7
e-91:522:90//AC004464
R-PLACE1010321
R-PLACE1010324//Caenorhabditis elegans DNA *** SEQUENCING IN PROGR
ESS *** from clone Y38E10, WORKING DRAFT SEQUENCE.//5.7e-08:484:57
//AL021149
R-PLACE1010329//Homo sapiens Chromosome 22q11.2 Cosmid Clone 50d10
in IGLC Region, complete sequence.//7.9e-35:328:79//AC000024
R-PLACE1010341//Homo sapiens clone DJ125K23, WORKING DRAFT SEQUEN
CE, 21 unordered pieces.//1.3e-31:418:66//AC004971
R-PLACE1010362
R-PLACE1010364//Mus cookii mitochondrion DNA fragment.//0.23:162:6
4//M77098
R-PLACE1010383//Homo sapiens chromosome 17, clone hCIT.186_H_2, co
mplete sequence.//1.4e-105:543:95//AC004675
R-PLACE1010401//Human Chromosome 15q11-q13 PAC clone pDJ223c9 from
the Prader-Willi/Angelman Syndrome region, complete sequence.//0.
00017:268:62//AC004137
R-PLACE1010481//Bos taurus C5-glucuronyl epimerase mRNA, partial c
ds.//8.6e-79:556:83//AF003927
R-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, comp
lete cds.//7.3e-88:438:96//AF039081
R-PLACE1010492//HS_3169_B2_B04_T7 CIT Approved Human Genomic Sperm
Library D Homo sapiens genomic clone Plate=3169 Col=8 Row=D, geno
mic survey sequence.//0.98:171:63//AQ169892
R-PLACE1010522//WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.34:
407:62//AC006082
R-PLACE1010547
R-PLACE1010562//CITBI-E1-2503B16.TF CITBI-E1 Homo sapiens genomic
clone 2503B16, genomic survey sequence.//6.4e-17:152:84//AQ265929
R-PLACE1010579//Torulopsis glabrata mitochondrial gene for ribosom
al protein var1.//1.7e-05:271:65//X02893
R-PLACE1010580
R-PLACE1010599
R-PLACE1010616//Human BAC clone RG343P13 from Tq31, complete seque
nce.//3.0e-13:151:75//AC002465
R-PLACE1010622//Arabidopsis thaliana BAC F1104.//0.00031:366:60//A
F096370
R-PLACE1010624//Homo sapiens chromosome 7q22 sequence, complete se
quence.//8.2e-34:322:79//AF053356
R-PLACE1010628//Homo sapiens clone DJ0647C14, WORKING DRAFT SEQUEN
CE, 21 unordered pieces.//2.3e-97:515:94//AC004846
R-PLACE1010629//HS_3003_A2_C08_MR CIT Approved Human Genomic Sperm
Library D Homo sapiens genomic clone Plate=3003 Col=16 Row=E, gen
omic survey sequence.//5.6e-60:321:95//AQ130493
R-PLACE1010630//Plasmodium falciparum chromosome 2, section 19 of
73 of the complete sequence.//0.051:372:59//AE001382
R-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cd
s.//2.6e-92:497:93//AB011102
R-PLACE1010661//CIT-HSP-2008K15.TR CIT-HSP Homo sapiens genomic cl
one 2008K15, genomic survey sequence.//5.7e-27:160:95//B57089
R-PLACE1010662//Caenorhabditis elegans cosmid C12C8, complete sequ
ence.//9.4e-09:151:73//Z81467
R-PLACE1010702//CIT-HSP-2314C3.TR CIT-HSP Homo sapiens genomic clo
ne 2314C3, genomic survey sequence.//1.3e-90:459:96//AQ028536
R-PLACE1010714//Saccharomyces douglasii mitochondrial tRNA-Ser and
tRNA-Phe genes, partial sequence, and Var1p (var1) gene, mitochon
drial gene encoding mitochondrial protein, complete cds.//5.3e-08:
478:58//U49822
R-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCA
P-C) mRNA, partial cds.//3.8e-55:300:95//AF092564
R-PLACE1010739//Human DNA sequence from clone 393P23 on chromosome
Xq21.1-21.33. Contains GSSs, complete sequence.//3.4e-89:507:90//
Z95400
R-PLACE1010743
R-PLACE1010761//Homo sapiens chromosome 17, clone hRPX.294_J_22, c
omplete sequence.//3.0e-103:511:97//AC005921
R-PLACE1010771
R-PLACE1010786
R-PLACE1010800//Homo sapiens clone NH0084K19, WORKING DRAFT SEQUEN
CE, 30 unordered pieces.//1.8e-43:545:71//AC005682
R-PLACE1010802//Phoebeis agarithe large subunit ribosomal RNA gene,
partial sequence: tRNA-Val gene, complete sequence: and small sub
unit ribosomal RNA gene, partial sequence, mitochondrial genes for
mitochondrial RNAs.//1.9e-09:492:59//AF044862
R-PLACE1010811//Homo sapiens Xp22 BAC GSHB-257G1 (Genome Systems B
AC Library) complete sequence.//0.041:415:59//AC002524
R-PLACE1010833
R-PLACE1010856//Plasmodium falciparum 3D7 chromosome 12 PFYAC812 g
enomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00
22:512:55//AC004153
R-PLACE1010857//Homo sapiens genomic DNA of Bp21.3-p22 anti-oncoge
ne of hepatocellular colorectal and non-small cell lung cancer, s
egment 11/11.//4.9e-85:507:90//AB020868
R-PLACE1010870//RPC111-59K21.TK RPC111 Homo sapiens genomic clone
R-59K21, genomic survey sequence.//8.2e-85:422:97//AQ195697
R-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cd
s.//7.0e-100:501:96//AB011182
R-PLACE1010891//Homo sapiens chromosome X, clone 592, WORKING DRAF
T SEQUENCE, 8 unordered pieces.//0.10:162:61//AC002489
R-PLACE1010896//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 g
enomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.00
032:409:59//AC005505
R-PLACE1010900//Homo sapiens DNA, trinucleotide repeats region.//
3.2e-07:180:71//AB018488
R-PLACE1010916//Plasmodium falciparum DNA *** SEQUENCING IN PROGRE
SS *** from MAL4P1, WORKING DRAFT SEQUENCE.//0.041:205:60//AL03455
7
R-PLACE1010917
R-PLACE1010925//HS_2027_B2_B09_T7 CIT Approved Human Genomic Sperm
Library D Homo sapiens genomic clone Plate=2027 Col=18 Row=D, gen
omic survey sequence.//1.6e-46:404:77//AQ247031
R-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cd
s.//4.2e-65:402:89//AB011126
R-PLACE1010942//Homo sapiens intersectin short form mRNA, complete
cds.//1.9e-80:441:93//AF064243
R-PLACE1010944
R-PLACE1010947//D.discoideum rasG gene.//0.00044:181:65//Z11533
R-PLACE1010954//Homo sapiens clone RG228D17, WORKING DRAFT SEQUEN
CE, 2 unordered pieces.//3.0e-51:518:74//AC005077
R-PLACE1010960//Human DNA sequence *** SEQUENCING IN PROGRESS ***
from clone 451821, WORKING DRAFT SEQUENCE.//0.022:292:63//AL033522
R-PLACE1010965//Human mariner1 transposase gene, complete consensu
s sequence.//1.0e-64:444:84//U52077

【表537】

R-PLACE1011026//Rickettsia prowazekii strain Madrid E, complete genome: segment 3/4.//0.59:345:61//AJ235272
 R-PLACE1011032//Human DNA sequence from PAC 389A20 on chromosome X contains ESTs STS, CpG islands and polymorphic CA repeat.//0.62:82:75//Z93242
 R-PLACE1011041//H.sapiens DNA sequence.//0.051:162:66//Z22248
 R-PLACE1011046//Homo sapiens mRNA for KIAA0581 protein, partial cds.//2.9e-100:563:91//AB011153
 R-PLACE1011054//Human DNA sequence from PAC 46H23, BRCA2 gene region on chromosome 13q12-13 contains Klotho, ESTs.//4.7e-29:280:73//Z84483
 R-PLACE1011056//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 341D10, WORKING DRAFT SEQUENCE.//1.7e-39:288:84//Z97985
 R-PLACE1011057//CIT-HSP-2014F10, TF CIT-HSP Homo sapiens genomic clone 2014F10, genomic survey sequence.//2.4e-60:370:90//B58896
 R-PLACE1011090//Homo sapiens chromosome 4 clone B20DN5 map 4q25, complete sequence.//0.12:489:59//AC005509
 R-PLACE1011099//Homo sapiens chromosome Y, clone 486, O, 2, complete sequence.//8.4e-43:427:76//AC002531
 R-PLACE1011114//Homo sapiens mRNA for HIV associated non-Hodgkin's lymphoma (clone h11-14).//1.7e-29:179:94//Y16709
 R-PLACE1011133//HS-1058-B1-H02-MF, abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 780 Col=3 Row=P, genomic survey sequence.//1.0:133:63//B44006
 R-PLACE1011143//H.sapiens CpG island DNA genomic MseI fragment, clone 127a4, forward read cpg127a4, fta.//1.0:127:67//Z56550
 R-PLACE1011160//Homo sapiens HRIHF82038 mRNA, partial cds.//2.4e-95:534:91//AB015333
 R-PLACE1011165//Human Cosmid g5129s232 from Tq31.3, complete sequence.//0.47:355:58//AC003968
 R-PLACE1011185//Homo sapiens clone DJ0038110, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.3e-26:403:70//AC004820
 R-PLACE1011203//paramoecium species 4.51er mt dna dimer: replication init. region, clone 1.//1.0e-10:379:60//K00908
 R-PLACE1011219//HS_3036_B1_F08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3036 Col=15 Row=L, genomic survey sequence.//2.6e-39:253:88//AQ104587
 R-PLACE1011221//Homo sapiens T-cell receptor alpha delta locus from bases 250472 to 501670 (section 2 of 5) of the Complete Nucleotide Sequence.//0.32:279:60//AE000559
 R-PLACE1011229//HS_3002_B1_E10_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3002 Col=19 Row=J, genomic survey sequence.//9.3e-31:317:74//AQ303626
 R-PLACE1011263//Homo sapiens BAC clone GS166A23 from Tp21, complete sequence.//1.2e-109:571:94//AC005014
 R-PLACE1011273//Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COX1) gene, complete cds.//0.00027:337:61//M97514
 R-PLACE1011291
 R-PLACE1011296//H.sapiens steroid reductase pseudogene.//4.2e-37:326:80//M68887
 R-PLACE1011310//H.sapiens 5' flanking sequence of gene for corticotropin.//0.0017:416:60//X67661
 R-PLACE1011325//Plasmodium falciparum chromosome 2, section 35 of 73 of the complete sequence.//3.0e-10:511:59//AE001398
 R-PLACE1011332//Homo sapiens chromosome 17, clone HCIT3L16, WORKING DRAFT SEQUENCE, 7 unordered pieces.//8.3e-06:250:64//AC002344
 R-PLACE1011340//Human BAC clone RG341D10 from Tpl5-p21, complete sequence.//0.67:290:58//AC002530
 R-PLACE1011375//Mus musculus Kv3.4 gene, exon 4.//6.8e-23:190:86//AJ010310
 R-PLACE1011399//Plasmodium falciparum 3D7 chromosome 12 PFYACB8-42 0 genomic sequence, WORKING DRAFT SEQUENCE, 14 unordered pieces.//0.22:359:60//AC005140
 R-PLACE1011419//Human DNA sequence from cosmid U90B3, on chromosome Xp11, contains ESTs.//5.1e-32:282:81//Z74022
 R-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds.//1.5e-112:600:94//AB011102
 R-PLACE1011452//Homo sapiens clone DJ0945F02, WORKING DRAFT SEQUENCE, 7 unordered pieces.//3.9e-77:303:85//AC006013
 R-PLACE1011465
 R-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds.//7.9e-103:515:96//AB018255
 R-PLACE1011492//A-B37A4, TP CIT978SK Homo sapiens genomic clone A-B37A4, genomic survey sequence.//6.5e-37:234:82//B14085
 R-PLACE1011503//Homo sapiens chromosome 17, clone hRPC.1171_1_10, complete sequence.//0.99:267:60//AC004687
 R-PLACE1011520//Homo sapiens clone DJ1119N05, complete sequence.//2.0e-116:591:96//AC004968
 R-PLACE1011563//Plasmodium falciparum 3D7 chromosome 12 PFYAC59 genomic sequence, WORKING DRAFT SEQUENCE, 4 unordered pieces.//1.2e-13:566:59//AC004688
 R-PLACE1011567//Plasmodium falciparum MAL3P6, complete sequence.//0.62:358:61//Z98551
 R-PLACE1011576//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//8.7e-45:400:78//AC003973
 R-PLACE1011586//Homo sapiens chromosome 17, clone HRPC890E16, complete sequence.//2.2e-59:338:93//AC004477
 R-PLACE1011635//C.pasteurianum pfl gene and act gene.//0.71:288:60//X93463
 R-PLACE1011641//Mycoplasma genitalium random genomic clone sg11, partial cds.//0.023:232:60//U02205
 R-PLACE1011643//Homo sapiens chromosome 19, cosmid R33590, complete sequence.//1.4e-21:432:67//AC005620
 R-PLACE1011649//Homo sapiens clone 24432 mRNA sequence.//7.8e-72:14:91//AF070535
 R-PLACE1011650//Human PAC clone DJ327A19 from Xq25-q26, complete sequence.//5.1e-27:174:79//AC002477
 R-PLACE1011664//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 460D19, WORKING DRAFT SEQUENCE.//7.4e-05:238:65//AL031905
 R-PLACE1011675//CIT-HSP-2370M16, TR CIT-HSP Homo sapiens genomic clone 2370M16, genomic survey sequence.//1.3e-27:233:81//AQ108283
 R-PLACE1011682//H.sapiens HLA-DMB gene.//2.3e-22:390:67//X76776
 R-PLACE1011719//Homo sapiens 12q24.2 BAC RPC111-360E11 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//3.1e-24:409:66//AC004806
 R-PLACE1011725//Homo sapiens unknown mRNA downregulated by induced differentiation with 13-cis retinoic acid.//0.13:143:65//AF026526
 R-PLACE1011729//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y73BF9, WORKING DRAFT SEQUENCE.//1.1e-15:157:82//AL022345
 R-PLACE1011749//Homo sapiens clone RG315H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.5e-38:314:81//AC005089
 R-PLACE1011762//Homo sapiens BAC clone RG067E13 from Tq21, complete sequence.//1.9e-35:538:68//AC002383
 R-PLACE1011778//CIT-HSP-2326C17, TV CIT-HSP Homo sapiens genomic clone 2326C17, genomic survey sequence.//2.8e-58:346:91//AQ028782
 R-PLACE1011783//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 229A8, WORKING DRAFT SEQUENCE.//4.6e-38:288:84//Z86090
 R-PLACE1011858//Human DNA sequence from clone 496M17 on chromosome 6p11.2-12.3 Contains EST, GSS, complete sequence.//4.1e-104:524:97//AL031321
 R-PLACE1011874//Homo Sapiens Chromosome X clone BWX0312, complete sequence.//2.1e-100:511:95//AC004478
 R-PLACE1011875
 R-PLACE1011891//Human lens membrane protein (mp19) gene, exon 11.//0.0011:195:64//L04193
 R-PLACE1011896//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2B adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two novel genes. Contains ESTs and GSSs, complete sequence.//0.010:110:74//AL022398
 R-PLACE1011922//Homo sapiens chromosome 21q22.3 PAC 171F15, complete sequence.//3.5e-10:152:74//AF042090
 R-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds.//7.0e-98:546:92//AF059617
 R-PLACE1011962//CIT-HSP-2294L24, TF CIT-HSP Homo sapiens genomic clone 2294L24, genomic survey sequence.//0.31:131:63//AQ006352
 R-PLACE1011964//Homo sapiens chromosome 17, clone HRPC987K16, complete sequence.//2.5e-08:393:63//AC002994
 R-PLACE1011982//Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MDJ14, complete sequence.//9.6e-09:463:62//AB016889
 R-PLACE1011995//Human Down Syndrome region of chromosome 21, clone A12H1-2H4.//2.7e-39:294:82//U44738
 R-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds.//2.5e-104:540:95//AB018256
 R-PLACE2000003//Human PAC clone DJ404F18 from Xq23, complete sequence.//4.9e-10:439:63//AC004000
 R-PLACE2000007//Human fibroblast growth factor receptor 3 (FGFR3) gene, intron 3.//1.0:151:66//L78722
 R-PLACE2000011//Homo sapiens clone 614 unknown mRNA, complete sequence.//1.5e-103:524:95//AF091080
 R-PLACE2000015//Homo sapiens PAC clone DJ269005 from Xq23, complete sequence.//0.94:372:57//AC005191
 R-PLACE2000017//Homo sapiens chromosome 17, clone hCIT.162_E_12, complete sequence.//3.0e-55:299:86//AC006236
 R-PLACE2000021//CIT-HSP-2343C18, TR CIT-HSP Homo sapiens genomic clone 2343C18, genomic survey sequence.//4.5e-54:295:94//AQ058140

【0838】

【表538】

R-PLACE2000033//H.sapiens gene for mitochondrial ATP synthase c subunit (P1 form).//6.5e-38:298:82//X69907
 R-PLACE2000034//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//5.3e-34:200:79//AC005628
 R-PLACE2000039//Homo sapiens BAC clone RG060N22 from 7q21, complete sequence.//1.8e-49:274:89//AC003083
 R-PLACE2000047//CIT-HSP-2373C2, TR CIT-HSP Homo sapiens genomic clone 2373C2, genomic survey sequence.//1.8e-48:389:79//AQ112243
 R-PLACE2000050//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 117715, WORKING DRAFT SEQUENCE.//0.0027:95:76//AL022315
 R-PLACE2000061//Homo sapiens mRNA for KIAA0575 protein, complete cds.//2.9e-39:429:72//AB011147
 R-PLACE2000062//Homo sapiens clone DJ0539M06, WORKING DRAFT SEQUENCE, 10 unordered pieces.//5.9e-40:310:84//AC004832
 R-PLACE2000072//Homo sapiens ZNF202 beta (ZNF202) mRNA, complete cds.//1.9e-109:550:95//AF027219
 R-PLACE2000097//Homo sapiens chromosome 12p13.3 clone RPC111-189M2 O, WORKING DRAFT SEQUENCE, 39 unordered pieces.//1.6e-106:553:95//AC005910
 R-PLACE2000100//Human DNA sequence from clone 301K23 on chromosome 1p35.1-36.21. Contains the 5' part of a novel gene similar to predicted yeast and worm genes. Contains ESTs and GSSs, complete sequence.//1.8e-38:285:84//AL031730
 R-PLACE2000103//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 20208, WORKING DRAFT SEQUENCE.//4.3e-113:559:97//AL031848
 R-PLACE2000111//Rat MLC1V gene encoding alkali myosin ventricular light chain, exon 1.//0.00041:347:61//X16325
 R-PLACE2000115//Cervus elaphus MHC class II DRB pseudogene, intron 2 microsatellite.//0.50:165:63//U63067
 R-PLACE2000132
 R-PLACE2000136//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from contig 3-30, complete sequence.//0.0032:310:61//AL008974
 R-PLACE2000140//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 11703, WORKING DRAFT SEQUENCE.//1.1e-111:566:96//AL020995
 R-PLACE2000164
 R-PLACE2000170//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0024K08: HTGS phase 1, WORKING DRAFT SEQUENCE, 5 unordered pieces.//3.9e-40:390:76//AC005598
 R-PLACE2000172
 R-PLACE2000176
 R-PLACE2000187//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 268H5, WORKING DRAFT SEQUENCE.//8.7e-45:298:87//AL008718
 R-PLACE2000216//Dog nonerythroid beta-spectrin mRNA, 3' end.//5.6e-88:495:92//L02897
 R-PLACE2000223
 R-PLACE2000235//HS_3159_B1_B06_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate-3159 Col=11 Row=D, genomic survey sequence.//1.8e-88:454:96//AQ179271
 R-PLACE2000246//Homo sapiens chromosome 3p clone RPC14-544D10, WORKING DRAFT SEQUENCE, 58 unordered pieces.//9.1e-41:282:86//AC005902
 R-PLACE2000264//Homo sapiens DNA sequence from PAC 95C20 on chromosome Xp11.3-11.4. Contains STSs and the DXS7 locus with GT and CTG repeat polymorphisms, complete sequence.//8.3e-35:305:80//Z97181
 R-PLACE2000274//Human Chromosome 16 BAC clone CIT987SK-A-211C6, complete sequence.//3.5e-18:325:67//AC002394
 R-PLACE2000302//Homo sapiens chromosome 17, clone HRPC1067M6, complete sequence.//1.5e-39:287:85//AC003043
 R-PLACE2000305//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 16915, WORKING DRAFT SEQUENCE.//1.2e-43:295:85//Z93015
 R-PLACE2000317//Human DNA sequence from clone 245G19 on chromosome Xp22.11-22.2 Contains serine-threonine kinase (Txp3) gene, a pseudogene similar to ALPHA-1 PROTEIN ((CONNEXIN 43, CX43, GAP JUNCTION 43 KD HEART PROTEIN)), and the 3' end of the RSL (X-linked juvenile retinoschisis precursor protein) gene. Contains ESTs, STSs and GSSs, complete sequence.//4.0e-05:284:65//Z92542
 R-PLACE2000335//Homo sapiens clone DJ0755D09, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.5e-26:334:70//AC006147
 R-PLACE2000342//Fugu rubripes cosmid 258N02 containing 1QF11, TH, MAP2 genes.//4.0e-05:254:64//AL021880
 R-PLACE2000347//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 799N4, WORKING DRAFT SEQUENCE.//1.1e-82:504:88//AL022147
 R-PLACE2000359//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 40E16, WORKING DRAFT SEQUENCE.//2.0e-36:314:80//AL031963
 R-PLACE2000366//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 796F18, WORKING DRAFT SEQUENCE.//2.0e-48:389:80//AL03191
 R-PLACE2000371
 R-PLACE2000373//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 324M8, WORKING DRAFT SEQUENCE.//0.61:231:61//AL008734
 R-PLACE2000379//Homo sapiens clone DJ0892G19, complete sequence.//3.5e-11:287:67//AC004917
 R-PLACE2000394//Human DNA sequence from clone 465N24 on chromosome 1p35.1-36.13. Contains two novel genes, ESTs, GSSs and CpG island s, complete sequence.//6.8e-108:553:96//AL031432
 R-PLACE2000398//Homo sapiens clone RG074A24, WORKING DRAFT SEQUENCE, 25 unordered pieces.//2.9e-26:326:73//AC005059
 R-PLACE2000399
 R-PLACE2000404//Homo sapiens chromosome 5, BAC clone 282B7 (LBNL H 192), complete sequence.//6.5e-84:434:96//AC005216
 R-PLACE2000411//P.clarkii mRNA: repeat region (ID 2R).//0.47:104:70//Z54273
 R-PLACE2000419
 R-PLACE2000425//Homo sapiens X-linked anhidrotic ectodermal dysplasia protein gene (EDA), exon 2 and flanking repeat regions.//1.9e-40:447:74//AF003528
 R-PLACE2000427
 R-PLACE2000433//Human Chromosome 15 pac pDJ24m8, complete sequence.//3.5e-40:286:85//AC000379
 R-PLACE2000435
 R-PLACE2000438//Homo sapiens full length insert cDNA clone ZE04D01.//2.2e-107:523:98//AF086521
 R-PLACE2000450
 4.1e-42:328:79//AC006257
 R-PLACE2000455
 R-PLACE2000458//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//5.1e-116:570:97//AC005740
 R-PLACE2000465//Human BAC clone RG191D16, complete sequence.//6.3e-37:408:75//AC002460
 R-PLACE2000477//M.musculus tex264 mRNA (3' region).//7.5e-06:117:76//X80427
 R-PLACE3000004
 R-PLACE3000029//Human DNA sequence from PAC 506G2 contains STSs and a CpG island.//5.8e-34:308:78//Z82976
 R-PLACE3000059//Mus musculus mRNA for ubiquitin conjugating enzyme.//1.1e-36:273:87//Y17267
 R-PLACE3000070//Homo sapiens chromosome 5, PAC clone 17e19 (LBNL H 148), complete sequence.//2.3e-10:181:71//AC004648
 R-PLACE3000103//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30A23, WORKING DRAFT SEQUENCE.//1.2e-48:495:74//AL022156
 R-PLACE3000119//Homo sapiens Chromosome 22q12 BAC Clone 58b8 in Me ningioma Deletion Region, complete sequence.//3.4e-39:283:85//AC000026
 R-PLACE3000124//Homo sapiens chromosome 5, P1 clone 793c5 (LBNL HS 7), complete sequence.//9.2e-23:171:76//AC005200
 R-PLACE3000136//U.arctos microsatellite DNA, clone UarMU23.//0.00052:171:65//Y09645
 R-PLACE3000142//HS_3037_B2_B02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3037 Col=4 Row=D, genomic survey sequence.//0.88:121:66//AQ097023
 R-PLACE3000147//Mus musculus DNA for ADAMTS-1, complete cds.//3.3e-23:472:66//AB001735
 R-PLACE3000148//Human DNA from cosmid L27h9, Huntington's Disease Region, chromosome 4p16.3 contains CpG island.//3.5e-11:176:73//Z49237
 R-PLACE3000155//Homo sapiens chromosome 17, clone hRPK.597_M_12, complete sequence.//6.9e-106:549:94//AC005277
 R-PLACE3000156//Homo sapiens BAC clone RG067E13 from 7q21, complete sequence.//7.0e-38:545:70//AC002383
 R-PLACE3000157
 R-PLACE3000158//, complete sequence.//1.4e-33:283:81//AC005500
 R-PLACE3000160
 R-PLACE3000169//Homo sapiens chromosome 19, BAC CIT-B-191n6, complete sequence.//5.2e-43:229:85//AC006130
 R-PLACE3000194
 R-PLACE3000197//Homo sapiens chromosome 17, clone hRPK.401_0_9, complete sequence.//7.2e-61:394:89//AC005291
 R-PLACE3000199//Homo sapiens Xq28 genomic DNA in the region of the L1CAM locus containing the genes for neural cell adhesion molecule L1 (L1CAM), arginine-vasopressin receptor (AVPR2), C1 p115 (C1), ARD1 N-acetyltransferase related protein (TE2), renin-binding protein (RbP), host cell factor 1 (HCF1), and interleukin-1 receptor-associated kinase (IRAK) genes, complete cds, and Xq28lu2 gene.//

【表539】

0.23:309:57//U52112
 R-PLACE3000207//CIT-HSP-384B14.TR CIT-HSP Homo sapiens genomic clone 384B14, genomic survey sequence.//1.1e-15:156:81//B54637
 R-PLACE3000208//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 591N18, WORKING DRAFT SEQUENCE.//1.3e-16:139:87//AL031594
 R-PLACE3000218//HS_3185_B1_801_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3185 Col=1 Row=D, genomic survey sequence.//3.5e-07:120:75//AQ155720
 R-PLACE3000220//Homo sapiens chromosome 17, clone HRP1096F1, complete sequence.//2.4e-44:363:80//AC004167
 R-PLACE3000226//Caenorhabditis elegans cosmid M01G5.//0.88:95:77//AF078786
 R-PLACE3000230//Homo sapiens ccr2b (ccr2), ccr2a (ccr2), ccr5 (ccr5) and ccr6 (ccr6) genes, complete cds, and lactoferrin (lactoferrin) gene, partial cds, complete sequence.//5.3e-68:536:81//U95626
 R-PLACE3000242//Sequence 1 from patent US 5599918.//3.2e-62:546:78//J35489
 R-PLACE3000244//M.musculus mRNA for 200 kD protein.//1.7e-45:404:75//X80169
 R-PLACE3000254//Human mRNA for KIAA0309 gene, partial cds.//7.5e-28:174:94//AB002307
 R-PLACE3000271//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 423B22, WORKING DRAFT SEQUENCE.//3.9e-54:492:77//AL034379
 R-PLACE3000276//Homo sapiens PAC clone DJ0320J15 from Xq23, complete sequence.//5.4e-12:176:69//AC004081
 R-PLACE3000304//Homo sapiens chromosome 19, cosmid R26660, complete sequence.//5.7e-114:555:97//AC005328
 R-PLACE3000310//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 467L1, WORKING DRAFT SEQUENCE.//6.2e-51:314:84//Z98884
 R-PLACE3000320//Homo sapiens elastin gene, exons 5-27 and alternatively spliced products, partial cds.//2.5e-44:289:90//U93037
 R-PLACE3000322//Human argininosuccinate lyase (ASL) gene, exon 3.//5.9e-20:153:88//M21006
 R-PLACE3000331//Homo sapiens clone DJ0592C07, WORKING DRAFT SEQUENCE, 3 unordered pieces.//1.1e-43:230:84//AC005480
 R-PLACE3000339
 R-PLACE3000341//Homo sapiens 3p22 Contig 7 PAC RPC14-672N11 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.5e-111:550:97//AC006055
 R-PLACE3000350//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//1.5e-44:314:78//AL022323
 R-PLACE3000352//HS_3095_B1_E09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3095 Col=17 Row=J, genomic survey sequence.//8.5e-73:356:99//AQ123142
 R-PLACE3000353//Caenorhabditis elegans DNA *** SEQUENCING IN PROGRESS *** from clone Y22F5, WORKING DRAFT SEQUENCE.//0.21:194:63//Z9712
 R-PLACE3000362//Plasmodium falciparum coronin gene, isolate 3D7.//0.26:360:60//AJ002197
 R-PLACE3000363
 R-PLACE3000365//Human BAC clone RG343P13 from Tq31, complete sequence.//4.6e-52:487:76//AC002465
 R-PLACE3000373//HS_3202_B1_G05_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3202 Col=9 Row=N, genomic survey sequence.//2.4e-75:437:90//AQ252699
 R-PLACE3000388//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 732E4, WORKING DRAFT SEQUENCE.//6.4e-61:515:81//AL008722
 R-PLACE3000399//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//0.00098:444:60//AC005231
 R-PLACE3000400//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//0.78:155:66//AC005506
 R-PLACE3000401//Homo sapiens clone DJ1147A01, WORKING DRAFT SEQUENCE, 25 unordered pieces.//8.0e-47:223:81//AC006023
 R-PLACE3000402//Homo sapiens chromosome 17, clone 104H12, complete sequence.//1.0:179:63//AC000003
 R-PLACE3000405//Homo sapiens chromosome 7qtel0 BAC F6, complete sequence.//2.4e-44:466:74//AF104455
 R-PLACE3000406//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 268H5, WORKING DRAFT SEQUENCE.//7.7e-49:471:75//AL008718
 R-PLACE3000413
 R-PLACE3000416//Homo sapiens *** SEQUENCING IN PROGRESS *** from PAC 1577, WORKING DRAFT SEQUENCE.//5.4e-42:416:77//AJ009612
 R-PLACE3000425//Human DNA sequence from PAC 130C2 on chromosome 6p22.2-22.3. Contains ribosomal protein L29 pseudogene, ESTs and STS
 s.//1.1e-41:366:78//AL008627
 R-PLACE3000455//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 469D22, WORKING DRAFT SEQUENCE.//3.8e-98:549:92//AL031284
 R-PLACE3000475//Human signal transducing adaptor molecule STAM mRNA, complete cds.//1.9e-82:440:92//U43899
 R-PLACE3000477
 R-PLACE4000009//R.norvegicus mRNA encoding 45kDa protein which binds to heyman nephritis antigen gp330.//6.6e-17:344:68//Z11995
 R-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cds.//2.7e-83:433:95//AB018352
 R-PLACE4000034//cSRL-S1C5-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-S1C5, genomic survey sequence.//0.54:116:66//B04984
 R-PLACE4000049//Human BAC clone GS165104 from Tq21, complete sequence.//0.29:313:59//AC002379
 R-PLACE4000052//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//0.0058:466:57//AL034557
 R-PLACE4000063//Homo sapiens chromosome 7q22 sequence, complete sequence.//0.98:246:61//AF053356
 R-PLACE4000089//RPC11-1511.TVB RPC1-11 Homo sapiens genomic clone RPC1-11-1511, genomic survey sequence.//3.2e-07:284:60//B82414
 R-PLACE4000093//Plasmodium falciparum 3D7 chromosome 12 PFYAC357 genomic sequence, WORKING DRAFT SEQUENCE, 7 unordered pieces.//2.4e-07:429:60//AC005506
 R-PLACE4000100
 R-PLACE4000106//Homo sapiens clone 24561 unknown mRNA, partial cds.//9.3e-100:419:91//AF055010
 R-PLACE4000128//Human Chromosome 16 BAC clone CIT987SK-A-61E3, complete sequence.//9.6e-45:284:90//AC003007
 R-PLACE4000129//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500.//1.6e-19:118:100//AB007969
 R-PLACE4000147//Homo sapiens BAC clone NH0342K06 from 2, complete sequence.//8.9e-17:208:73//AC005034
 R-PLACE4000156//Homo sapiens DNA sequence from PAC 352A20 on chromosome 6q24.1-25.1. Contains a pseudogene similar to yeast, bacterial, worm and slime mold hypothetical genes, and a gene coding for an aldehyde dehydrogenase family protein. Contains ESTs, STSs and GSSs, complete sequence.//3.7e-43:281:90//AL021939
 R-PLACE4000192
 R-PLACE4000222//Homo sapiens clone DJ1129J21, WORKING DRAFT SEQUENCE, 25 unordered pieces.//5.4e-44:280:82//AC005631
 R-PLACE4000233//Homo sapiens full length insert cDNA YHS9C06.//1.8e-79:414:97//AF074981
 R-PLACE4000247//Homo sapiens chromosome 17, clone hRPK.156_L14, complete sequence.//5.7e-59:558:76//AC005821
 R-PLACE4000250//CIT-HSP-2335L20.TR CIT-HSP Homo sapiens genomic clone 2335L20, genomic survey sequence.//1.7e-44:313:84//AQ037381
 R-PLACE4000252//Homo sapiens chromosome 17, clone hRPK.700_H6, complete sequence.//1.5e-39:311:83//AC005920
 R-PLACE4000261//H.sapiens BF1P-gIH03np gene for immunoglobulin heavy chain variable region.//0.33:197:61//Z80410
 R-PLACE4000269//Homo sapiens chromosome 4 clone B368A9 map 4q25, complete sequence.//1.4e-31:327:68//AC005510
 R-PLACE4000270//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.3e-32:345:74//D87675
 R-PLACE4000300//Sequence 61 from patent US 5744300.//0.0017:51:98//AR003339
 R-PLACE4000320//Human DNA sequence from clone 441J1 on chromosome 6p24 Contains STS, GSS, complete sequence.//8.2e-41:295:85//Z99495
 R-PLACE4000323//Human chromosome 11 187a8 cosmid, complete sequence.//1.3e-32:404:75//U73640
 R-PLACE4000326
 R-PLACE4000344//Homo sapiens PAC clone DJ0988G15 from Tq33-q35, complete sequence.//0.32:135:68//AC005587
 R-PLACE4000367//H.sapiens gene encoding RING finger protein.//0.61:146:67//Y07829
 R-PLACE4000369//HS_3181_A1_B02_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3181 Col=3 Row=C, genomic survey sequence.//7.1e-80:424:94//AQ173222
 R-PLACE4000379//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1104E15, WORKING DRAFT SEQUENCE.//1.7e-05:160:65//AL022312
 R-PLACE4000387//Homo sapiens clone DJ0876A24, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.4e-47:351:81//AC004913
 R-PLACE4000392//Human DNA sequence from clone 751H9 on chromosome 6q13. Contains part of an unknown gene, ESTs, STSs and GSSs, complete sequence.//8.5e-88:541:88//AL034377
 R-PLACE4000401//Human Chromosome 11 overlapping pacs pDJ235k10 and

【0840】

【表540】

pDJ239622, WORKING DRAFT SEQUENCE, 17 unordered pieces.//2.7e-17:143.83//AC000406
 R-PLACE4000411
 R-PLACE4000445//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0.028:91:78//AC005628
 R-PLACE4000465//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30A23, WORKING DRAFT SEQUENCE.//1.6e-43:532:71//AL022156
 R-PLACE4000489//Plasmodium falciparum chromosome 2, section 64 of 73 of the complete sequence.//4.1e-06:357:61//AE001427
 R-PLACE4000494//Homo sapiens 12p13.3 PAC RPC15-1063M23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.7e-37:416:74//AC005855
 R-PLACE4000522
 R-PLACE4000548//Homo sapiens 12p13.3 PAC RPC15-1096D14 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.0020:383:60//AC005342
 R-PLACE4000558//Homo sapiens 12q24 BAC RPC111-162P23 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.9e-44:465:75//AC002996
 R-THYR01000026//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 37E16, WORKING DRAFT SEQUENCE.//2.2e-43:354:82//Z83844
 R-THYR01000034//Plasmodium falciparum chromosome 2, section 59 of 73 of the complete sequence.//0.022:327:60//AE001422
 R-THYR01000035//HS_3018_B2_F10_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3018 Col=20 Row=L, genomic survey sequence.//2.3e-36:228:91//AQ092318
 R-THYR01000040//Plasmodium falciparum 3D7 chromosome 12 PFYAC293 genomic sequence, WORKING DRAFT SEQUENCE, 9 unordered pieces.//1.0:367:56//AC004157
 R-THYR01000070//***ALU WARNING: Human Alu-Sq subfamily consensus sequence.//1.1e-44:284:89//U14573
 R-THYR01000072//***ALU WARNING: Human Alu-J subfamily consensus sequence.//6.6e-33:150:63//U14567
 R-THYR01000085
 R-THYR01000092//Homo sapiens chromosome 7qtel0 BAC F6, complete sequence.//3.3e-36:301:78//AF104455
 R-THYR01000107//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 12513, WORKING DRAFT SEQUENCE.//1.4e-35:282:82//AL033528
 R-THYR01000111//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//4.0e-32:351:65//AC002300
 R-THYR01000121//Human chromosome 16 BAC clone CIT987SK-A-962B4, complete sequence.//6.6e-77:507:85//U91318
 R-THYR01000124//High throughput sequencing of human chromosome 12, WORKING DRAFT SEQUENCE, 1 ordered pieces.//0.66:334:59//AC005840
 R-THYR01000129//Homo sapiens TED protein (TED) mRNA, complete cds.//2.3e-88:449:96//AF087142
 R-THYR01000132//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 212A2, WORKING DRAFT SEQUENCE.//1.1e-40:298:84//Z95114
 R-THYR01000156//Homo sapiens chromosome 17, clone hRPK.849_M_15, complete sequence.//3.4e-37:425:73//AC005703
 R-THYR01000163//RPC111-1B20, TVB RPC1-11 Homo sapiens genomic clone RPC1-11-1B20, genomic survey sequence.//8.4e-38:276:84//B63536
 R-THYR01000173//Human DNA sequence from PAC 323B6 on chromosome X contains ESTs CpG island.//1.1e-70:553:81//Z83841
 R-THYR01000186//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 41018, WORKING DRAFT SEQUENCE.//6.7e-41:345:81//AL031732
 R-THYR01000187//Human thymopoietin (TMPO) gene, partial exon 6, complete exon 7, partial exon 8, and partial cds for thymopoietin beta.//1.3e-43:356:80//U18271
 R-THYR01000190//Homo sapiens chromosome 17, clone HRP843B9, complete sequence.//2.6e-40:385:77//AC004139
 R-THYR01000197//Homo sapiens mRNA for poly(A)-specific ribonuclease.//1.1e-108:535:97//AJ005698
 R-THYR01000199//Homo sapiens mRNA for KIAA0652 protein, complete cds.//1.4e-113:559:97//AB014552
 R-THYR01000206//Rat PMSG-induced ovarian mRNA, 3' sequence, N4.//4.0e-43:318:86//D84482
 R-THYR01000221//Human DNA from overlapping chromosome 19 cosmid R31396, F25451, and R31076 containing CCK6B and UPKA, genomic sequence, complete sequence.//2.7e-44:452:76//AC002115
 R-THYR01000241//Homo sapiens Cosmid Clone p129d11 unknown chromosomal location, complete sequence.//4.8e-58:447:81//AC000039
 R-THYR01000242
 R-THYR01000253//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//3.4e-56:300:84//Z95152
 R-THYR01000270
 R-THYR01000279//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 531H16, WORKING DRAFT SEQUENCE.//4.8e-113:584:96//AL031664
 R-THYR01000288//Homo sapiens mRNA for Hs Ste24p, complete cds.//1.1e-98:566:91//AB016068
 R-THYR01000320//HS_2033_B1_A07_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2033 Col=13 Row=8, genomic survey sequence.//0.97:211:63//AQ233366
 R-THYR01000327//Sequence 1 from patent US 5541298.//2.8e-52:289:93//I24058
 R-THYR01000343//Homo sapiens mRNA for KIAA0790 protein, partial cds.//1.1e-111:559:96//AB018333
 R-THYR01000358//Human selenium-binding protein (hSBP) mRNA, complete cds.//4.6e-47:317:87//U29091
 R-THYR01000368//HS_3049_A1_E12_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3049 Col=23 Row=1, genomic survey sequence.//7.0e-11:111:83//AQ126777
 R-THYR01000381
 R-THYR01000387//Homo sapiens PAC clone DJ104BB16 from 7q34-q36, complete sequence.//2.4e-101:545:93//AC006019
 R-THYR01000394//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//1.6e-46:233:88//AC006078
 R-THYR01000395//Mouse MIPP mRNA for a placenta-expressed gene.//2.3e-57:395:85//X58523
 R-THYR01000401
 3.3e-111:546:97//AF051907
 R-THYR01000438//Homo sapiens clone DJ1186P10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//2.7e-44:289:89//AC005231
 R-THYR01000452//Homo sapiens chromosome 17, clone hRPK.243_K_12, complete sequence.//6.7e-27:222:82//AC005668
 R-THYR01000471//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 102024, WORKING DRAFT SEQUENCE.//2.4e-36:369:76//AL021391
 R-THYR01000484//Homo sapiens clone DJ1099N07, complete sequence.//1.6e-43:288:81//AC004962
 R-THYR01000488//Homo sapiens chromosome 5p, BAC clone 50g21 (LBNL H154), complete sequence.//1.6e-95:512:94//AC005740
 R-THYR01000501//HS_2208_A1_G11_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2208 Col=21 Row=M, genomic survey sequence.//0.0063:189:63//AQ091586
 R-THYR01000502//Homo sapiens eIF-1A, Y isoform (EIF1AY) mRNA, complete cds.//0.19:468:60//AF000987
 R-THYR01000505//Homo sapiens chromosome 19, cosmid R31546, complete sequence.//0.20:214:58//AC004798
 R-THYR01000558
 R-THYR01000569
 R-THYR01000570//Homo sapiens full length insert cDNA clone ZD76G10.//4.3e-41:209:100//AF086408
 R-THYR01000585//Homo sapiens protein associated with Myc mRNA, complete cds.//8.2e-107:533:97//AF075587
 R-THYR01000596//Mus musculus mitochondrial DNA polymerase accessory subunit (MtPol8) mRNA, nuclear gene encoding mitochondrial protein, partial cds.//0.35:170:67//AF006072
 R-THYR01000602//Homo sapiens DNA for amyloid precursor protein, complete cds.//2.2e-53:289:92//D87675
 R-THYR01000605
 R-THYR01000625//Homo sapiens chromosome 19, cosmid R29425, complete sequence.//1.3e-31:261:82//AC005546
 R-THYR01000637//Human DNA sequence from clone 243E7 on chromosome 22q12.1. Contains ESTs, STSs and GSSs, complete sequence.//4.0e-06:249:63//AL022323
 R-THYR01000641//P. falciparum glutamic acid-rich protein gnen, complete cds.//3.1e-08:244:68//J03998
 R-THYR01000658//***ALU WARNING: Human Alu-Sp subfamily consensus sequence.//3.9e-49:282:93//U14572
 R-THYR01000662
 R-THYR01000666//Homo sapiens DNA sequence from PAC 329E20 on chromosome 1p34.4-36.13. Contains endothelin-converting-enzyme 1 (ECE-1), EST, STS, CA repeat, complete sequence.//1.9e-20:215:77//AL031005
 R-THYR01000676//Homo sapiens chromosome 4 clone B71M12 map 4q25, complete sequence.//1.1e-06:227:64//AC004069
 R-THYR01000684
 R-THYR01000699
 R-THYR01000712
 R-THYR01000734//Human BAC clone RG191D16, complete sequence.//3.7

【表541】

e-14:468:64//AC002460
 R-THYR01000748//Homo sapiens cosmid 123E15, complete sequence.//2.6e-11:182:73//AF024533
 R-THYR01000756//Sequence 21 from patent US 5552281.//1.4e-15:106:98//125660
 R-THYR01000777//Plasmodium falciparum MAL3P2, complete sequence.//1.0:175:66//AL034558
 R-THYR01000783//CIT-HSP-2335P6.TF CIT-HSP Homo sapiens genomic clone 2335P6, genomic survey sequence.//1.2e-81:391:99//AQ038226
 R-THYR01000787//Homo sapiens chromosome Y, clone 264.M.20, complete sequence.//9.4e-07:494:58//AC004617
 R-THYR01000793
 R-THYR01000796//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 167P19, WORKING DRAFT SEQUENCE.//1.7e-42:379:79//Z93014
 R-THYR01000805//Human Chromosome 11 pac pDJ610120, WORKING DRAFT SEQUENCE, 18 unordered pieces.//4.7e-40:362:76//AC002555
 R-THYR01000815//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 316D5, WORKING DRAFT SEQUENCE.//4.0e-58:295:92//Z82199
 R-THYR01000829//Sequence 7 from patent US 5716622.//0.97:362:61//187788
 R-THYR01000843//Homo sapiens Chromosome 15q11-q13 PAC clone pDJ351h23 from the Prader-Willi/Angelman Syndrome region, complete sequence.//3.3e-57:522:76//AC004738
 R-THYR01000852//Homo sapiens chromosome 11 clone CIT-HSP-1337H24, WORKING DRAFT SEQUENCE, 9 unordered pieces.//4.2e-17:291:69//AC005849
 R-THYR01000855//Human DNA sequence from clone 366B10 on chromosome 22q12.2-12.3. Contains GSSs, complete sequence.//1.1e-41:419:75//AL031592
 R-THYR01000865//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1125A11, WORKING DRAFT SEQUENCE.//9.0e-47:294:84//AL034549
 R-THYR01000895//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 380F5, WORKING DRAFT SEQUENCE.//3.7e-111:569:96//AL031719
 R-THYR01000916//Homo sapiens clone DJ0965K10, WORKING DRAFT SEQUENCE, 6 unordered pieces.//1.0e-97:554:92//AC006015
 R-THYR01000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds.//9.6e-109:566:94//AF079529
 R-THYR01000934//Homo sapiens full length insert cDNA clone ZD69A10.//1.6e-104:539:95//AF086378
 R-THYR01000951//Homo sapiens Chromosome 11q12 pac pDJ57114, WORKING DRAFT SEQUENCE, 29 unordered pieces.//8.9e-61:479:81//AC004229
 R-THYR01000952//Human autoimmune thyroid disease-related antigen mRNA.//5.3e-16:116:93//Z82639
 R-THYR01000974//Homo sapiens ribosomal protein L33-like protein mRNA, complete cds.//3.2e-59:321:95//AF047440
 R-THYR01000975//Homo sapiens chromosome 19, cosmid F18718, complete sequence.//1.9e-44:396:79//AC006126
 R-THYR01000983//Homo sapiens chromosome 17, clone hRPK.271_K_11, complete sequence.//0.99:71:78//AC005562
 R-THYR01000984//Homo sapiens Chromosome 11q12.2 PAC clone pDJ688p12 containing uteroglobin gene, WORKING DRAFT SEQUENCE, 11 unordered pieces.//6.7e-42:320:84//AC006078
 R-THYR01000988//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence.//6.7e-39:292:78//Z84466
 R-THYR01001003//HS_3051_B1_H01_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3051 Col=1 Row=P, genomic survey sequence.//2.5e-39:310:83//AQ253727
 R-THYR01001031//Homo sapiens DNA sequence from PAC 230G1 on chromosome Xp11.3. Contains EST, STS and GSS, complete sequence.//2.5e-50:300:88//Z84466
 R-THYR01001033//CIT-HSP-2007J14.TF CIT-HSP Homo sapiens genomic clone 2007J14, genomic survey sequence.//5.1e-26:143:100//B56677
 R-THYR01001062//CIT-HSP-2386P3.TF.1 CIT-HSP Homo sapiens genomic clone 2386P3, genomic survey sequence.//1.4e-48:316:87//AQ239882
 R-THYR01001093
 R-THYR01001100//Homo sapiens BAC clone RG152G17 from 7q22-q31.1, complete sequence.//0.47:102:73//AC005070
 R-THYR01001120
 R-THYR01001121//Homo sapiens mRNA for beta-tubulin folding cofactor D.//8.9e-81:429:94//AJ006417
 R-THYR01001133//CIT-HSP-2381110.TR CIT-HSP Homo sapiens genomic clone 2381110, genomic survey sequence.//4.7e-12:237:67//AQ111077
 R-THYR01001134
 R-THYR01001142//H.sapiens CpG island DNA genomic MseI fragment, clone 81d1, reverse read cp81d1.rta.//0.95:214:60//Z56037
 R-THYR01001173//cSRL-27c11-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-27c11, genomic survey sequence.//4.6e-26:262:77//B04145
 R-THYR01001177
 R-THYR01001189//Homo sapiens DNA from chromosome 19, BAC 33152, complete sequence.//1.0e-41:281:87//AC003973
 R-THYR01001204
 R-THYR01001213//Human Alu repeat sequence A6.//3.8e-38:236:88//U12581
 R-THYR01001262//Homo sapiens, clone hRPK.16_A_1, complete sequence.//8.7e-53:442:79//AC006227
 R-THYR01001271//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0224P12: HTGS phase 1, WORKING DRAFT SEQUENCE, 13 unordered pieces.//0.53:330:61//AC004630
 R-THYR01001290
 R-THYR01001313//H.sapiens CpG island DNA genomic MseI fragment, clone 195h3, forward read cp9195h3.ftlb.//0.046:126:66//Z57783
 R-THYR01001320//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 424J12, WORKING DRAFT SEQUENCE.//3.0e-58:476:80//Z82207
 R-THYR01001321//Plasmodium falciparum MAL3P2, complete sequence.//1.0e-08:408:62//AL034558
 R-THYR01001322
 R-THYR01001347//Homo sapiens mRNA for KIAA0745 protein, partial cds.//3.2e-08:266:64//AB018288
 R-THYR01001363//cSRL-72f5-u cSRL flow sorted Chromosome 11 specific cosmid Homo sapiens genomic clone cSRL-72f5, genomic survey sequence.//1.7e-85:471:92//B05884
 R-THYR01001365//Homo sapiens chromosome 10 clone CIT987SK-1163G10 map 10q25, complete sequence.//1.8e-109:584:94//AC005660
 R-THYR01001374
 R-THYR01001401//Human pigment epithelium-derived factor gene, complete cds.//4.2e-51:333:88//U29953
 R-THYR01001403//Human PAC clone DJ222H05 from Xq25-q26, complete sequence.//8.7e-38:307:82//AC002377
 R-THYR01001405
 R-THYR01001406//RPC111-69F22.TX RPC111 Homo sapiens genomic clone R-69F22, genomic survey sequence.//1.9e-67:400:90//AQ238297
 R-THYR01001411//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone B0N2, WORKING DRAFT SEQUENCE.//2.2e-06:349:63//AL031123
 R-THYR01001426//*** SEQUENCING IN PROGRESS *** Homo sapiens genomic DNA (PAC 1118i22) from chromosome 11: HTGS phase 1, WORKING DRAFT SEQUENCE.//2.2e-89:506:86//AJ002553
 R-THYR01001434//Microcentus carayae 12S mitochondrial ribosomal RNA, small subunit, mitochondrial gene, partial sequence.//1.0:176:61//U77877
 R-THYR01001458//Human DNA sequence from clone 453C12 on chromosome 20q12-13.12 Contains SDC4 (syndecan 4 (amphiglycan, ryudocan)) predicts a gene like the mouse transcription factor RBP-L, MATN4 (matrilin-4) STS, GSS, CpG island, complete sequence.//3.3e-07:196:67//AL021578
 R-THYR01001480//Homo sapiens clone DJ0756H11, WORKING DRAFT SEQUENCE, 5 unordered pieces.//1.2e-99:517:95//AC006001
 R-THYR01001487//Homo sapiens, WORKING DRAFT SEQUENCE, 97 unordered pieces.//8.5e-14:221:70//AC004085
 R-THYR01001534//HS_2242_B2_H04_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2242 Col=8 Row=P, genomic survey sequence.//0.00012:141:68//AQ182326
 R-THYR01001537//Human DNA sequence from clone 111F4 on chromosome Xq23 Contains GSSs, complete sequence.//0.42:323:60//AL023876
 R-THYR01001541//Homo sapiens clone RG228D17, WORKING DRAFT SEQUENCE, 2 unordered pieces.//1.7e-42:370:78//AC005077
 R-THYR01001559//Homo sapiens 12q24.2 PAC RPC15-944M2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//1.0:144:67//AC005868
 R-THYR01001570//Plasmodium falciparum 3D7 chromosome 12 PFYAC92 genomic sequence, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.43:268:61//AC005308
 R-THYR01001573//M.avium rpsL gene.//0.98:131:66//X80120
 R-THYR01001584//A. longa plastid genes for ribosomal proteins and tRNAs.//0.29:502:58//X75653
 R-THYR01001595//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone Y313F4, WORKING DRAFT SEQUENCE.//1.5e-33:319:78//AL023808
 R-THYR01001602//Homo sapiens chromosome 17, clone hRPK.142_H_9, complete sequence.//4.4e-13:320:67//AC005919
 R-THYR01001605//Human DNA sequence from PAC 358H7 on chromosome X.//1.9e-32:391:76//Z77249
 R-THYR01001617//Homo sapiens cDNA for dihydroxyacetone phosphate acyltransferase (DAP-AT).//1.9e-81:448:92//AJ002190
 R-THYR01001637//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 688G8, WORKING DRAFT SEQUENCE.//5.4e-41:381:78//AL031671

【表542】

R-THYR01001656//HS_2201_B2_A08_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2201 Col=16 Row=B, genomic survey sequence.//0.096:162:63//AQ293168

R-THYR01001661//Human immunoglobulin-associated (B29) gene, promoter and exon 1, partial cds.//1.0:229:62//U22954

R-THYR01001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform.//4.8e-110:562:95//AJ225089

R-THYR01001673//CIT-HSP-2327D12.TR CIT-HSP Homo sapiens genomic clone 2327D12, genomic survey sequence.//1.5e-17:224:68//AQ042426

R-THYR01001703//Homo sapiens clone 198 unknown mRNA, partial sequence.//1.6e-44:251:93//AF091072

R-THYR01001706//Homo sapiens clone DJ0935K16, complete sequence.//1.8e-26:378:68//AC006011

R-THYR01001721//, complete sequence.//1.3e-101:571:92//AC005500

R-THYR01001738

R-THYR01001745//Homo sapiens chromosome 5, PAC clone 24713 (LBNL H85), complete sequence.//1.1e-15:193:70//AC004777

R-THYR01001746//Human inter-alpha-trypsin inhibitor light chain (IT1) gene, exon 3.//0.54:260:61//M88244

R-THYR01001772//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 30A23, WORKING DRAFT SEQUENCE.//1.6e-12:285:64//AL022156

R-THYR01001793

R-THYR01001809//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 1071N3, WORKING DRAFT SEQUENCE.//2.5e-43:486:74//AL031728

R-THYR01001854//Homo sapiens chromosome 17, clone hRPK.74_E_22, complete sequence.//5.0e-41:245:87//AC005696

R-THYR01001895//Human Chromosome 11p14.3 PAC clone 6-106123, complete sequence.//4.4e-12:419:61//AC005137

R-THYR01001907//Homo sapiens Chromosome 22q11.2 Cosmid Clone 24b1 n DCCR Region, complete sequence.//8.1e-35:340:78//AC000075

R-VESEN1000122//Homo sapiens Human mRNA, complete cds.//1.3e-23:138:98//AF009368

R-Y79AA1000013

R-Y79AA1000033//Homo sapiens BAC clone GS114109 from 7p14-p15, complete sequence.//9.9e-112:551:97//AC006027

R-Y79AA1000037//CIT-HSP-2334F3.TR CIT-HSP Homo sapiens genomic clone 2334F3, genomic survey sequence.//0.16:308:60//AQ036673

R-Y79AA1000059//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-279B10, complete sequence.//6.1e-56:314:88//AC002300

R-Y79AA1000065//Human carboxylesterase gene, exon 5.//0.64:203:63//D021079

R-Y79AA1000131//*** SEQUENCING IN PROGRESS *** Homo sapiens chromosome 4, BAC clone C0548N01: HTGS phase 1, WORKING DRAFT SEQUENCE, 31 unordered pieces.//7.0e-18:169:79//AC004795

R-Y79AA1000181//Human DNA sequence from clone 612B18 on chromosome 1q24-25.3 Contains exon from gene similar to 40S ribosomal protein, first coding exon of dynamin 2 (DYNI1). ESTs, STS, GSS, CpG island, complete sequence.//1.1e-106:474:98//AL031864

R-Y79AA1000202//CIT978SK-A-518G2.TP CIT978SK Homo sapiens genomic clone A-518G2, genomic survey sequence.//1.0e-10:78:97//B68074

R-Y79AA1000214//Homo sapiens clone DJ0673M15, WORKING DRAFT SEQUENCE, 33 unordered pieces.//6.5e-59:386:90//AC004854

R-Y79AA1000230//Cytosine zoon felis 18S ribosomal RNA.//1.0:167:62//L19080

R-Y79AA1000231//HS_3009_A1_H03_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3009 Col=5 Row=0, genomic survey sequence.//6.4e-52:348:88//AQ090225

R-Y79AA1000258//Hepatitis C virus HCV-B9 gene for NS5, partial cds.//0.65:127:65//D10558

R-Y79AA1000268//Human DNA sequence from PAC 162H14 on chromosome 2. Contains 3' part of a FIBULIN 1 like gene and ESTs, complete sequence.//4.7e-40:300:84//Z98047

R-Y79AA1000313//Human DNA sequence from PAC 179115, BRCA2 gene region chromosome 13q12-q13 contains Klotho ESTs and CpG island.//5.0e-14:136:83//Z92540

R-Y79AA1000328

R-Y79AA1000342//S.clavuligerus linear plasmid pSCL (complete sequence).//0.55:189:65//X54107

R-Y79AA1000346//Human MEST mRNA, complete cds.//0.00013:52:100//D78611

R-Y79AA1000349//M.musculus Spnr mRNA for RNA binding protein.//8.8e-36:300:81//X84692

R-Y79AA1000355//Human DNA sequence from clone 551E13 on chromosome Xp11.2-11.3 Contains farnesyl pyrophosphate synthetase pseudogene, Vt4 protein pseudogene, EST, GSS, complete sequence.//5.7e-45:403:80//AL022163

R-Y79AA1000368

R-Y79AA1000405//RPC111-16B12.TPB RPC111 Homo sapiens genomic clone

R-THYR010016812, genomic survey sequence.//0.10:171:65//B88000

R-Y79AA1000410//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 92N15, WORKING DRAFT SEQUENCE.//4.1e-50:361:83//Z93097

R-Y79AA1000420//Plasmodium falciparum merozoite surface protein 4, merozoite surface protein 5, merozoite surface protein 2, and adenylosuccinate lyase genes, complete cds.//0.071:474:57//AF033037

R-Y79AA1000469//Homo sapiens clone NHD140K04, complete sequence.//1.8e-86:221:90//AC005033

R-Y79AA1000480//Homo sapiens chromosome 4 clone B240N9 map 4q25, complete sequence.//2.1e-14:179:72//AC004057

R-Y79AA1000538//Homo sapiens clone DJ0826E18, WORKING DRAFT SEQUENCE, 4 unordered pieces.//4.5e-43:321:83//AC005282

R-Y79AA1000539//Homo sapiens PAC clone DJ0074M20 from X, complete sequence.//0.0012:275:59//AC006143

R-Y79AA1000540//Z.dioplerennis repetitive DNA (clone ZEAR 260).//0.0017:258:62//X53609

R-Y79AA1000560//Mouse mRNA for alpha-adaptin (C).//6.1e-32:390:70//X14972

R-Y79AA1000574//Homo sapiens chromosome 9q34, clone 23B4, complete sequence.//0.96:224:61//AC002325

R-Y79AA1000627//Homo sapiens full length insert cDNA ZA77G02.//6.3e-100:533:94//AF075117

R-Y79AA1000705//RPC111-76G7.TV RPC111 Homo sapiens genomic clone, R-76G7, genomic survey sequence.//4.6e-88:429:98//AQ268433

R-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds.//2.7e-112:586:95//AF093670

R-Y79AA1000748

R-Y79AA1000752

R-Y79AA1000774//CIT-HSP-2288K24.TF CIT-HSP Homo sapiens genomic clone 2288K24, genomic survey sequence.//5.3e-45:316:86//AQ005014

R-Y79AA1000782//Human mRNA for KIAA0246 gene, partial cds.//5.0e-7:107:100//D87433

R-Y79AA1000784//Plasmodium falciparum 3D7 chromosome 12 PFYAC181 genomic sequence, WORKING DRAFT SEQUENCE, 8 unordered pieces.//0.0034:520:55//AC005505

R-Y79AA1000794//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 989H11, WORKING DRAFT SEQUENCE.//0.015:322:60//Z83851

R-Y79AA1000800//M.musculus tex264 mRNA (3' region).//1.1e-06:104:78//X80427

R-Y79AA1000802//CIT-HSP-2295G6.TF CIT-HSP Homo sapiens genomic clone 2295G6, genomic survey sequence.//0.67:152:62//AQ007605

R-Y79AA1000805//Human Chromosome 11 Cosmid cSRL30h11, complete sequence.//3.1e-26:423:68//U73642

R-Y79AA1000824//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 329A5, WORKING DRAFT SEQUENCE.//1.1e-08:449:61//Z97832

R-Y79AA1000827//Triticum aestivum heat shock protein 101 kDa (HSP101) mRNA, complete cds.//1.0:101:69//AF083344

R-Y79AA1000850//Homo sapiens small optic lobes homolog (SOLH) mRNA, complete cds.//0.40:386:59//U85647

R-Y79AA1000962//CIT-HSP-2298N11.TR CIT-HSP Homo sapiens genomic clone 2298N11, genomic survey sequence.//0.00019:253:65//AQ013111

R-Y79AA1000968//Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds.//1.7e-58:446:80//U38253

R-Y79AA1000969

R-Y79AA1000976//CIT-HSP-2350C4.TF CIT-HSP Homo sapiens genomic clone 2350C4, genomic survey sequence.//3.3e-60:295:100//AQ061422

R-Y79AA1000985//Mus musculus pericentrin mRNA, complete cds.//5.9e-38:348:76//U05823

R-Y79AA1001023

R-Y79AA1001041

R-Y79AA1001048

R-Y79AA1001061//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-427H10, complete sequence.//1.2e-60:537:78//AC004626

R-Y79AA1001068//Homo sapiens P1 clone GSP13996 from Sgl2, complete sequence.//2.3e-41:405:77//AC005031

R-Y79AA1001077

R-Y79AA1001078//Homo sapiens 12q13.1 PAC RPC11-228P16 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//2.0e-09:534:59//AC004801

R-Y79AA1001105//Staphylococcus epidermidis trimethoprim resistance plasmid pSK639.//0.0072:309:63//U40259

R-Y79AA1001145//RPC111-59N12.TK RPC111 Homo sapiens genomic clone R-59N12, genomic survey sequence.//3.7e-07:256:64//AQ200068

R-Y79AA1001167//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 5/15, WORKING DRAFT SEQUENCE.//0.55:223:61//AP000012

R-Y79AA1001177//Human gene for G13 alpha protein, intron 7 through exon 9, variant U6 gene, and snRNP E protein pseudogene LH87.//7.0e-09:203:69//X54048

R-Y79AA1001185

【0843】

【表543】

R-Y79AA1001211//Homo sapiens 12p13.3 BAC RPC111-543P15 (Roswell Park Cancer Institute Human BAC Library) complete sequence.//2.1e-3 2:277:81//AC005912
 R-Y79AA1001216//Human chromosome 12p13 sequence, complete sequence.//0.98:325:59//U47924
 R-Y79AA1001228//Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MAB16, complete sequence.//0.0034:378:59//AB018112
 R-Y79AA1001233//Homo sapiens clone DJ1178G13, WORKING DRAFT SEQUENCE, 5 unordered pieces.//0.19:106:72//AC004988
 R-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LNLc1101133QT (RZPD Berlin)).//3.4e-109:549:95//AJ005892
 R-Y79AA1001281
 R-Y79AA1001299//Homo sapiens SNF5/INI1 gene, exon 9.//6.3e-24:133:100//V17126
 R-Y79AA1001312//Human immunodeficiency virus type 1 variant 43 polymerase pseudogene, partial cds.//0.0070:284:58//U45372
 R-Y79AA1001323//Fugu rubripes GSS sequence, clone 027L23aG3, genomic survey sequence.//0.11:125:70//AL025355
 R-Y79AA1001384//W. makkii mitochondrial CYTB and tRNA genes.//0.07 0:209:65//X66594
 R-Y79AA1001391//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL1P2, WORKING DRAFT SEQUENCE.//0.80:163:62//AL031745
 R-Y79AA1001394//Homo sapiens DNA from chromosome 19, cosmid R2914 4, complete sequence.//0.99:241:63//AC004221
 R-Y79AA1001402//Homo sapiens Chr.14 PAC RPC14-794B2 (Roswell Park Cancer Institute Human PAC Library) complete sequence.//0.25:81:80 //AC005924
 R-Y79AA1001493
 R-Y79AA1001511//Human DNA sequence from clone 931K24 on chromosome 20p12 Contains ESTs and GSSs, complete sequence.//1.3e-35:207:95//AL034430
 R-Y79AA1001533//Mouse mRNA for RNA polymerase I associated factor (PAF53), complete cds.//2.7e-44:285:81//D14336
 R-Y79AA1001541//Human DNA sequence from clone 113J7 on chromosome Xp11.22-11.4. Contains part of a putative Homeobox (pseudo?) gene, ESTs and an STS, complete sequence.//0.70:365:60//AL023574
 R-Y79AA1001548//Homo sapiens phosphatidylinositol 4-kinase mRNA, complete cds.//5.9e-95:517:91//L36151
 R-Y79AA1001555
 R-Y79AA1001585
 R-Y79AA1001594//Human DNA sequence from PAC 60G11 on chromosome X: contains STS.//6.6e-19:241:76//Z94722
 R-Y79AA1001603//H. sapiens CpG island DNA genomic MseI fragment, clone 72f8, forward read cpg72f8. flla.//3.3e-21:131:96//Z62766
 R-Y79AA1001613
 R-Y79AA1001647//Human DNA sequence from PAC 3EJ3, between markers DXS1192 and DXS102 on chromosome X.//6.3e-08:338:63//Z82975
 R-Y79AA1001665//Homo sapiens genomic DNA, chromosome 21q22.2 (Down Syndrome region), segment 1/15, WORKING DRAFT SEQUENCE.//3.2e-11:114:84//AP000008
 R-Y79AA1001679//O. coniculus lambda-crystallin mRNA, complete cds.//3.9e-15:270:68//M22743
 R-Y79AA1001692//RPC111-42M5.TJ RPC111 Homo sapiens genomic clone R-42M5, genomic survey sequence.//0.013:64:89//AQ052792
 R-Y79AA1001696//Apis mellifera ligustica complete mitochondrial genome.//9.3e-09:428:58//L06178
 R-Y79AA1001705
 R-Y79AA1001711//Mus musculus 60 kDa ribonucleoprotein Ro gene, partial cds.//2.2e-45:554:75//AF042139
 R-Y79AA1001781//Plasmodium falciparum chromosome 2, section 39 of 73 of the complete sequence.//1.0:414:57//AE001402
 R-Y79AA1001805//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone S10D11, WORKING DRAFT SEQUENCE.//2.8e-05:329:61//Z98044
 R-Y79AA1001827//Oryctolagus cuniculus PIUS mRNA, complete cds.//2.3e-90:557:89//U74297
 R-Y79AA1001846//Homo sapiens DNA sequence from PAC 179N16 on chromosome 6p21.1-21.33. Contains the SAPK4 (MAPK p38delta) gene, and the alternatively spliced SAPK2 gene coding for CSaids binding protein CSBP2 and a MAPK p38beta LIKE protein. Contains ESTs, STSs and two predicted CpG islands, complete sequence.//2.1e-34:306:78//Z9 5152
 R-Y79AA1001848//Sequence 11 from patent US 5449616.//1.0:221:59//I 14369
 R-Y79AA1001866//Arabidopsis thaliana genomic DNA, chromosome 5, TA C clone: K23L20, complete sequence.//0.0089:527:58//AB016874
 R-Y79AA1001874
 R-Y79AA1001875//M. musculus mRNA for Rab7 protein.//5.8e-45:170:92//X89650
 R-Y79AA1001923//Human DNA sequence from clone 353H6 on chromosome, Xq25-26.2. Contains the alternatively spliced SMARCA1 gene for SWI /SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1 (SNF2L1) and a 40S Ribosomal Protein S26 pseudogene. Contains ESTs, STSs and GSSs, complete sequence.//1.0:138:68//AL022577
 R-Y79AA1002027//Liverwort Marchantia polymorpha chloroplast genome DNA.//0.71:153:67//X04465
 R-Y79AA1002083//Human DNA sequence *** SEQUENCING IN PROGRESS *** from clone 172B20, WORKING DRAFT SEQUENCE.//1.0:178:64//AL022319
 R-Y79AA1002089//Homo sapiens clone GS111G14, WORKING DRAFT SEQUENCE, 5 unordered pieces.//6.3e-49:377:81//AC005011
 R-Y79AA1002093//Homo sapiens (clone SEL366) 17q YAC (368C7) RNA.//4.0e-32:174:99//L77612
 R-Y79AA1002103//CIT-HSP-232B121.TR CIT-HSP Homo sapiens genomic clone 232B121, genomic survey sequence.//1.9e-44:245:96//AQ044502
 R-Y79AA1002115//CITB1-E1-2514F10.TF CITB1-E1 Homo sapiens genomic clone 2514F10, genomic survey sequence.//1.8e-24:249:78//AQ265752
 R-Y79AA1002125//RPC111-15J6.TV RPC111-Homo sapiens genomic clone RPC111-15J6, genomic survey sequence.//8.5e-21:147:91//B75354
 R-Y79AA1002139
 R-Y79AA1002204
 R-Y79AA1002208//Human ankyrin G (ANK-3) mRNA, complete cds.//0.04 0:319:59//U13616
 R-Y79AA1002209//Psilotum nudum RT gene for reverse transcriptase (PT4).//0.99:106:65//X65415
 R-Y79AA1002210
 R-Y79AA1002211//H. sapiens HGAL gene.//1.0:311:59//X99133
 R-Y79AA1002220//Plasmodium falciparum DNA *** SEQUENCING IN PROGRESS *** from MAL4P1, WORKING DRAFT SEQUENCE.//5.9e-07:535:57//AL034 557
 R-Y79AA1002229
 R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds.//6.1e-117:564:98//AB014592
 R-Y79AA1002246
 R-Y79AA1002258//Homo sapiens mRNA for HIP3, complete cds.//1.3e-9 2:453:97//AB013384
 R-Y79AA1002298//HS_3071_B2_E08_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3071 Col=16 Row=J, genomic survey sequence.//1.9e-56:384:87//AQ171331
 R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds.//2.5e-108:403:99//AB014534
 R-Y79AA1002311//Homo sapiens chromosome 10 clone CIT987SK-1173112 map 10q25, complete sequence.//1.1e-07:368:61//AC005887
 R-Y79AA1002351
 R-Y79AA1002361//H. sapiens CpG island DNA genomic MseI fragment, clone 65b9, reverse read cpg65b9.rlla.//0.57:59:79//Z62206
 R-Y79AA1002399//Homo sapiens chromosome 17, clone hRPK.700_H_6, complete sequence.//2.0e-98:385:99//AC005920
 R-Y79AA1002407//Homo sapiens chromosome 17, clone hRPC.842_A_23, complete sequence.//5.4e-59:490:76//AC004662
 R-Y79AA1002416//Homo sapiens Xp22 GSHB-314C4 (Genome Systems Human BAC library) complete sequence.//6.3e-08:103:80//AC004087
 R-Y79AA1002431
 R-Y79AA1002433//Mouse transcriptional control element.//0.064:84:7 1//M17284
 R-Y79AA1002472//Homo sapiens chromosome 19, BAC CIT-B-393i15 (BC30 1323), complete sequence.//1.6e-103:525:96//AC006116
 R-Y79AA1002482//Homo sapiens chromosome 18, clone hRPK.474_M_24, complete sequence.//9.7e-38:302:83//AC006238
 R-Y79AA1002487//P. falciparum complete gene map of plastid-like DNA (IR-B).//0.23:266:61//X95276

【0844】

5'末端クローン配列に対するHuman Unigene相同性検索結果データ

各データは、

クローン配列名、

トップヒットデータのTitle、

P値:比較配列の長さ (base):相同性(%)、

トップヒットデータのAccession No.の順に//で区切って記載した。

なお、相同性のスコアのP値が1より大であった場合はデータは示さない。

【0845】

【表544】

F-HEMBA1000005//EST//4.3e-87:422:97//Hs.147830:A122069	F-HEMBA1000442//EST//1.0:201:61//Hs.162434:AA577398
F-HEMBA1000012//Human endosome-associated protein (EEA1) mRNA, complete cds//0.82:170:64//Hs.2864:L40157	F-HEMBA1000456//Fanconi anemia complementation group C//0.58:362:59//Hs.37953:X66893
F-HEMBA1000020//Homo sapiens beta 2 gene//4.0e-74:529:83//Hs.150244:U83668	F-HEMBA1000459//EST//9.2e-21:157:86//Hs.132635:A1032875
F-HEMBA1000030//ESTs//1.1e-91:494:93//Hs.7958:W22078	F-HEMBA1000460//ESTs//2.9e-77:409:95//Hs.27135:W49590
F-HEMBA1000042//ESTs//3.5e-22:228:77//Hs.145406:A1253247	F-HEMBA1000464//ESTs//6.6e-17:365:65//Hs.150675:AA127853
F-HEMBA1000046//ESTs, Highly similar to PRE-MRNA SPLICING FACTOR RNA HELICASE PRP22 [Saccharomyces cerevisiae]//0.00019:192:65//Hs.7900:W22411	F-HEMBA1000469
F-HEMBA1000050//EST//0.81:74:72//Hs.156298:A1336759	F-HEMBA1000488//Homo sapiens HIV-1 inducer of short transcripts binding protein (FB11) mRNA, complete cds//0.15:253:58//Hs.104640:AF000561
F-HEMBA1000076//ESTs//0.11:252:62//Hs.131939:A1417910	F-HEMBA1000490//Homo sapiens kinectin mRNA, complete cds//0.71:539:56//Hs.82709:Z22551
F-HEMBA1000111//ESTs//8.5e-89:449:96//Hs.41105:N66734	F-HEMBA1000491//ESTs//2.0e-21:361:65//Hs.152453:AA864970
F-HEMBA1000129//Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds//0.27:342:61//Hs.14207:U86453	F-HEMBA1000501//Homo sapiens tapasin (NGS-17) mRNA, complete cds//2.5e-39:312:77//Hs.5247:AF029750
F-HEMBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cds//6.8e-169:791:98//Hs.27197:AB018340	F-HEMBA1000504//Homo sapiens mRNA for osteoblast specific factor 2 (OSF-2os)//1.3e-08:57:100//Hs.155095:D13666
F-HEMBA1000150//Homo sapiens mRNA for KIAA0788 protein, partial cds//1.4e-37:243:88//Hs.2397:Z70200	F-HEMBA1000505//Homo sapiens KED4p mRNA, complete cds//1.0:197:62//Hs.131962:AF064093
F-HEMBA1000156//ESTs, Weakly similar to The KIAA0138 gene product is novel. [H. sapiens]//5.3e-80:383:98//Hs.135552:A1215187	F-HEMBA1000508//EST//0.67:156:60//Hs.162898:AA659646
F-HEMBA1000158//Homo sapiens OPA-containing protein mRNA, complete cds//2.1e-07:265:63//Hs.85313:AF071309	F-HEMBA1000518
F-HEMBA1000168//ESTs//6.1e-35:257:85//Hs.13533:H23079	F-HEMBA1000519//EST//6.8e-52:300:91//Hs.149580:A1281881
F-HEMBA1000180//ESTs, Moderately similar to RETROVIRUS-RELATED POLYPROTEIN [H. sapiens]//1.3e-18:111:96//Hs.163863:W28729	F-HEMBA1000520//ESTs, Weakly similar to coded for by C. elegans CDNA CEESB82F [C. elegans]//2.9e-16:132:84//Hs.155871:AA533783
F-HEMBA1000185//H. sapiens ERF-2 mRNA//1.0:125:68//Hs.78909:U07802	F-HEMBA1000523//ESTs, Highly similar to TESTIS-SPECIFIC PROTEIN P6513 [Mus musculus]//2.1e-25:192:87//Hs.22383:R51067
F-HEMBA1000193//EST//1.5e-48:266:95//Hs.160642:A1240133	F-HEMBA1000531//ESTs, Weakly similar to heat shock protein [H. sapiens]//2.4e-57:288:97//Hs.116022:AA455706
F-HEMBA1000201//Human Inl1 mRNA, complete cds//6.5e-75:440:92//Hs.155626:U04847	F-HEMBA1000534//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.8e-47:153:88//Hs.113283:AF018080
F-HEMBA1000213//ESTs//0.21:239:62//Hs.26838:AA527529	F-HEMBA1000540//ESTs//8.6e-07:60:100//Hs.109755:AA180809
F-HEMBA1000216//Homo sapiens clone 23698 mRNA sequence//1.1e-57:529:68//Hs.8136:U81984	F-HEMBA1000542//Human lysyl oxidase-like protein mRNA, complete cds//0.088:581:57//Hs.65436:U24389
F-HEMBA1000227//Human RNA-binding protein CUG-BP/hNAB50 (NAB50) mRNA, complete cds//1.3e-05:311:64//Hs.81248:U63289	F-HEMBA1000545//Human knpi repeat mRNA (cdna clone pcd-kpni-4), 3' end//7.8e-106:731:83//Hs.139107:K00629
F-HEMBA1000231	F-HEMBA1000555//Human mRNA for KIAA0242 gene, partial cds//0.75:283:58//Hs.77495:D87684
F-HEMBA1000243//EST//5.9e-52:359:85//Hs.141433:N23377	F-HEMBA1000557//ESTs//3.9e-27:389:71//Hs.125087:AA495729
F-HEMBA1000244//H. sapiens mRNA for cytokine inducible nuclear protein//0.0022:350:60//Hs.74019:X83703	F-HEMBA1000561//Homo sapiens mRNA for KIAA0760 protein, partial cds//3.8e-64:665:72//Hs.137168:AB018303
F-HEMBA1000251//ESTs//3.2e-84:443:95//Hs.21068:N47460	F-HEMBA1000563//ESTs//3.8e-51:257:98//Hs.47122:A1338977
F-HEMBA1000264//ESTs//0.76:227:61//Hs.5159:AA588562	F-HEMBA1000568//EST//0.12:270:61//Hs.134833:A1091046
F-HEMBA1000280//EST//1.7e-12:149:75//Hs.103418:AA035568	F-HEMBA1000569//H. sapiens mRNA encoding GPI-anchored protein p137//3.8e-19:409:62//Hs.119283:Z48042
F-HEMBA1000282//ESTs//1.7e-16:164:79//Hs.123111:AA813186	F-HEMBA1000575//EST//0.060:156:64//Hs.126277:AA826681
F-HEMBA1000288//ESTs//5.4e-06:154:68//Hs.54174:N64406	F-HEMBA1000588//ESTs, Weakly similar to weakly similar to myosin heavy chain [C. elegans]//7.7e-41:217:96//Hs.55084:AA479162
F-HEMBA1000290//Human novel homeobox mRNA for a DNA binding protein//3.8e-07:412:61//Hs.37035:U07664	F-HEMBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein//2.3e-44:228:97//Hs.155218:AJ007509
F-HEMBA1000302//EST//1.2e-41:238:94//Hs.147245:A1206095	F-HEMBA1000592//ESTs, Weakly similar to sorting nexin 1 [H. sapiens]//1.7e-27:463:65//Hs.13794:AA203241
F-HEMBA1000303	F-HEMBA1000594//Human clone 230971 defective mariner transposon Hs mar2 mRNA sequence//4.0e-68:574:79//Hs.159176:U92019
F-HEMBA1000304//ESTs//3.5e-11:96:87//Hs.163057:AA728946	F-HEMBA1000604//ESTs//3.3e-21:158:74//Hs.142924:A1092535
F-HEMBA1000307//EST//7.7e-05:280:62//Hs.146462:A1124898	F-HEMBA1000608//Homo sapiens mRNA for KIAA0456 protein, partial cds//3.7e-120:561:99//Hs.5003:AB007925
F-HEMBA1000327//ESTs//5.3e-92:435:99//Hs.100605:AA305965	F-HEMBA1000622//Homo sapiens DEC-205 mRNA, complete cds//5.2e-34:592:68//Hs.153563:AF011333
F-HEMBA1000333//Human mRNA for KIAA0206 gene, partial cds//0.84:395:56//Hs.79299:D86961	F-HEMBA1000636//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E. coli]//7.4e-22:166:84//Hs.26252:AA643235
F-HEMBA1000338//ESTs, Moderately similar to novel stromal cell protein [M. musculus]//2.4e-38:317:80//Hs.99189:X84712	F-HEMBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cds//2.1e-138:639:99//Hs.60103:AB014590
F-HEMBA1000351//Human Line-1 repeat mRNA with 2 open reading frame s//0.020:334:59//Hs.23094:M19503	F-HEMBA1000655//ESTs//1.2e-54:503:77//Hs.140864:AA176174
F-HEMBA1000355//Myosin, heavy polypeptide 11, smooth muscle//0.11:336:61//Hs.78344:AF001548	F-HEMBA1000657//Mucin 1, transmembrane//0.99:219:61//Hs.89603:J05582
F-HEMBA1000356//H. sapiens ERF-2 mRNA//0.031:317:59//Hs.78909:U07802	F-HEMBA1000662//ESTs//2.2e-52:257:99//Hs.63243:A1123912
F-HEMBA1000357//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:441:78//Hs.154326:D42087	F-HEMBA1000673//H. sapiens mRNA for translin associated protein X//1.7e-47:366:79//Hs.96247:X95073
F-HEMBA1000366//ESTs//0.025:56:87//Hs.141629:H74010	F-HEMBA1000682//Oxytocin receptor//4.7e-59:673:72//Hs.2820:X64878
F-HEMBA1000369//Homo sapiens PAC clone DJ0669B10 from 7q33-q35//0.99:433:58//Hs.159899:AC004853	F-HEMBA1000686
F-HEMBA1000376//Oxytocin receptor//3.4e-43:569:70//Hs.2820:X64878	F-HEMBA1000702
F-HEMBA1000387//ESTs//8.2e-104:535:94//Hs.78110:AA741320	F-HEMBA1000705//EST//0.047:363:60//Hs.136379:AA521309
F-HEMBA1000390//Homo sapiens BAC clone RG119C02 from Tp15//2.3e-141:712:95//Hs.22900:AC004520	F-HEMBA1000719//ESTs//2.7e-68:333:98//Hs.146195:A1039850
F-HEMBA1000392//Homo sapiens clone 24619 mRNA sequence//1.7e-47:461:74//Hs.139088:AF070533	F-HEMBA1000722//ESTs//0.49:283:60//Hs.21108:N92630
F-HEMBA1000396//ESTs, Weakly similar to hypothetical protein [H. sapiens]//1.2e-26:351:70//Hs.138992:C14008	F-HEMBA1000726//EST//1.1e-45:183:87//Hs.149580:A1281881
F-HEMBA1000411//EST//2.8e-27:401:71//Hs.138719:N52915	F-HEMBA1000727//ESTs//4.8e-95:442:100//Hs.22119:AA885491
F-HEMBA1000418//ESTs//0.0094:375:61//Hs.40140:A1079253	F-HEMBA1000747
F-HEMBA1000422//EST//6.2e-23:225:78//Hs.132635:A1032875	F-HEMBA1000749//ESTs//8.0e-14:108:77//Hs.154892:A1091568
F-HEMBA1000428//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//7.6e-31:616:66//Hs.159897:AB007970	F-HEMBA1000752//EST//1.3e-25:344:69//Hs.160992:HS2716
F-HEMBA1000434//EST//0.0031:157:64//Hs.162328:AA559034	F-HEMBA1000769//ESTs//0.0018:206:63//Hs.153268:AA887239

【0846】

【表545】

F-HEMBA1000773//ESTs//0.56:336:58//Hs.105964:N35803	F-HEMBA1001109//Homo sapiens tapasin (NCS-17) mRNA, complete cds//
F-HEMBA1000774//EST//4.0e-38:312:79//Hs.162197:AA535216	2.4e-61:341:85//Hs.5247:AF029750
F-HEMBA1000791//ESTs//2.8e-87:413:99//Hs.112050:AA431300	F-HEMBA1001121//EST//7.3e-13:265:64//Hs.142423:AA412497
F-HEMBA1000817//ESTs//5.6e-124:617:96//Hs.101366:AA167536	F-HEMBA1001122//Homo sapiens mRNA for KIAA0471 protein, complete c
F-HEMBA1000822//ESTs//0.94:347:58//Hs.23905:AA928542	ds//0.066:649:56//Hs.5347:AB007940
F-HEMBA1000827//EST//0.064:133:60//Hs.138738:N58367	F-HEMBA1001123//Homo sapiens mRNA for KIAA0448 protein, complete c
F-HEMBA1000843	ds//1.5e-10:231:68//Hs.27349:AB007917
F-HEMBA1000851//Fragile X mental retardation 1//0.014:219:62//Hs.8	F-HEMBA1001133//EST//0.50:222:63//Hs.131018:AI015747
9764:X69962	F-HEMBA1001137//Homo sapiens mRNA for KIAA0798 protein, complete c
F-HEMBA1000852//Arylsulfatase D//6.7e-38:244:75//Hs.43887:X83572	ds//2.2e-73:527:77//Hs.159277:AB018341
F-HEMBA1000867	F-HEMBA1001140//Homo sapiens mRNA for KIAA0682 protein, complete c
F-HEMBA1000869//ESTs//5.1e-33:166:77//Hs.141186:R99609	ds//0.020:141:65//Hs.7482:AB014582
F-HEMBA1000870//EST//0.032:130:66//Hs.157351:AI367237	F-HEMBA1001172//EST//0.77:158:60//Hs.158894:AI378457
F-HEMBA1000872//ESTs//2.4e-20:134:92//Hs.155982:AA406047	F-HEMBA1001174//ESTs//1.4e-63:363:92//Hs.132798:AA922226
F-HEMBA1000876//EST//5.3e-20:233:72//Hs.124339:AA829660	F-HEMBA1001197//ESTs, Weakly similar to Rap2 interacting protein 8
F-HEMBA1000908//ESTs//5.4e-28:219:84//Hs.12247:AI203154	[M.musculus]//5.0e-54:555:71//Hs.55165:AA573499
F-HEMBA1000910//Human DNA sequence from clone 1409 on chromosome X	F-HEMBA1001208//EST//6.2e-26:213:77//Hs.146964:AI183463
pl1.1-11.4. Contains a inter-Alpha-Trypsin Inhibitor Heavy Chain L	F-HEMBA1001213//Human mRNA for KIAA0013 gene, complete cds//0.026:
IKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE	569:57//Hs.48824:D87717
LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphospha	F-HEMBA1001226//ESTs//1.9e-11:407:65//Hs.157977:AI369694
tase) LIKE pseudogene. Contains ESTs, STSs and genomic marker OX58	F-HEMBA1001235//ESTs//0.0042:161:63//Hs.155170:AA167748
032//2.8e-11:309:65//Hs.4943:Z98046	F-HEMBA1001247//ESTs//1.2e-91:429:99//Hs.143304:AI084058
F-HEMBA1000918//ESTs//0.11:234:59//Hs.96499:AA252537	F-HEMBA1001257//Human zinc finger protein (MAZ) mRNA//0.017:330:62
F-HEMBA1000919//Human mRNA for histone H1x, complete cds//0.18:22	//Hs.7647:M94046
1:64//Hs.109804:D64142	F-HEMBA1001265
F-HEMBA1000934//Homo sapiens mRNA for KIAA0547 protein, complete c	F-HEMBA1001281
ds//3.8e-09:350:62//Hs.36850:AB011119	F-HEMBA1001286//Natriuretic peptide precursor B//0.75:163:63//Hs.9
F-HEMBA1000942//ESTs, Highly similar to PMS4 homolog mismatch repa	37:AL021155
ir protein [H.sapiens]//9.4e-10:77:93//Hs.111445:H00596	F-HEMBA1001289//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69
F-HEMBA1000943//ESTs, Highly similar to ZINC FINGER PROTEIN 10 [H	G12//5.1e-30:530:64//Hs.154050:AC004131
sapiens]//0.0039:54:92//Hs.58338:AA609476	F-HEMBA1001294//Homo sapiens mRNA for matrilin-3//0.00023:657:56//
F-HEMBA1000946//Phosphoribosylglycinamide formyltransferase, phosph	Hs.119534:AJ224741
horibosylglycinamide synthetase, phosphoribosylaminoimidazole synt	F-HEMBA1001299//Small inducible cytokine A5 (RANTES)//2.2e-27:271:
hetase//0.93:132:66//Hs.82285:X54199	77//Hs.155464:AF088219
F-HEMBA1000960//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX	F-HEMBA1001302//ESTs, Moderately similar to Cab45a [M.musculus]//
WARNING ENTRY !!!! [H.sapiens]//0.080:128:71//Hs.118972:AA761369	3.3e-53:272:97//Hs.154563:AI129590
F-HEMBA1000968//Human transposon-like element mRNA//2.8e-95:352:87	F-HEMBA1001303//ESTs, Weakly similar to RNA splicing-related prote
//Hs.84775:M23161	in [R.norvegicus]//2.6e-66:241:99//Hs.120847:AA731201
F-HEMBA1000971//ESTs//8.4e-88:417:98//Hs.128631:AI127903	F-HEMBA1001310//ESTs//2.0e-21:133:93//Hs.159116:W55873
F-HEMBA1000972//EST//0.75:134:64//Hs.117228:AA682775	F-HEMBA1001319//Homo sapiens mRNA for KIAA0758 protein, partial cd
F-HEMBA1000974//ESTs//1.3e-103:497:98//Hs.126786:U74314	s//0.23:562:58//Hs.22039:AB018301
F-HEMBA1000975//Homo sapiens diacylglycerol kinase iota (DGK1) mRN	F-HEMBA1001323//Wingless-type MMTV integration site 5A, human homo
A, complete cds//1.3e-05:424:59//Hs.159564:AF061936	log//2.5e-31:165:99//Hs.152213:L20861
F-HEMBA1000985//Homo sapiens mRNA, chromosome 1 specific transcrip	F-HEMBA1001326//ESTs, Highly similar to HYPOTHETICAL 55.1 KD PROT
t KIAA0492//0.0036:389:60//Hs.127338:AB007961	EIN IN FABI-PES4 INTERGENIC REGION [Saccharomyces cerevisiae]//8.9
F-HEMBA1000986//ESTs//0.00025:272:64//Hs.12364:H09132	e-08:185:68//Hs.108734:AI073427
F-HEMBA1000991//Homo sapiens mRNA for Hrs, complete cds//3.9e-24:1	F-HEMBA1001327//ESTs//0.085:337:60//Hs.114157:AA703013
93:84//Hs.24756:U43895	F-HEMBA1001330//EST//0.0018:225:63//Hs.127987:AA970569
F-HEMBA1001007//EST//0.96:70:71//Hs.163258:AA828835	F-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VA
F-HEMBA1001008//Human G protein-coupled receptor (STRL22) mRNA, co	P-33) mRNA, complete cds//3.6e-105:516:97//Hs.9006:AF057358
mplete cds//4.9e-43:472:74//Hs.46468:U45984	F-HEMBA1001361//ESTs//1.2e-62:317:97//Hs.6639:R39794
F-HEMBA1001009//Immunoglobulin mu//0.18:367:59//Hs.75758:X58529	F-HEMBA1001375//ESTs//0.93:180:60//Hs.148425:AI198074
F-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete c	F-HEMBA1001377//ESTs//9.2e-87:414:99//Hs.48469:N62156
ds//1.4e-140:661:98//Hs.158287:AB007937	F-HEMBA1001383//ESTs//0.0023:336:60//Hs.140622:AA844353
F-HEMBA1001019//EST//4.1e-14:251:68//Hs.148769:AI239572	F-HEMBA1001387//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Ho
F-HEMBA1001020//Von Hippel-Lindau syndrome//2.2e-28:253:69//Hs.781	mo sapiens]//1.0e-132:643:97//Hs.124217:AA020848
60:AF010238	F-HEMBA1001388
F-HEMBA1001022	F-HEMBA1001391//ESTs//5.6e-32:191:93//Hs.71628:N41660
F-HEMBA1001024//Homo sapiens mRNA, chromosome 1 specific transcrip	F-HEMBA1001398
t KIAA0501//6.8e-28:376:72//Hs.159897:AB007970	F-HEMBA1001405//EST//1.0:135:63//Hs.146833:AI151117
F-HEMBA1001026//Homo sapiens klotho mRNA, complete cds//1.3e-05:74	F-HEMBA1001407//ESTs//0.53:390:57//Hs.150447:AI017798
5:57//Hs.94592:AB005142	F-HEMBA1001411//EST//8.8e-06:270:62//Hs.145386:AI253108
F-HEMBA1001043//ESTs//2.1e-28:448:67//Hs.112469:AA598515	F-HEMBA1001413
F-HEMBA1001051//EST//3.1e-48:310:87//Hs.149580:AI281881	F-HEMBA1001415//EST//1.3e-12:176:75//Hs.133172:AI051605
F-HEMBA1001052//EST//0.94:149:67//Hs.131216:AI017971	F-HEMBA1001432//RING3 PROTEIN//0.57:345:59//Hs.75243:D42040
F-HEMBA1001059//N-ACETYLGLACTOSAMINE-6-SULFATASE PRECURSOR//4.6e-	F-HEMBA1001433//ESTs//1.3e-21:333:69//Hs.131648:AI025726
165:777:98//Hs.159479:U06088	F-HEMBA1001435//Cytochrome P450, subfamily I (aromatic compound-in
F-HEMBA1001060//ESTs//6.8e-14:150:78//Hs.24821:AA044813	ducible), polypeptide 2//1.2e-74:469:80//Hs.1361:M55053
F-HEMBA1001071//Alpha-1 type 3 collagen//3.5e-32:181:96//Hs.11957	F-HEMBA1001442//EST//0.29:181:64//Hs.116883:AA663031
1:XI4420	F-HEMBA1001446//ESTs, Weakly similar to Rap2 interacting protein 8
F-HEMBA1001077//ESTs, Moderately similar to transcription intermed	[M.musculus]//6.8e-47:550:71//Hs.55165:AA573499
iary factor 1 [H.sapiens]//1.1e-98:487:97//Hs.147802:R71297	F-HEMBA1001450//Homo sapiens GTPase-activating protein (SIP1) mRN
F-HEMBA1001080//Human N-type calcium channel alpha-1 subunit mRNA,	A, complete cds//0.82:312:58//Hs.7019:AB005666
complete cds//0.013:385:58//Hs.69949:M94172	F-HEMBA1001454//ESTs//1.2e-46:297:80//Hs.152395:AA533107
F-HEMBA1001085//Human hSAH2 mRNA, complete cds//0.55:338:59//Hs.2	F-HEMBA1001455//ESTs//7.3e-103:502:97//Hs.112860:AA442412
0191:U76248	F-HEMBA1001463//Human mRNA for KIAA0392 gene, partial cds//8.7e-5
F-HEMBA1001088//Human PINCH protein mRNA, complete cds//7.3e-73:30	1:323:88//Hs.40100:AB002390
3:78//Hs.83987:U09284	F-HEMBA1001476//Homo sapiens mRNA for KIAA0572 protein, partial cd
F-HEMBA1001094//Interleukin 8//0.092:530:58//Hs.624:M17017	s//6.2e-104:489:99//Hs.14409:AB011144
F-HEMBA1001099	F-HEMBA1001478//EST//0.013:205:61//Hs.157309:AI365451

【0847】

【表546】

F-HEMBA1001497//Small inducible cytokine A5 (RANTES)//5.9e-45:307:84//Hs.155464:AF088219

F-HEMBA1001510//H.sapiens mRNA for G13 protein//2.1e-71:405:92//Hs.42853:X98054

F-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frame s//4.5e-105:773:82//Hs.23094:M19503

F-HEMBA1001517//EST//3.6e-09:271:65//Hs.162347:AA564902

F-HEMBA1001522//ESTs//4.3e-13:85:95//Hs.126707:A1376869

F-HEMBA1001526

F-HEMBA1001533//EST//1.0:75:73//Hs.145360:A1252476

F-HEMBA1001557//EST//3.5e-13:261:64//Hs.161496:N66580

F-HEMBA1001566//EST//3.7e-07:354:64//Hs.43830:N26652

F-HEMBA1001569//Homo sapiens mRNA for vesicle associated membrane protein 2 (VAMP2)//8.0e-68:338:97//Hs.91589:M36205

F-HEMBA1001570//ESTs//1.5e-47:369:82//Hs.107657:AA126814

F-HEMBA1001579//Homo sapiens mRNA for NS1-binding protein (NS1-BP) //7.0e-175:678:99//Hs.159597:AJ012449

F-HEMBA1001581//ESTs//4.4e-07:237:67//Hs.152304:AA605184

F-HEMBA1001585//ESTs//1.1e-11:81:100//Hs.16364:A1357228

F-HEMBA1001589//Human mRNA for KIAA0166 gene, complete cds//0.82:210:64//Hs.115778:D79988

F-HEMBA1001595//Human mRNA for KIAA0128 gene, partial cds//2.6e-110:855:78//Hs.90998:D50918

F-HEMBA1001608//EST//1.0:201:60//Hs.136747:AA749210

F-HEMBA1001620//ESTs//1.5e-39:211:98//Hs.131063:A1016400

F-HEMBA1001635//ESTs//4.0e-33:168:100//Hs.122655:A1361870

F-HEMBA1001636//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//0.038:198:64//Hs.34579:A1338536

F-HEMBA1001640//ESTs//1.1e-24:315:71//Hs.34114:AA776899

F-HEMBA1001647//Human plectin (PLEC1) mRNA, complete cds//0.00049:629:61//Hs.79706:U53204

F-HEMBA1001651//EST//3.6e-07:285:63//Hs.132558:AA948560

F-HEMBA1001655//ESTs//1.4e-95:497:96//Hs.59563:AA203283

F-HEMBA1001658//EST//0.18:251:59//Hs.117724:H47121

F-HEMBA1001661

F-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//7.9e-146:669:99//Hs.107254:AC005943

F-HEMBA1001675//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//2.0e-57:447:79//Hs.158095:AB007953

F-HEMBA1001678//ESTs//4.0e-50:360:83//Hs.146811:AA410788

F-HEMBA1001681//EST//1.0:165:58//Hs.136790:AA776060

F-HEMBA1001702//EST//0.015:312:61//Hs.162839:AA648760

F-HEMBA1001709//EST//0.85:131:65//Hs.131451:A1023995

F-HEMBA1001711//ESTs//0.084:425:56//Hs.125346:A1302836

F-HEMBA1001712//EST//0.26:214:59//Hs.159088:A1383114

F-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHONDRIAL PRECURSOR [Rattus norvegicus]//3.0e-30:195:92//Hs.132948:AA194452

F-HEMBA1001718//EST//0.0044:275:60//Hs.125969:AA889554

F-HEMBA1001723//INTERLEUKIN ENHANCER-BINDING FACTOR//0.24:501:57//Hs.101524:U58197

F-HEMBA1001731//EST//1.2e-06:261:63//Hs.132331:A1028363

F-HEMBA1001734//ESTs//0.018:177:63//Hs.129631:A1000415

F-HEMBA1001744//EST//8.7e-77:420:92//Hs.133226:A1052250

F-HEMBA1001745//Homo sapiens mRNA for TSC403 protein, complete cds//0.37:300:62//Hs.10887:AB013924

F-HEMBA1001746//ESTs//0.31:168:66//Hs.27237:N68328

F-HEMBA1001761//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//0.76:218:60//Hs.135553:M41598

F-HEMBA1001781//Homo sapiens chromosome 19, cosmid R30953//0.98:219:60//Hs.98776:AC005622

F-HEMBA1001784//Homo sapiens mRNA for KIAA0474 protein, complete cds//6.4e-09:265:67//Hs.158232:AB007943

F-HEMBA1001791

F-HEMBA1001800//EST//3.1e-41:331:81//Hs.127142:AA937570

F-HEMBA1001803//EST//0.0062:269:59//Hs.49075:N64817

F-HEMBA1001804//Human POU domain protein (Brn-3b) mRNA, complete cds//1.8e-07:439:59//Hs.266:U06233

F-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0500//2.5e-175:809:98//Hs.118164:AB007969

F-HEMBA1001809//ESTs//6.0e-101:497:97//Hs.155127:AA625305

F-HEMBA1001815

F-HEMBA1001819//Human kruppel-related zinc finger protein (ZNF184) mRNA, partial cds//4.9e-80:842:70//Hs.158174:U66561

F-HEMBA1001820//EST//0.057:214:62//Hs.148715:A1223845

F-HEMBA1001822//Homo sapiens intersectin short form mRNA, complete cds//6.7e-42:510:65//Hs.56392:AF064244

F-HEMBA1001824//Homo sapiens OPA-containing protein mRNA, complete cds//5.2e-13:253:68//Hs.85313:AF071309

F-HEMBA1001835//Human mRNA for KIAA0235 gene, partial cds//0.96:288:60//Hs.6151:D87078

F-HEMBA1001844//ESTs//1.1e-29:197:80//Hs.155243:N70293

F-HEMBA1001847//Human mRNA for KIAA0326 gene, partial cds//2.0e-23:379:68//Hs.6833:AB002324

F-HEMBA1001861//Homo sapiens mRNA for KIAA0517 protein, complete cds//2.8e-185:865:98//Hs.78946:AB014517

F-HEMBA1001864//EST//0.27:145:63//Hs.162585:AA593121

F-HEMBA1001866//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR [D.melanogaster]//3.2e-39:293:84//Hs.152332:A1141922

F-HEMBA1001869//ESTs, Weakly similar to ASH1 [D.melanogaster]//8.1e-70:367:95//Hs.15423:T84036

F-HEMBA1001888//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//5.4e-86:835:76//Hs.158095:AB007953

F-HEMBA1001896

F-HEMBA1001910//Human calpain-like protease (htra-3) mRNA, complete cds//0.43:114:71//Hs.6133:U94346

F-HEMBA1001912//ESTs//4.1e-79:398:97//Hs.26660:A1312633

F-HEMBA1001913//Homo sapiens TNF-alpha stimulated ABC protein (ABC50) mRNA, complete cds//0.00031:200:62//Hs.9573:AF027302

F-HEMBA1001915//EST//0.082:128:64//Hs.126542:AA916511

F-HEMBA1001918//Homo sapiens SEC63 (SEC63) mRNA, complete cds//0.46:374:59//Hs.31575:AF100141

F-HEMBA1001921//Homo sapiens germinal center kinase related protein kinase mRNA, complete cds//6.7e-186:855:99//Hs.154934:AF000145

F-HEMBA1001939//ESTs//4.9e-34:342:77//Hs.132711:A1377295

F-HEMBA1001940//ESTs//8.6e-15:149:81//Hs.141129:R86221

F-HEMBA1001942//ESTs//0.0014:271:62//Hs.124514:A1219882

F-HEMBA1001945//EST//0.98:142:64//Hs.161540:N85943

F-HEMBA1001950//ESTs//0.99:188:64//Hs.28639:R78360

F-HEMBA1001960//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//0.30:85:69//Hs.25674:AF072242

F-HEMBA1001962//EST//0.0012:289:59//Hs.125492:AA938930

F-HEMBA1001964//EST//0.73:153:64//Hs.112161:AA477708

F-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (pre sequence isolate of a Rat gene) and a novel alternatively spliced gene. Contains a putative CpG island, ESTs and CSSs//4.6e-156:720:99//Hs.11050:AL031178

F-HEMBA1001979//ESTs//0.86:184:67//Hs.77208:AA044732

F-HEMBA1001987//ESTs, Moderately similar to hTAIF168 [H.sapiens]//2.8e-29:151:100//Hs.124106:AA948100

F-HEMBA1001991//Homo sapiens clone 24540 mRNA sequence//0.049:121:70//Hs.153529:AF070581

F-HEMBA1002003//Keratin 10 (epidermolytic hyperkeratosis: keratosis palmaris et plantaris)//9.8e-09:294:63//Hs.99936:X14487

F-HEMBA1002008//ESTs//0.12:299:59//Hs.132803:W63582

F-HEMBA1002018//PROTEIN-TYROSINE PHOSPHATASE ZETA PRECURSOR//0.98:212:64//Hs.78867:M93426

F-HEMBA1002022//Human p37NB mRNA, complete cds//0.00044:58:96//Hs.155545:U32907

F-HEMBA1002035//EST//6.4e-07:145:68//Hs.135336:A1049827

F-HEMBA1002039//EST//0.99:79:67//Hs.98451:AA426057

F-HEMBA1002049//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-26:223:81//Hs.105292:AA504776

F-HEMBA1002084

F-HEMBA1002092

F-HEMBA1002100//Homo sapiens zinc finger homeodomain protein (ATBF1-A) mRNA, complete cds//5.6e-21:124:96//Hs.101842:L32832

F-HEMBA1002102//ESTs, Highly similar to ANKYRIN [Mus musculus]//5.9e-09:434:62//Hs.135102:A1190276

F-HEMBA1002113//ESTs//0.049:255:63//Hs.106137:A1129973

F-HEMBA1002119

F-HEMBA1002125//H.sapiens ERF-2 mRNA//0.026:341:59//Hs.78909:U07802

F-HEMBA1002139//ESTs//0.082:309:60//Hs.36383:W52393

F-HEMBA1002144//Human mRNA for KIAA0227 gene, partial cds//5.6e-06:601:60//Hs.79170:D86980

F-HEMBA1002150//Homo sapiens mRNA for KIAA0720 protein, partial cds//5.6e-06:353:62//Hs.23741:AB018263

F-HEMBA1002151

F-HEMBA1002153//EST//0.014:328:60//Hs.149115:A1244695

F-HEMBA1002160//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//5.6e-49:303:79//Hs.158241:AB007976

F-HEMBA1002161//Myosin, heavy polypeptide 7, cardiac muscle, beta//1.2e-40:616:67//Hs.929:M57965

F-HEMBA1002162//Homo sapiens mRNA for XPR2 protein//3.4e-48:749:67//Hs.44766:AJ007590

F-HEMBA1002166//Small inducible cytokine A5 (RANTES)//2.1e-60:485:79//Hs.155464:AF088219

【0848】

【表547】

F-HEMBA1002177//Homo sapiens yotiao mRNA, complete cds//2.4e-19:151:86//Hs.114808:AF026245	s.79385:U90905
F-HEMBA1002185//EST//0.00011:233:65//Hs.125552:AA884141	F-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds//4.3e-142:457:99//Hs.151411:AF075587
F-HEMBA1002189//EST//5.1e-24:193:81//Hs.163161:AA778363	F-HEMBA1002583//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//2.8e-30:156:100//Hs.32170:AB015132
F-HEMBA1002191//Homo sapiens mRNA for KIAA0689 protein, partial cds//0.27:382:59//Hs.21992:AB014589	F-HEMBA1002590//ESTs//1.0e-30:277:77//Hs.139158:AA226159
F-HEMBA1002199//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.2e-14:199:72//Hs.159897:AB007970	F-HEMBA1002592//ESTs//2.4e-20:233:75//Hs.159329:AI378363
F-HEMBA1002204//ESTs//0.46:312:59//Hs.61210:AA024696	F-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds//1.4e-176:820:99//Hs.20141:AB011169
F-HEMBA1002212//ESTs//1.0:191:63//Hs.149752:AI285767	F-HEMBA1002621//EST//0.99:208:60//Hs.159127:AI384013
F-HEMBA1002215//ESTs, Highly similar to TESTIN 2 PRECURSOR [Mus musculus]//1.6e-47:251:96//Hs.59906:AA001281	F-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//9.2e-189:632:97//Hs.91338:AB018351
F-HEMBA1002226//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//2.4e-57:375:71//Hs.67619:AB007957	F-HEMBA1002628//Human mRNA for KIAA0336 gene, complete cds//0.079:231:65//Hs.125129:AB002334
F-HEMBA1002229//Homo sapiens KIAA0395 mRNA, partial cds//7.9e-47:377:80//Hs.43681:AL022394	F-HEMBA1002629//Human density enhanced phosphatase-1 mRNA, complete cds//1.3e-07:473:61//Hs.1177:U10886
F-HEMBA1002237//EST//0.044:137:66//Hs.144448:AA812455	F-HEMBA1002645//ESTs//2.6e-32:209:88//Hs.141323:N80390
F-HEMBA1002241	F-HEMBA1002651
F-HEMBA1002253//EST//2.2e-41:219:96//Hs.137065:AA888887	F-HEMBA1002659//Human vascular endothelial growth factor related protein VRP mRNA, complete cds//0.74:223:60//Hs.79141:U43142
F-HEMBA1002257//Homo sapiens diacylglycerol kinase iota (DGK ι) mRNA, complete cds//1.1e-152:731:97//Hs.159564:AF061936	F-HEMBA1002661//Human LINE-1 repeat mRNA with 2 open reading frames//1.4e-122:781:85//Hs.23094:M19503
F-HEMBA1002265//ESTs//5.4e-11:337:65//Hs.112639:AI125420	F-HEMBA1002666//ESTs//0.39:117:65//Hs.3794:T08497
F-HEMBA1002267//Homo sapiens GDP-L-fucose pyrophosphorylase (CFPP) mRNA, complete cds//1.0:395:60//Hs.150926:AF017445	F-HEMBA1002678//EST//0.0081:148:64//Hs.156768:AI351368
F-HEMBA1002270//ESTs//2.5e-87:504:89//Hs.124440:H95404	F-HEMBA1002679//Cyclic nucleotide gated channel (photoreceptor), cGMP gated 1 (alpha)//0.00096:418:61//Hs.1323:S42457
F-HEMBA1002321//Homo sapiens oxidized low-density lipoprotein receptor mRNA, complete cds//0.17:338:60//Hs.77729:AB010710	F-HEMBA1002688//Homo sapiens hyperpolarization-activated channel 1 (IH1) mRNA, partial cds//1.8e-11:541:60//Hs.124161:AF065164
F-HEMBA1002328//ESTs//7.9e-103:480:99//Hs.123318:AI201982	F-HEMBA1002696//Homo sapiens DNA from chromosome 19, cosmid R29144//1.9e-06:345:61//Hs.155647:AC004221
F-HEMBA1002337//Human mRNA for KIAA0118 gene, partial cds//0.93:220:61//Hs.154326:D42087	F-HEMBA1002703//Homo sapiens mRNA for KIAA0455 protein, complete cds//6.0e-12:327:62//Hs.13245:AB007924
F-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cds//7.8e-187:872:98//Hs.6162:AB018314	F-HEMBA1002712
F-HEMBA1002348//EST//1.0e-19:285:70//Hs.121860:AA776692	F-HEMBA1002716//EST//1.2e-56:284:97//Hs.131329:AA922800
F-HEMBA1002349//EST//0.011:385:59//Hs.148533:AI200996	F-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.7e-127:614:97//Hs.132942:AB014521
F-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//2.4e-189:872:99//Hs.119023:AF092563	F-HEMBA1002730//Homo sapiens microsomal glutathione S-transferase 3 (MGST3) mRNA, complete cds//0.21:157:66//Hs.111811:AB007867
F-HEMBA1002381//EST//7.9e-34:236:77//Hs.162197:AA535216	F-HEMBA1002742//EST//0.97:138:60//Hs.160545:AI271596
F-HEMBA1002389//ESTs//4.3e-59:342:92//Hs.133391:AA535144	F-HEMBA1002746//Human HOX4C mRNA for a homeobox protein//0.72:347:58//Hs.74061:X59372
F-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//2.2e-159:775:97//Hs.25527:AC005954	F-HEMBA1002748//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.24:83:74//Hs.40806:AA018786
F-HEMBA1002419//EST, Moderately similar to ROD CGMP-SPECIFIC 3', 5'-CYCLIC PHOSPHODIESTERASE BETA-SUBUNIT [H.sapiens]//1.0:144:65//Hs.136096:W27141	F-HEMBA1002750//ESTs//5.8e-37:185:76//Hs.140577:AA827817
F-HEMBA1002430//Human clone 23695 mRNA sequence//2.7e-06:563:59//Hs.90798:U79289	F-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//2.9e-178:834:98//Hs.74750:AB011126
F-HEMBA1002439//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//0.11:111:67//Hs.162154:AA528561	F-HEMBA1002770//ESTs, Highly similar to TIP120 [R.norvegicus]//8.0e-98:492:96//Hs.11833:AI299947
F-HEMBA1002458//ESTs, Weakly similar to hypothetical protein B. 6.8K [H.sapiens]//1.3e-71:346:98//Hs.136121:W26490	F-HEMBA1002777//Homo sapiens prostate apoptosis response protein par-4 mRNA, complete cds//3.9e-05:528:59//Hs.128208:U63809
F-HEMBA1002460//ESTs//2.1e-94:484:96//Hs.106441:R53160	F-HEMBA1002779//ESTs//8.1e-134:662:96//Hs.107295:W80392
F-HEMBA1002462//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//0.00024:240:64//Hs.113286:U77783	F-HEMBA1002780//ESTs//3.8e-41:421:74//Hs.141576:N80326
F-HEMBA1002469//Human mRNA for KIAA0122 gene, partial cds//1.3e-109:603:92//Hs.154583:D50912	F-HEMBA1002794//Protein kinase C, mu//4.8e-06:244:67//Hs.2891:X75756
F-HEMBA1002475//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.025:261:63//Hs.89631:U48508	F-HEMBA1002801//ESTs//2.1e-24:182:87//Hs.124633:AA856938
F-HEMBA1002477//Homo sapiens mRNA for KIAA0561 protein, partial cds//2.8e-45:331:83//Hs.6189:AB011133	F-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds//3.4e-169:820:97//Hs.28307:AF071185
F-HEMBA1002486//EST//0.00039:174:67//Hs.96680:AA303235	F-HEMBA1002816//ESTs//2.5e-91:387:94//Hs.8008:R52744
F-HEMBA1002495	F-HEMBA1002818//Homo sapiens UPH1 (UPH1) mRNA, complete cds//7.0e-122:733:89//Hs.6059:AF093119
F-HEMBA1002498//ESTs//1.2e-91:460:97//Hs.118327:W79161	F-HEMBA1002826//ESTs//0.00015:235:62//Hs.119383:AI279904
F-HEMBA1002503//H.sapiens mRNA for MACH-alpha-2 protein//4.8e-13:164:74//Hs.19949:X98173	F-HEMBA1002833
F-HEMBA1002508//Homo sapiens PYRIN (MEFV) mRNA, complete cds//6.1e-79:460:83//Hs.113283:AF018080	F-HEMBA1002850//EST//0.0014:201:65//Hs.156235:AA770550
F-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//9.0e-159:738:98//Hs.6764:AJ011972	F-HEMBA1002863//ESTs//1.2e-50:295:91//Hs.57980:W68823
F-HEMBA1002515//ESTs//3.6e-08:185:69//Hs.118701:AA420795	F-HEMBA1002876//ESTs, Weakly similar to HYPOTHETICAL 26.4 KD PROTEIN EEE08.8 IN CHROMOSOME II [C.elegans]//4.9e-18:110:94//Hs.13322:AA151730
F-HEMBA1002538//ESTs//0.97:58:73//Hs.134672:AI087951	F-HEMBA1002886//EST//0.99:184:65//Hs.160684:AI279429
F-HEMBA1002542//Homo sapiens mRNA for chemokine LEC precursor, complete cds//6.1e-46:238:87//Hs.10458:AF088219	F-HEMBA1002896//ESTs//2.1e-11:72:100//Hs.149215:AI051679
F-HEMBA1002547//Homo sapiens agrin precursor mRNA, partial cds//1.1e-138:655:98//Hs.68900:AF016903	F-HEMBA1002921
F-HEMBA1002552//Human Hep2 protein mRNA, complete cds//2.8e-08:173:68//Hs.102137:U31875	F-HEMBA1002924//EST//3.7e-05:291:64//Hs.134677:AI088001
F-HEMBA1002555//Homo sapiens mRNA for APC 2 protein, complete cds//0.00020:603:57//Hs.20912:AB012162	F-HEMBA1002934//ESTs//2.3e-42:324:80//Hs.141658:M77915
F-HEMBA1002558//ESTs//6.0e-25:262:77//Hs.136304:AA431205	F-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds//1.6e-174:803:99//Hs.14687:AB011148
F-HEMBA1002561//Human clone 23574 mRNA sequence//4.7e-17:268:72//Hs.79385:U90905	F-HEMBA1002937//ESTs, Weakly similar to homologous to mouse gene P326:GenBank Accession Number M95564 [H.sapiens]//8.1e-36:256:85//Hs.36899:AA130053
	F-HEMBA1002939//H.sapiens mRNA for cytokine inducible nuclear protein//1.1e-05:479:59//Hs.74019:X83703
	F-HEMBA1002944//Human putative endothelin receptor type B-like pro

【0849】

【表548】

tein mRNA, complete cds//0.83:326:58//Hs.27747:U87460	0//Hs.154782:X99459
F-HEMBA1002951//ESTs//6.1e-08:137:70//Hs.126762:AA913925	F-HEMBA1003327//EST//7.7e-10:165:72//Hs.114826:AA056254
F-HEMBA1002954//ESTs//9.3e-39:249:89//Hs.146185:R19099	F-HEMBA1003328//EST//0.00023:128:67//Hs.126467:AA913328
F-HEMBA1002968//ESTs//0.73:142:64//Hs.136371:AA506092	F-HEMBA1003330
F-HEMBA1002970//EST//2.9e-10:103:82//Hs.162580:AA593828	F-HEMBA1003348//Human mRNA for KIAA0331 gene, complete cds//4.8e-2
F-HEMBA1002971//ESTs//3.5e-21:190:81//Hs.61170:AA454219	6:256:78//Hs.146395:AB002329
F-HEMBA1002973//Phosphodiesterase 4B, cAMP-specific (dunce (Drosop	F-HEMBA1003369//Homo sapiens DNA from chromosome 19p13.2 cosmid R
hila)-homolog phosphodiesterase 4E//1.5e-37:247:89//Hs.188:L20971	31240, R30272 and R28549 containing the EKLF, GCDH, CRT, and RAD2
F-HEMBA1002987//Homo sapiens chromosome-associated protein-C (hCA	3A genes, genomic sequence//0.37:187:65//Hs.80265:AD000092
P-C) mRNA, partial cds//1.7e-05:797:58//Hs.50758:AF092564	F-HEMBA1003370//ESTs//8.2e-36:196:79//Hs.139158:AA226159
F-HEMBA1002999//EST//9.9e-38:453:70//Hs.161635:W22525	F-HEMBA1003373//ESTs//1.0:195:61//Hs.127307:AI263819
F-HEMBA1003021//Small inducible cytokine A5 (RANTES)//4.6e-49:373:	F-HEMBA1003376//Clathrin, light polypeptide (Lcb)//2.3e-29:606:64//
81//Hs.155464:AF088219	/Hs.73919:X81637
F-HEMBA1003033//ESTs//5.0e-64:340:95//Hs.154270:N26486	F-HEMBA1003380//ESTs//2.5e-21:303:70//Hs.37528:HS8017
F-HEMBA1003034//Homo sapiens PYRIN (MEFY) mRNA, complete cds//7.4	F-HEMBA1003384//ESTs//0.14:281:61//Hs.159650:N95552
e-70:330:78//Hs.113283:AF018080	F-HEMBA1003395//ESTs//0.53:121:70//Hs.144873:AI202488
F-HEMBA1003035//Homo sapiens mRNA for testican-3//0.041:623:57//H	F-HEMBA1003402//EST//0.029:148:66//Hs.116798:AA633813
s.159425:AJ001454	F-HEMBA1003403//Adducin 2 (beta) (alternative products)//5.0e-05:4
F-HEMBA1003037//EST//0.53:59:74//Hs.148011:AI268003	45:61//Hs.30951:U43959
F-HEMBA1003041//ESTs. Weakly similar to F58C11.6 [C.elegans]//1.7	F-HEMBA1003408//ESTs//9.0e-12:87:98//Hs.70268:Z78309
e-64:337:95//Hs.105907:AA186514	F-HEMBA1003417//Glutamate-cysteine ligase (gamma-glutamylcysteine
F-HEMBA1003046//Homo sapiens mitochondrial processing peptidase be	synthetase), regulatory (30.8kD)//9.5e-05:541:58//Hs.89709:L35546
ta-subunit mRNA, complete cds//3.2e-166:777:98//Hs.44097:AF054182	F-HEMBA1003418//ESTs//3.5e-85:399:100//Hs.154489:AA564962
F-HEMBA1003064//ESTs//3.2e-07:320:65//Hs.23466:AI223438	F-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//2.0
F-HEMBA1003067	e-149:686:99//Hs.25812:AF058696
F-HEMBA1003071//Homo sapiens hyperpolarization-activated channel 1	F-HEMBA1003447//Human mRNA for KIAA0380 gene, complete cds//0.43:2
(IH1) mRNA, partial cds//1.5e-15:611:59//Hs.124161:AF065164	71:60//Hs.47822:AB002378
F-HEMBA1003077//Homo sapiens KIAA0405 mRNA, complete cds//2.2e-29:	F-HEMBA1003461//Glycoprotein Ib (platelet), beta polypeptide//4.8
542:62//Hs.48998:AB007865	e-08:775:58//Hs.3847:U59632
F-HEMBA1003078//CYTOCHROME P450 1VF3//2.0e-29:452:67//Hs.106242:AB	F-HEMBA1003463//ESTs//3.3e-22:121:99//Hs.130847:AA058578
002454	F-HEMBA1003480//Homo sapiens mRNA for KIAA0700 protein, partial cd
F-HEMBA1003079//EST//2.0e-20:273:73//Hs.138001:AI034461	s//0.16:321:60//Hs.13999:AB014600
F-HEMBA1003083//EST//2.0e-48:314:86//Hs.149580:AI281881	F-HEMBA1003528//ESTs//3.8e-53:315:91//Hs.129688:AA057443
F-HEMBA1003086//ESTs//2.6e-20:237:73//Hs.129331:AI090721	F-HEMBA1003531//Human mRNA for KIAA0033 gene, partial cds//4.9e-5
F-HEMBA1003096//ESTs. Weakly similar to HMG-box transcription fact	1:451:78//Hs.22271:026067
or [H.musculus]//0.98:216:61//Hs.97865:AA405872	F-HEMBA1003538//ESTs//1.2e-82:415:96//Hs.162075:AI392811
F-HEMBA1003098//EST//2.9e-19:239:73//Hs.152366:AA486721	F-HEMBA1003545//ISL1 transcription factor, LIM/homeodomain, (isle
F-HEMBA1003117//H.sapiens ERF-2 mRNA//0.0048:447:59//Hs.78909:U078	t-1)//5.0e-75:736:73//Hs.505:U07559
02	F-HEMBA1003548//ESTs//8.7e-77:411:95//Hs.163443:R23311
F-HEMBA1003129//Homo sapiens clone 24407 mRNA sequence//1.9e-06:50	F-HEMBA1003555//Human nucleotide-binding protein mRNA, complete cd
7:58//Hs.12432:AF070575	s//3.6e-33:562:64//Hs.81469:U01833
F-HEMBA1003133//Homo sapiens mRNA for KIAA0771 protein, partial cd	F-HEMBA1003556
s//0.038:288:63//Hs.6162:AB018314	F-HEMBA1003560//EST//3.7e-29:202:86//Hs.136858:AA767122
F-HEMBA1003136	F-HEMBA1003568//ESTs//2.4e-06:214:65//Hs.143371:AI342327
F-HEMBA1003142//ESTs//3.6e-112:526:99//Hs.55982:AA284279	F-HEMBA1003569//Human metastasis-associated metal mRNA, complete cd
F-HEMBA1003148//Homo sapiens mRNA for dachshund protein//2.2e-184:	s//2.0e-58:455:66//Hs.101448:U35113
850:99//Hs.63931:AJ005670	F-HEMBA1003571//ESTs//0.0025:198:63//Hs.116448:AA648972
F-HEMBA1003166//Homo sapiens mRNA for KIAA0688 protein, complete c	F-HEMBA1003579//ESTs//6.0e-110:513:99//Hs.97372:AA398546
ds//1.1e-24:171:83//Hs.141874:AB014588	F-HEMBA1003581//ESTs. Highly similar to TALIN [Mus musculus]//3.6
F-HEMBA1003175//EST//0.91:168:60//Hs.123335:AA810740	e-19:108:99//Hs.18420:AA599232
F-HEMBA1003179//EST. Weakly similar to hypothetical protein in pur	F-HEMBA1003591//ESTs. Weakly similar to R74.5 [C.elegans]//5.2e-8
B 5' region [E.coli]//4.7e-20:118:97//Hs.118831:AA211895	S:487:92//Hs.57937:W68285
F-HEMBA1003197//ESTs//0.049:265:58//Hs.153718:AI215523	F-HEMBA1003595//Membrane cofactor protein (CD46, trophoblast-lymph
F-HEMBA1003199//SDX-3 PROTEIN//0.00034:383:60//Hs.157429:X71135	ocyte cross-reactive antigen)//2.8e-06:439:62//Hs.83532:X59405
F-HEMBA1003202//ESTs//7.1e-84:408:98//Hs.130134:AA905412	F-HEMBA1003597//ESTs//0.0025:200:64//Hs.8473:T40827
F-HEMBA1003204//Homo sapiens PYRIN (MEFY) mRNA, complete cds//4.6	F-HEMBA1003598//ESTs//0.18:187:63//Hs.98641:AA429916
e-33:154:85//Hs.113283:AF018080	F-HEMBA1003615//ESTs. Highly similar to phosphorylation regulatory
F-HEMBA1003212//ESTs//1.0e-31:159:84//Hs.134067:AI076765	protein HP-10 [H.sapiens]//2.4e-133:644:97//Hs.3566:AA314782
F-HEMBA1003220//EST//8.6e-29:317:73//Hs.150552:AI053784	F-HEMBA1003617//Homo sapiens mRNA for HRHFB2157, partial cds//7.9
F-HEMBA1003222//ESTs//0.77:208:62//Hs.85451:AA181310	e-171:501:97//Hs.124956:AB015344
F-HEMBA1003229//EST//0.084:233:60//Hs.98176:AA417012	F-HEMBA1003621//Homo sapiens protein inhibitor of activated STAT p
F-HEMBA1003235//Homo sapiens antigen NY-CO-16 mRNA, complete cds//	rotein PIAs-alpha mRNA, complete cds//4.4e-16:161:78//Hs.111323:A
0.00054:432:58//Hs.132206:AF039694	F077954
F-HEMBA1003250	F-HEMBA1003622//EST//0.0085:251:62//Hs.97343:AA401750
F-HEMBA1003257//Homo sapiens fibroblast growth factor 18 (FGF18) m	F-HEMBA1003630//ESTs//7.5e-05:304:61//Hs.87131:AA233159
RNA, complete cds//4.3e-08:426:64//Hs.49585:AF075292	F-HEMBA1003637//Homo sapiens homolog of the Aspergillus nidulans s
F-HEMBA1003273//EST//0.00078:195:65//Hs.158019:AA867991	udd gene product mRNA, complete cds//7.9e-26:546:63//Hs.109901:AF0
F-HEMBA1003276//EST//6.6e-09:159:74//Hs.162664:AA605020	13591
F-HEMBA1003278//ESTs//0.89:257:63//Hs.23207:R42864	F-HEMBA1003640//ESTs//1.1e-11:267:66//Hs.34359:AI122791
F-HEMBA1003281//ESTs//2.6e-33:175:98//Hs.122278:AA781867	F-HEMBA1003645
F-HEMBA1003286//Homo sapiens chromosome 3q13 beta-1,4-galactosyltr	F-HEMBA1003646
ansferase mRNA, complete cds//2.9e-145:539:97//Hs.13225:AF038662	F-HEMBA1003656
F-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete c	F-HEMBA1003662
ds//1.6e-167:799:98//Hs.12836:AB011109	F-HEMBA1003667//ESTs//1.5e-27:235:81//Hs.55855:AA621381
F-HEMBA1003296//EST//0.0013:49:97//Hs.137157:R44912	F-HEMBA1003679//ESTs//4.3e-49:251:97//Hs.152811:AA630906
F-HEMBA1003304//ESTs//0.047:164:64//Hs.94448:AA770160	F-HEMBA1003680//Human plectin (PLEC1) mRNA, complete cds//3.4e-06:
F-HEMBA1003309//ESTs//7.8e-123:589:98//Hs.105486:AA521012	464:61//Hs.79706:U53204
F-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinas	F-HEMBA1003684//ESTs. Weakly similar to zinc finger protein C2H2-1
e, complete cds//1.5e-189:865:99//Hs.124224:AB001872	71 [H.sapiens]//1.6e-100:478:98//Hs.118866:AI017072
F-HEMBA1003322//H.sapiens mRNA for sigma 3B protein//4.5e-49:399:8	F-HEMBA1003690//Homo sapiens mRNA for KIAA0600 protein, partial cd

【0850】

【表549】

s//9.5e-74:606:77//Hs.9028:AF039691
 F-HEMBA1003692//ESTs//4.2e-43:252:92//Hs.39748:AA487187
 F-HEMBA1003711//Homo sapiens mRNA for KIAA0544 protein, partial cd
 s//0.81:254:62//Hs.32316:AB011116
 F-HEMBA1003714//ESTs//6.4e-98:495:95//Hs.43846:N49995
 F-HEMBA1003715//ESTs//1.3e-11:228:69//Hs.101237:AA708760
 F-HEMBA1003720//Homo sapiens clone 23892 mRNA sequence//5.5e-45:69
 2:68//Hs.91916:AF035317
 F-HEMBA1003725//EST//2.5e-46:228:100//Hs.160069:AA926921
 F-HEMBA1003729//ESTs//4.1e-48:253:96//Hs.26270:AA258839
 F-HEMBA1003733//Human Line-1 repeat mRNA with 2 open reading frame
 s//8.6e-102:753:81//Hs.23094:M19503
 F-HEMBA1003742//Homo sapiens chromosome 19, cosmid R31180//0.16:24
 2:62//Hs.153325:AC005390
 F-HEMBA1003758//ESTs//9.3e-12:408:61//Hs.148459:A1198946
 F-HEMBA1003760//Homo sapiens clone 23698 mRNA sequence//9.7e-35:43
 0:69//Hs.8136:U81984
 F-HEMBA1003773//EST//0.76:191:61//Hs.127020:AA934920
 F-HEMBA1003783//ESTs. Weakly similar to COIH5.7 [C.elegans]//1.7e-
 24:224:81//Hs.18171:AA524327
 F-HEMBA1003784//ESTs//0.13:120:67//Hs.161993:AA503172
 F-HEMBA1003799//Interleukin 9 receptor//2.0e-17:263:70//Hs.1702:L3
 9064
 F-HEMBA1003803//Homo sapiens calcium-activated potassium channel
 (KCNH3) mRNA, complete cds//0.13:222:61//Hs.89230:AF031815
 F-HEMBA1003804//ESTs//1.4e-112:275:98//Hs.72132:AF039239
 F-HEMBA1003805//Human p62 mRNA, complete cds//1.1e-11:523:60//Hs.1
 19537:N88108
 F-HEMBA1003807//ESTs//4.1e-08:279:68//Hs.115679:A1379721
 F-HEMBA1003827//Homo sapiens mRNA for KIAA0616 protein, partial cd
 s//3.3e-85:586:87//Hs.6051:AB014516
 F-HEMBA1003836//EST//6.8e-06:98:74//Hs.145447:A1204220
 F-HEMBA1003838//ESTs. Moderately similar to !!!! ALU SUBFAMILY SC
 WARNING ENTRY !!!! [H.sapiens]//3.8e-40:151:88//Hs.139007:H74314
 F-HEMBA1003856//ESTs//8.6e-53:286:95//Hs.116645:A1005167
 F-HEMBA1003864//Human mRNA for KIAA0369 gene, complete cds//0.11:1
 44:66//Hs.21355:AB002367
 F-HEMBA1003866//Homo sapiens semaphorin F homolog mRNA, complete c
 ds//4.3e-30:580:63//Hs.27621:U52840
 F-HEMBA1003879//Nuclear cap binding protein, 80kD//6.7e-10:87:95//
 Hs.89563:O32002
 F-HEMBA1003880
 F-HEMBA1003885//Homo sapiens mRNA for KIAA0752 protein, partial cd
 s//4.2e-18:302:67//Hs.23711:AB018295
 F-HEMBA1003893//ESTs. Weakly similar to HYPOTHETICAL 27.8 KD PROTE
 IN IN YMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.2e-49:295:92
 //Hs.114673:W72675
 F-HEMBA1003902//ESTs//1.1e-11:165:74//Hs.54632:AA976236
 F-HEMBA1003908//Homo sapiens mRNA for KIAA0525 protein, partial cd
 s//0.081:345:58//Hs.78494:AB011097
 F-HEMBA1003926//EST//2.5e-32:253:83//Hs.132635:A1032875
 F-HEMBA1003937//Human mRNA for KIAA0391 gene, complete cds//2.9e-3
 8:313:69//Hs.154668:AB002389
 F-HEMBA1003939//ESTs//3.4e-07:150:71//Hs.148926:R59562
 F-HEMBA1003942//EST. Weakly similar to 24 KD PROTEIN [Xenopus laevis]
 is//0.0029:222:61//Hs.144236:W52380
 F-HEMBA1003950//ESTs//0.98:200:62//Hs.163912:W20055
 F-HEMBA1003953//Zinc finger protein 7 (KIX 4, clone HF.16)//0.0001
 4:271:66//Hs.2076:M29580
 F-HEMBA1003958//ESTs. Moderately similar to !!!! ALU SUBFAMILY J W
 ARNING ENTRY !!!! [H.sapiens]//2.1e-44:243:76//Hs.91146:N73230
 F-HEMBA1003959//ESTs//0.067:251:59//Hs.39915:H78567
 F-HEMBA1003976//EST//6.7e-09:109:81//Hs.154635:A1138965
 F-HEMBA1003978
 F-HEMBA1003985//EST//0.32:115:69//Hs.102617:N47009
 F-HEMBA1003987//ESTs//7.8e-07:60:100//Hs.66058:AA424456
 F-HEMBA1003989//Homo sapiens HIV-1 inducer of short transcripts bi
 nding protein (FBI1) mRNA, complete cds//0.022:349:58//Hs.104640:A
 F000561
 F-HEMBA1004000//EST//7.2e-07:200:66//Hs.119082:AA358468
 F-HEMBA1004011//EST//0.019:241:62//Hs.116989:AA676493
 F-HEMBA1004012//ESTs//3.6e-09:177:68//Hs.106132:AA812573
 F-HEMBA1004015//ESTs//3.0e-86:407:99//Hs.115679:A1379721
 F-HEMBA1004024//Homo sapiens mRNA for KIAA0772 protein, complete c
 ds//5.2e-51:359:84//Hs.15519:AB018315
 F-HEMBA1004038//ESTs//1.2e-58:324:94//Hs.61658:A1239930
 F-HEMBA1004042//EST//0.00088:272:61//Hs.155763:A1312281
 F-HEMBA1004045//EST//2.7e-20:408:66//Hs.162529:AA584160
 F-HEMBA1004048//Transforming growth factor beta//0.026:462:57//Hs.
 6101:M60315
 F-HEMBA1004049//ESTs//8.1e-68:430:86//Hs.146307:AA584638
 F-HEMBA1004055//Human chromosome 3p21.1 gene sequence//1.5e-10:45
 7:58//Hs.82837:L13435
 F-HEMBA1004056//Homo sapiens mRNA for alpha(1,2)fucosyltransferas
 e, complete cds//1.5e-46:199:80//Hs.46328:D87942
 F-HEMBA1004074//ESTs//3.0e-23:219:74//Hs.70279:AA757426
 F-HEMBA1004086//EST//0.36:189:62//Hs.156218:AA770107
 F-HEMBA1004097//NADH-CYTOCHROME B5 REDUCTASE//1.0:302:57//Hs.7566
 6:M28713
 F-HEMBA1004111//Human G protein-coupled receptor (STRL22) mRNA, co
 mplete cds//4.3e-39:335:79//Hs.46468:U45984
 F-HEMBA1004131//Human mRNA for KIAA0202 gene, partial cds//1.9e-2
 4:610:61//Hs.80712:D86957
 F-HEMBA1004132//EST//3.5e-06:143:70//Hs.136799:AA780064
 F-HEMBA1004133//ESTs//1.0:157:68//Hs.161226:A1419759
 F-HEMBA1004138//H.sapiens mRNA for RanGTPase activating protein 1/
 /0.00055:343:62//Hs.5923:X82260
 F-HEMBA1004143
 F-HEMBA1004146
 F-HEMBA1004150//EST//0.0046:402:57//Hs.147027:A1186056
 F-HEMBA1004164//Homo sapiens mRNA for KIAA0798 protein, complete c
 ds//1.8e-15:591:60//Hs.159277:AB018341
 F-HEMBA1004168//Homo sapiens geminin mRNA, complete cds//1.5e-134:
 649:97//Hs.59888:AF067855
 F-HEMBA1004199
 F-HEMBA1004200//ESTs//0.0083:150:66//Hs.116424:A1375427
 F-HEMBA1004202//ESTs. Weakly similar to GTP-BINDING PROTEIN YPTB1
 [Zea mays]//1.2e-35:205:94//Hs.10092:A1189282
 F-HEMBA1004203//ESTs//3.9e-14:237:70//Hs.118273:AA626040
 F-HEMBA1004207//Leptin receptor//1.1e-167:791:98//Hs.54515:U50748
 F-HEMBA1004225//ESTs//0.00087:231:64//Hs.13109:AA192514
 F-HEMBA1004227//ESTs. Weakly similar to F55A11.4 [C.elegans]//0.01
 2:156:67//Hs.163588:A1073878
 F-HEMBA1004238
 F-HEMBA1004241//ESTs//8.7e-05:51:96//Hs.162826:AA679571
 F-HEMBA1004246//EST//1.2e-36:198:96//Hs.121343:AA758522
 F-HEMBA1004248//Homo sapiens insulin induced protein 1 (INSIG1) ge
 ne, complete cds//1.1e-28:295:72//Hs.56205:U96876
 F-HEMBA1004264//Human HCF1 gene related mRNA sequence//3.1e-07:55
 3:60//Hs.83634:U52112
 F-HEMBA1004267//Homo sapiens mRNA for KIAA0588 protein, complete c
 ds//4.9e-73:490:77//Hs.141874:AB014588
 F-HEMBA1004272
 F-HEMBA1004274//EST//0.43:154:61//Hs.125347:AA876444
 F-HEMBA1004275//Human mRNA for KIAA0333 gene, partial cds//0.71:11
 8:65//Hs.155313:AB002331
 F-HEMBA1004276//Homo sapiens mRNA for KIAA0800 protein, complete c
 ds//1.0:364:56//Hs.118738:AB018343
 F-HEMBA1004286//Homo sapiens TGF beta receptor associated protein-
 1 mRNA, complete cds//6.9e-187:868:99//Hs.101766:AF022795
 F-HEMBA1004289
 F-HEMBA1004295//EST//0.20:149:62//Hs.162415:AA573484
 F-HEMBA1004306//ESTs//0.041:177:64//Hs.158234:A1270047
 F-HEMBA1004312//ESTs//0.83:253:59//Hs.121898:A1336314
 F-HEMBA1004321//Zinc finger protein 136 (clone pHZ-20)//2.3e-40:45
 2:65//Hs.69740:U09367
 F-HEMBA1004323//EST//0.44:134:64//Hs.145464:A1204532
 F-HEMBA1004327//Homo sapiens SOX22 protein (SOX22) mRNA, complete
 cds//0.017:209:64//Hs.43627:U35612
 F-HEMBA1004330//ESTs//4.5e-27:171:91//Hs.112838:AA614062
 F-HEMBA1004334//EST//2.4e-53:556:75//Hs.139093:AA166888
 F-HEMBA1004335//Homo sapiens mRNA for KIAA0706 protein, complete c
 ds//0.49:80:73//Hs.139648:AB014606
 F-HEMBA1004341
 F-HEMBA1004353//Homo sapiens mRNA for c-myc binding protein, compl
 ete cds//2.7e-39:270:86//Hs.80686:D89667
 F-HEMBA1004354//Human CHL1 potential helicase (CHL1), complete cd
 s//1.3e-46:190:92//Hs.27424:U75968
 F-HEMBA1004356//Thyrotropin-releasing hormone receptor//0.15:296:6
 2//Hs.3022:D85376
 F-HEMBA1004366//ESTs. Weakly similar to transposon LRE2 reverse tr
 ansriptase homolog [H.sapiens]//7.8e-10:396:61//Hs.33688:AA020928
 F-HEMBA1004372//ESTs//0.90:172:62//Hs.145611:R68800
 F-HEMBA1004389//Zinc finger protein 148 (pHZ-52)//8.0e-28:359:67//
 Hs.112180:AF039019
 F-HEMBA1004394//ESTs//0.023:357:58//Hs.47212:N51250
 F-HEMBA1004396//EST//3.4e-22:244:74//Hs.162554:AA584818
 F-HEMBA1004405//EST//4.0e-43:214:100//Hs.33100:H42199
 F-HEMBA1004408//ESTs. Weakly similar to The hal539 protein is rela
 ted to cyclophilin. [H.sapiens]//1.4e-20:144:88//Hs.121076:A124642

【表550】

6	57//Hs.41587:U63139
F-HEMBA1004429//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//4.8e-18:248:72//Hs.6974:7:N35531	F-HEMBA1004771
F-HEMBA1004433//Small inducible cytokine A5 (RANTES)//8.2e-39:248:81//Hs.155464:AF088219	F-HEMBA1004776//ESTs, Weakly similar to progesterone receptor-related protein p23 [H.sapiens]//1.0:158:63//Hs.62004:AF039235
F-HEMBA1004460//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.6e-87:650:81//Hs.113283:AF018080	F-HEMBA1004778//ESTs//1.2e-70:336:99//Hs.113052:A1222106
F-HEMBA1004461//ESTs//0.057:217:61//Hs.26989:Z41606	F-HEMBA1004795
F-HEMBA1004479//Homo sapiens clone 23698 mRNA sequence//4.9e-17:223:71//Hs.8136:U81984	F-HEMBA1004803//ESTs//5.0e-75:454:88//Hs.138632:H97952
F-HEMBA1004482//EST//0.0056:261:59//Hs.45012:N39450	F-HEMBA1004806//EST//0.080:142:65//Hs.160268:A1148971
F-HEMBA1004499//ESTs//4.1e-68:340:97//Hs.134266:AA92600	F-HEMBA1004807//Human HIV1 tat element modulatory factor mRNA sequence from chromosome 3//4.5e-48:171:92//Hs.134510:L01042
F-HEMBA1004502//ESTs//7.7e-32:195:91//Hs.134906:H93431	F-HEMBA1004816//EST//1.0e-17:175:71//Hs.140680:AA873646
F-HEMBA1004506//Human Line-1 repeat mRNA with 2 open reading frame s//9.0e-89:758:76//Hs.23094:M19503	F-HEMBA1004820//ESTs//1.3e-136:629:99//Hs.160726:A1300481
F-HEMBA1004507//ESTs, Weakly similar to T19810.6 [C.elegans]//1.4e-61:296:99//Hs.114622:AA693492	F-HEMBA1004847//ESTs//2.1e-09:66:98//Hs.158161:AA312511
F-HEMBA1004509//Homo sapiens suppressor of white apricot homolog 2 (SWAP2) mRNA, complete cds//0.014:265:61//Hs.43543:AF042800	F-HEMBA1004850//EST//0.033:253:64//Hs.158782:A1376601
F-HEMBA1004534//Filamin 1 (actin-binding protein-280)//5.0e-74:678:74//Hs.76279:U53416	F-HEMBA1004863//Homo sapiens mRNA for KIAA0578 protein, partial cds//0.83:179:62//Hs.22998:AB011150
F-HEMBA1004538//EST//0.00047:268:58//Hs.136870:AA805381	F-HEMBA1004864//ESTs, Weakly similar to ANON-66Db [D.melanogaster]//1.7e-13:81:100//Hs.75884:AA446987
F-HEMBA1004542//Human butyrophilin protein (BT3.3) mRNA, partial cds//0.74:74:75//Hs.87497:U90552	F-HEMBA1004865//ESTs//0.92:148:65//Hs.126980:AA934077
F-HEMBA1004554	F-HEMBA1004880//H.sapiens mRNA for retrotransposon//1.2e-30:264:79//Hs.6940:Z48633
F-HEMBA1004560//ESTs//3.1e-19:240:73//Hs.112637:AA805331	F-HEMBA1004889//Growth arrest-specific 1//0.20:146:68//Hs.65029:L13698
F-HEMBA1004573//EST//2.4e-59:290:99//Hs.112908:AA620802	F-HEMBA1004900//ESTs//1.6e-32:196:93//Hs.132032:R85304
F-HEMBA1004577//ESTs, Weakly similar to UTR1 PROTEIN [S.cerevisiae]//1.2e-17:334:67//Hs.24536:AA479825	F-HEMBA1004909//ESTs//3.4e-13:154:75//Hs.151467:N51106
F-HEMBA1004586//Von Hippel-Lindau syndrome//5.1e-35:337:78//Hs.78160:AF010238	F-HEMBA1004918//EST//0.78:122:61//Hs.145491:A1254348
F-HEMBA1004596//ESTs//3.3e-32:189:94//Hs.42530:N41661	F-HEMBA1004923//ELK1, member of ETS oncogene family//1.6e-40:340:79//Hs.116549:AL009172
F-HEMBA1004604//Human hindlimb expressed homeobox protein backfoot (Bft) mRNA, complete cds//0.42:186:66//Hs.84136:U70370	F-HEMBA1004929//Cardiac gap junction protein//0.0048:588:57//Hs.74471:X52947
F-HEMBA1004610//ESTs, Moderately similar to !!!! ALU SUBFAMILY J W ARNING ENTRY !!!! [H.sapiens]//2.3e-16:297:68//Hs.106008:AA147606	F-HEMBA1004930//ESTs//1.5e-17:227:74//Hs.148739:A1224959
F-HEMBA1004617//EST//0.027:188:61//Hs.159094:A1383198	F-HEMBA1004933//Human pseudoautosomal homeodomain-containing protein (PHOG) mRNA, complete cds//0.11:182:65//Hs.105932:U89331
F-HEMBA1004629//ESTs//7.8e-09:348:63//Hs.138358:T66178	F-HEMBA1004934
F-HEMBA1004631//EST//0.0012:268:60//Hs.150685:AA923416	F-HEMBA1004944//EST//1.2e-67:349:96//Hs.162281:AA553981
F-HEMBA1004632//ESTs//0.82:125:67//Hs.143619:A1360891	F-HEMBA1004954//ESTs//0.014:404:60//Hs.11177:AA417813
F-HEMBA1004637//ESTs//0.0034:229:64//Hs.157178:A1346780	F-HEMBA1004956//EST//2.3e-05:208:64//Hs.146958:A1144478
F-HEMBA1004638//ESTs//2.0e-11:166:71//Hs.128657:A1017522	F-HEMBA1004960//ESTs//0.79:169:62//Hs.11637:W03274
F-HEMBA1004666//EST//0.44:294:58//Hs.44780:N36083	F-HEMBA1004972
F-HEMBA1004669//ESTs//1.7e-28:200:86//Hs.8084:W22796	F-HEMBA1004973//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.073:574:58//Hs.154139:AB007914
F-HEMBA1004670//Mucin 1, transmembrane//0.060:416:57//Hs.89603:J05582	F-HEMBA1004977//EST//4.4e-12:86:94//Hs.157819:A1361946
F-HEMBA1004672//ESTs//0.27:44:95//Hs.86237:AA206141	F-HEMBA1004978//ESTs//0.097:337:60//Hs.114157:AA703013
F-HEMBA1004693//ESTs//5.3e-55:301:95//Hs.159066:A1093252	F-HEMBA1004980//EST//3.2e-10:169:65//Hs.149123:A1244750
F-HEMBA1004697//H.sapiens mRNA for ribosomal protein L18a homolog a//0.64:313:61//Hs.118578:X08021	F-HEMBA1004983//EST//0.93:85:71//Hs.162267:AA553589
F-HEMBA1004705//Homo sapiens KIAA0432 mRNA, complete cds//4.5e-19:230:73//Hs.155174:AB007892	F-HEMBA1004995//ESTs//0.46:296:61//Hs.135168:A1394026
F-HEMBA1004709//ESTs//3.1e-31:176:88//Hs.152413:AA780515	F-HEMBA1005008//ESTs//1.5e-20:156:85//Hs.114140:U35429
F-HEMBA1004711//Cholinergic receptor, nicotinic, delta polypeptide//1.0:244:57//Hs.99975:X55019	F-HEMBA1005009//Homo sapiens chromosome 7q22 sequence//1.5e-52:379:72//Hs.151887:AF053356
F-HEMBA1004725//Homo sapiens agrin precursor mRNA, partial cds//0.24:328:60//Hs.68900:AF016903	F-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cds//4.5e-148:693:98//Hs.31921:AB014548
F-HEMBA1004730//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//5.9e-32:476:70//Hs.116874:AA524909	F-HEMBA1005029//Homo sapiens mRNA for KIAA0660 protein, complete cds//1.0:215:65//Hs.6727:AB014560
F-HEMBA1004733//ESTs//3.8e-16:96:79//Hs.152413:AA780515	F-HEMBA1005035//ESTs, Weakly similar to HYPOTHETICAL 82.8 KD PROTEIN B0303.4 IN CHROMOSOME III [C.elegans]//9.4e-106:503:98//Hs.21362:AF039237
F-HEMBA1004734//Human epidermoid carcinoma mRNA for ubiquitin-conjugating enzyme E2 similar to Drosophila bendless gene product, complete cds//0.16:329:58//Hs.75355:D83004	F-HEMBA1005039//Human kpni repeat mRNA (cdna clone pcd-kpni-8), 3' end//5.8e-60:272:89//Hs.103948:K00627
F-HEMBA1004736//Human Line-1 repeat mRNA with 2 open reading frame s//2.0e-61:663:71//Hs.23094:M19503	F-HEMBA1005047//Homo sapiens MAD-related gene SMAD7 (SMAD7) mRNA, complete cds//0.078:442:59//Hs.100602:AF010193
F-HEMBA1004748//ESTs//1.5e-05:343:63//Hs.42241:H96813	F-HEMBA1005050//H.sapiens ERF-2 mRNA//0.0025:251:63//Hs.78909:U07802
F-HEMBA1004751//ESTs//3.7e-32:147:80//Hs.138788:N54504	F-HEMBA1005062//ESTs//0.020:268:59//Hs.146181:A1264462
F-HEMBA1004752//Homo sapiens mRNA for KIAA0288 gene, complete cds//0.00020:521:59//Hs.91400:AB006626	F-HEMBA1005066//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//1.5e-59:411:85//Hs.129727:AF035587
F-HEMBA1004753//Homo sapiens DEC-205 mRNA, complete cds//5.1e-46:337:84//Hs.153563:AF011333	F-HEMBA1005075//Human mRNA for KIAA0383 gene, partial cds//0.00010:395:57//Hs.27590:AB002381
F-HEMBA1004756//Human transporter protein (glT) mRNA, complete cds//3.1e-24:416:65//Hs.76460:U49082	F-HEMBA1005079//Dihydrolypoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex)//3.5e-26:344:72//Hs.89479:X66785
F-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds//1.2e-136:769:91//Hs.153088:L39060	F-HEMBA1005083//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.59:631:59//Hs.27910:AF049105
F-HEMBA1004763//Loricrin//0.0018:227:62//Hs.155657:M61120	F-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, complete cds//4.1e-163:762:98//Hs.11170:AF080561
F-HEMBA1004768//Human Line-1 repeat mRNA with 2 open reading frame s//4.5e-115:909:78//Hs.23094:M19503	F-HEMBA1005113//ESTs//0.52:109:68//Hs.106330:A1031916
F-HEMBA1004770//Human Rad50 (Rad50) mRNA, complete cds//0.020:728:	F-HEMBA1005123//Homo sapiens mRNA for KIAA0761 protein, partial cds//1.3e-52:468:78//Hs.93121:AB018304
	F-HEMBA1005133//ESTs//1.6e-27:366:73//Hs.151467:N51106
	F-HEMBA1005149//EST//3.3e-37:304:80//Hs.132635:A1032875

【0852】

【表551】

F-HEMBA1005152//ESTs//3.9e-09:285:62//Hs.155876:AA593021	76//Hs.155464:AF088219
F-HEMBA1005159//EST//8.4e-05:289:64//Hs.125563:AA884216	F-HEMBA1005528//ESTs. Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//1.2e-30:166:96//Hs.17035:AI080471
F-HEMBA1005185//ESTs//1.4e-22:129:96//Hs.14920:AA910914	F-HEMBA1005530
F-HEMBA1005201//EST//4.0e-16:96:98//Hs.89002:AA282197	F-HEMBA1005548//Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds//4.6e-18:391:64//Hs.30250:AF055376
F-HEMBA1005202	F-HEMBA1005552//ESTs//1.8e-46:238:88//Hs.138856:H47461
F-HEMBA1005206//Homo sapiens sox1 gene//0.0079:431:58//Hs.144029:Y13436	F-HEMBA1005558//Human involucrin mRNA//3.0e-07:501:60//Hs.157091:M13903
F-HEMBA1005219//ESTs//4.3e-47:299:88//Hs.5019:W26547	F-HEMBA1005568//ESTs//0.013:259:63//Hs.13669:H47257
F-HEMBA1005223//ESTs//0.00030:168:66//Hs.76487:N37081	F-HEMBA1005570//ESTs//0.0084:442:59//Hs.125384:AI346507
F-HEMBA1005232//EST//0.0078:209:61//Hs.46852:N48302	F-HEMBA1005576//Homo sapiens mRNA for KIAA0463 protein, partial cds//1.9e-128:610:98//Hs.77738:AB007932
F-HEMBA1005241//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//6.0e-54:399:79//Hs.129735:AF010144	F-HEMBA1005577//ESTs//0.98:199:61//Hs.146226:AI312873
F-HEMBA1005244//ESTs//2.5e-14:85:100//Hs.128744:AI191922	F-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//9.1e-53:830:64//Hs.57929:AB011538
F-HEMBA1005251//ESTs//0.012:49:95//Hs.161554:AA393896	F-HEMBA1005582
F-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cds//4.7e-151:705:98//Hs.72660:AB011157	F-HEMBA1005583
F-HEMBA1005274//ESTs//7.1e-09:298:64//Hs.145522:AI261380	F-HEMBA1005588//ESTs//1.3e-35:386:70//Hs.55855:AA621381
F-HEMBA1005275//ESTs//7.9e-13:375:63//Hs.148974:AA001777	F-HEMBA1005593//S-ADENOSYLMETHIONINE SYNTHETASE ALPHA AND BETA FOR MS//0.54:439:59//Hs.2137:D49357
F-HEMBA1005293//Homo sapiens clone 23662 mRNA sequence//7.7e-22:338:65//Hs.12451:U97018	F-HEMBA1005595//Human mRNA for KIAA0325 gene, partial cds//5.5e-06:378:57//Hs.7720:AB002323
F-HEMBA1005296//ESTs//0.055:299:60//Hs.86320:AI149232	F-HEMBA1005605//EST//2.0e-60:324:94//Hs.5062:D19609
F-HEMBA1005304//Small inducible cytokine A5 (RANTES)//1.7e-45:322:85//Hs.155464:AF088219	F-HEMBA1005609//ESTs//6.0e-39:378:76//Hs.142242:H06982
F-HEMBA1005311	F-HEMBA1005616//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//8.2e-22:721:61//Hs.144563:AF057280
F-HEMBA1005314//ESTs//8.1e-39:199:98//Hs.119974:AI279516	F-HEMBA1005621//ESTs. Weakly similar to MITOTIC MAD2 PROTEIN [S. cerevisiae]//1.8e-89:454:96//Hs.19400:AA662845
F-HEMBA1005315//ESTs//1.9e-07:266:64//Hs.141440:N21615	F-HEMBA1005627//EST//1.0:161:60//Hs.162765:AA622535
F-HEMBA1005318//ESTs//5.3e-06:161:72//Hs.119411:AA937117	F-HEMBA1005631//EST//0.74:124:62//Hs.156185:AA723734
F-HEMBA1005331//Human checkpoint suppressor 1 mRNA, complete cds//0.00075:310:63//Hs.111597:U68723	F-HEMBA1005632//ESTs//1.0:96:70//Hs.141321:N70199
F-HEMBA1005338//Homo sapiens mRNA for matrilin-4, partial//4.4e-153:740:97//Hs.129361:AJ007581	F-HEMBA1005634//EST//6.6e-10:105:73//Hs.159692:AI416956
F-HEMBA1005353//EST//5.4e-09:222:68//Hs.119508:AA485732	F-HEMBA1005666
F-HEMBA1005359//Zinc finger protein 137 (clone pHZ-30)//5.7e-100:500:88//Hs.151689:U09414	F-HEMBA1005670//Homo sapiens mRNA for KIAA0570 protein, complete cds//2.7e-45:255:79//Hs.114293:AB011142
F-HEMBA1005367//Homo sapiens melanostatin 1 (MLSN1) mRNA, complete cds//2.5e-70:572:73//Hs.43265:AF071787	F-HEMBA1005679//Human knpi repeat mRNA (cdna clone pcd-kpni-4), 3' end//1.2e-37:356:77//Hs.139107:K00629
F-HEMBA1005372//ESTs//0.00045:163:66//Hs.164058:AI417905	F-HEMBA1005680
F-HEMBA1005374//Human melanoma antigen recognized by T-cells (MART-1) mRNA//6.1e-43:341:81//Hs.154069:U06452	F-HEMBA1005685
F-HEMBA1005382//EST//2.4e-32:167:99//Hs.147186:AI193053	F-HEMBA1005699//Human putative EPH-related PTK receptor ligand LERK-8 (Eplg8) mRNA, complete cds//3.3e-71:497:85//Hs.26988:U66406
F-HEMBA1005389//ESTs//0.0021:245:59//Hs.104463:AA804448	F-HEMBA1005705//ESTs//0.00093:149:65//Hs.163564:R43678
F-HEMBA1005394//ESTs. Weakly similar to No definition line found [C.elegans]//1.0e-130:620:98//Hs.108990:N25951	F-HEMBA1005717//EST//0.018:115:66//Hs.160541:AI270143
F-HEMBA1005403//ESTs. Weakly similar to No definition line found [C.elegans]//7.7e-151:727:97//Hs.17118:AI033807	F-HEMBA1005732//Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase)//2.6e-20:151:88//Hs.77393:D14697
F-HEMBA1005408//ESTs//3.2e-70:426:89//Hs.158078:H24513	F-HEMBA1005737//ESTs//9.5e-34:235:88//Hs.160197:AA393754
F-HEMBA1005410//EST//2.5e-25:460:67//Hs.138765:N70347	F-HEMBA1005746//ESTs//0.20:260:59//Hs.112451:AI264024
F-HEMBA1005411	F-HEMBA1005755//Human knpi repeat mRNA (cdna clone pcd-kpni-8), 3' end//1.8e-48:425:78//Hs.103948:K00627
F-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CDKN2C) mRNA, complete cds//3.3e-171:537:99//Hs.4854:AF041248	F-HEMBA1005765//Small inducible cytokine A5 (RANTES)//1.3e-36:280:81//Hs.155464:AF088219
F-HEMBA1005426//EST//1.0:148:64//Hs.44469:N33323	F-HEMBA1005780//ESTs//1.0:139:67//Hs.88684:AA885141
F-HEMBA1005443//Zinc finger protein 157 (HZF2)//9.0e-34:259:72//Hs.89997:U28687	F-HEMBA1005813//ESTs//0.012:209:63//Hs.113365:R77747
F-HEMBA1005447//EST//3.9e-10:211:70//Hs.145960:AI276783	F-HEMBA1005815//Human calpain-like protease (htra-3) mRNA, complete cds//2.0e-07:439:62//Hs.6133:U94346
F-HEMBA1005468//ESTs//8.4e-53:390:81//Hs.152395:AA533107	F-HEMBA1005822//ESTs//9.3e-06:444:59//Hs.124344:T10577
F-HEMBA1005469//Human (clone ES.1) RNA-binding protein mRNA, complete cds//3.1e-29:155:99//Hs.75104:L37368	F-HEMBA1005829//ESTs//1.1e-47:394:80//Hs.146811:AA410788
F-HEMBA1005472//Human Line-1 repeat mRNA with 2 open reading frame s//1.4e-88:481:92//Hs.23094:M19503	F-HEMBA1005834//Human Line-1 repeat mRNA with 2 open reading frame s//7.9e-42:690:66//Hs.23094:M19503
F-HEMBA1005474//Small inducible cytokine A5 (RANTES)//4.2e-29:257:78//Hs.155464:AF088219	F-HEMBA1005852//Human plectin (PLEC1) mRNA, complete cds//0.17:47:0:56//Hs.79706:U53204
F-HEMBA1005475//Homo sapiens antigen NY-CO-16 mRNA, complete cds//5.3e-09:414:60//Hs.132206:AF039694	F-HEMBA1005853//EST//0.013:211:60//Hs.162604:AA595150
F-HEMBA1005497//Glucocorticoid receptor alpha (alternative products)//8.7e-41:588:69//Hs.102761:U25029	F-HEMBA1005884//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.4e-53:332:83//Hs.158095:AB007953
F-HEMBA1005500//Homo sapiens PAC clone DJ1093017 from Tq11.23-q21//1.1e-28:318:73//Hs.159530:AC004957	F-HEMBA1005891//ESTs//1.1e-77:393:97//Hs.28545:AI268097
F-HEMBA1005506//Human mRNA for KIAA0010 gene, complete cds//0.67:351:58//Hs.155287:D13635	F-HEMBA1005894//Human G protein-coupled receptor (STRL22) mRNA, complete cds//7.2e-45:411:77//Hs.46468:U45984
F-HEMBA1005508//ESTs//0.45:326:59//Hs.102756:AA526911	F-HEMBA1005909//Human neuropeptide y2 receptor mRNA, complete cds//0.00054:477:59//Hs.37125:U42766
F-HEMBA1005511//Human mRNA for KIAA0355 gene, complete cds//4.2e-49:400:79//Hs.153014:AB002353	F-HEMBA1005911//Thromboxane A2 receptor//4.1e-45:419:75//Hs.89887:D38081
F-HEMBA1005513//ESTs. Weakly similar to males-absent on the first [D.melanogaster]//5.3e-76:378:97//Hs.22767:N99220	F-HEMBA1005921//Homo sapiens haemopoietic progenitor homeobox HPX4 ZB (HPX4ZB) mRNA, complete cds//2.0e-46:434:78//Hs.125231:AF068006
F-HEMBA1005517//Homo sapiens transcription factor forkhead-like 7 (FKHL7) gene, complete cds//0.54:623:56//Hs.143551:AF048693	F-HEMBA1005931//ESTs. Weakly similar to kruppel-related zinc finger protein [H.sapiens]//1.2e-46:228:100//Hs.152178:AI224880
F-HEMBA1005518//ESTs//0.10:207:60//Hs.72447:AA160575	F-HEMBA1005934//EST//3.1e-14:121:85//Hs.150003:AI291588
F-HEMBA1005520//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.1e-55:288:85//Hs.144563:AF057280	F-HEMBA1005962//EST//0.0010:212:62//Hs.163197:AA767883
F-HEMBA1005526//Small inducible cytokine A5 (RANTES)//5.4e-48:176:	F-HEMBA1005963

【0853】

【表552】

F-HEMBA1005990//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//4.2e-151:697:99//Hs.26285:AF082516
 F-HEMBA1005991//EST//3.0e-07:361:59//Hs.146442:A1127530
 F-HEMBA1005999//EST//1.2e-14:350:66//Hs.122326:AA782526
 F-HEMBA1006002
 F-HEMBA1006005//ESTs, Weakly similar to TH1 protein [D.melanogaster]//0.98:197:61//Hs.5184:AA709151
 F-HEMBA1006031
 F-HEMBA1006035
 F-HEMBA1006036//Homo sapiens PYRIN (NEFV) mRNA, complete cds//5.4e-92:617:84//Hs.113283:AF018080
 F-HEMBA1006042//ESTs//6.3e-41:161:81//Hs.141186:R99609
 F-HEMBA1006067//ESTs//2.0e-74:354:99//Hs.143321:A1139422
 F-HEMBA1006081
 F-HEMBA1006090//EST//1.2e-12:340:62//Hs.161195:A1418788
 F-HEMBA1006091//ESTs//4.7e-98:473:98//Hs.9658:AA506313
 F-HEMBA1006100//ESTs//7.1e-22:273:73//Hs.144407:AA737799
 F-HEMBA1006108//ESTs, Weakly similar to ZK792.1 [C.elegans]//2.1e-26:273:66//Hs.8763:W30741
 F-HEMBA1006121//EST//0.00012:232:59//Hs.117096:AA677968
 F-HEMBA1006124//EST//0.047:251:62//Hs.132257:A1027222
 F-HEMBA1006130//Human H0X4C mRNA for a homeobox protein//1.0:150:62//Hs.74061:X59372
 F-HEMBA1006138//ESTs//1.8e-27:132:84//Hs.141575:AA211734
 F-HEMBA1006142//EST//2.5e-47:310:87//Hs.149580:A1281881
 F-HEMBA1006155
 F-HEMBA1006158//ESTs//5.1e-105:506:98//Hs.93468:AA0575
 F-HEMBA1006173//ESTs//2.5e-24:195:84//Hs.79092:H29627
 F-HEMBA1006182//ESTs//2.5e-19:237:72//Hs.141840:AA028117
 F-HEMBA1006198//ESTs//0.017:133:67//Hs.142168:AA292540
 F-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//8.6e-177:836:98//Hs.109268:AF070557
 F-HEMBA1006248//Human zinc finger protein (MAZ) mRNA//0.0014:221:67//Hs.7647:M94046
 F-HEMBA1006252
 F-HEMBA1006253//EST//1.3e-100:467:100//Hs.146619:A1140706
 F-HEMBA1006259//Homo sapiens mRNA for KIAA0798 protein, complete cds//0.00037:158:69//Hs.159277:AB018341
 F-HEMBA1006268//ESTs//1.1e-20:376:67//Hs.72814:AA706631
 F-HEMBA1006272//EST//4.8e-20:252:69//Hs.162992:AA688140
 F-HEMBA1006278//H.sapiens PAP mRNA//6.5e-57:610:71//Hs.49007:X76770
 F-HEMBA1006283
 F-HEMBA1006284//ESTs//0.00017:248:63//Hs.143840:A1189964
 F-HEMBA1006291
 F-HEMBA1006293
 F-HEMBA1006309//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA, complete cds//0.76:416:58//Hs.46465:U45285
 F-HEMBA1006310//Homo sapiens mRNA for KIAA0602 protein, partial cds//9.3e-49:637:68//Hs.37656:AB011174
 F-HEMBA1006328//ESTs//1.8e-71:429:88//Hs.139922:AA281350
 F-HEMBA1006334//EST//0.082:267:57//Hs.136449:AA572789
 F-HEMBA1006344//ESTs//6.2e-08:67:94//Hs.42302:A1032142
 F-HEMBA1006347//ESTs, Weakly similar to males-absent on the first [D.melanogaster]//5.3e-76:378:97//Hs.22767:M99220
 F-HEMBA1006349//ESTs//0.87:276:60//Hs.23628:H03287
 F-HEMBA1006359//Zinc finger protein 43 (HTF6)//4.4e-117:823:81//Hs.74107:X59244
 F-HEMBA1006364//EST//0.0012:168:66//Hs.156756:A1351026
 F-HEMBA1006377//Homo sapiens RalBP1-interacting protein (POBI) mRNA, complete cds//0.0028:422:59//Hs.80567:AF010233
 F-HEMBA1006380//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds//0.41:265:61//Hs.8813:AF032922
 F-HEMBA1006381//ESTs//3.8e-78:382:98//Hs.132171:A1042531
 F-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frame s//2.1e-49:395:80//Hs.23094:M19503
 F-HEMBA1006416//EST//7.3e-12:154:77//Hs.134086:A1077477
 F-HEMBA1006419//EST//4.6e-51:179:86//Hs.149580:A1281881
 F-HEMBA1006421//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.9e-46:517:72//Hs.51048:X68830
 F-HEMBA1006424//ESTs//2.7e-08:380:60//Hs.44369:A1206835
 F-HEMBA1006426//ESTs//3.0e-98:465:99//Hs.129251:AA993264
 F-HEMBA1006438//EST//1.3e-29:183:93//Hs.147412:A1209194
 F-HEMBA1006445
 F-HEMBA1006446//EST//0.14:200:59//Hs.160695:A1282889
 F-HEMBA1006461//Thiopurine S-methyltransferase//1.4e-29:210:72//Hs.51124:AF019369
 F-HEMBA1006467
 F-HEMBA1006471//ESTs//1.4e-05:391:60//Hs.121282:A1091453
 F-HEMBA1006474//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]//1.1e-13:346:63//Hs.31257:AA875998
 F-HEMBA1006483//Thromboxane A2 receptor//2.2e-51:386:82//Hs.89887:D38081
 F-HEMBA1006485//EST//5.4e-111:516:99//Hs.61925:AA039532
 F-HEMBA1006486//EST//4.7e-23:286:72//Hs.137800:AA886897
 F-HEMBA1006489//ESTs//2.5e-06:137:71//Hs.128621:AA910431
 F-HEMBA1006492
 F-HEMBA1006494//ESTs//8.5e-24:299:72//Hs.153413:A1248625
 F-HEMBA1006497//EST//0.00034:431:61//Hs.130057:AA903389
 F-HEMBA1006502//ESTs//2.6e-11:131:80//Hs.141267:H22072
 F-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//7.3e-141:470:98//Hs.153858:AB014566
 F-HEMBA1006521//ESTs, Weakly similar to 3-oxoacyl-[acyl-carrier protein] reductase [E.coli]//3.9e-98:483:97//Hs.94811:AA011185
 F-HEMBA1006530//EST//1.7e-42:530:71//Hs.163207:AA808002
 F-HEMBA1006535//ESTs//2.9e-84:404:98//Hs.128679:A1160081
 F-HEMBA1006540//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//4.4e-173:654:98//Hs.21301:AF093419
 F-HEMBA1006546//ESTs//2.8e-45:391:78//Hs.146307:AA584638
 F-HEMBA1006559//Homo sapiens KIAA0438 mRNA, complete cds//2.1e-47:363:79//Hs.21490:AB007898
 F-HEMBA1006562//ESTs//4.5e-09:116:75//Hs.142368:A1198425
 F-HEMBA1006566//EST//0.85:100:68//Hs.13052:T67136
 F-HEMBA1006569//ESTs//2.7e-06:213:64//Hs.144372:A1346522
 F-HEMBA1006579//EST//0.064:160:62//Hs.126244:AA873479
 F-HEMBA1006583//Homo sapiens Jagged 2 mRNA, complete cds//1.7e-07:533:60//Hs.106387:AF029778
 F-HEMBA1006595//Small inducible cytokine A5 (RANTES)//6.8e-69:328:81//Hs.155464:AF088219
 F-HEMBA1006597//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.6e-38:441:69//Hs.23711:AB018295
 F-HEMBA1006612//ESTs//8.8e-135:668:97//Hs.7942:AA205862
 F-HEMBA1006617//EST//4.6e-31:254:81//Hs.132635:A1032875
 F-HEMBA1006624//ESTs, Weakly similar to HYPOTHETICAL 41.9 KD PROTEIN IN SDS3-THS1 INTERGENIC REGION [S.cerevisiae]//2.5e-75:379:97//Hs.40911:A1391502
 F-HEMBA1006631//ESTs//1.4e-126:612:98//Hs.131737:A1343331
 F-HEMBA1006635//EST//0.65:145:63//Hs.104560:AA340589
 F-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]//9.1e-27:170:92//Hs.109818:AA411185
 F-HEMBA1006643//ESTs, Moderately similar to putative p150 [H.sapiens]//9.7e-05:259:65//Hs.105747:AA505003
 F-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds//3.9e-28:108:93//Hs.6196:U40282
 F-HEMBA1006652//ESTs, Highly similar to 60S RIBOSOMAL PROTEIN L7 [Drosophila melanogaster]//3.0e-87:452:96//Hs.159574:AA190615
 F-HEMBA1006653
 F-HEMBA1006659//Homo sapiens PAC clone DJ0905J08 from Tpl2-p14//2.9e-92:438:98//Hs.8173:AC005189
 F-HEMBA1006665//Homo sapiens clone 23892 mRNA sequence//2.8e-18:180:80//Hs.91916:AF035317
 F-HEMBA1006674//Homo sapiens mRNA for nucleolar protein hMop56//1.6e-16:122:90//Hs.5092:Y12065
 F-HEMBA1006676
 F-HEMBA1006682//EST//0.12:193:61//Hs.128367:AA974575
 F-HEMBA1006695//ESTs//5.6e-27:110:80//Hs.159510:AA297145
 F-HEMBA1006696//EST//3.2e-12:160:75//Hs.146472:A1128198
 F-HEMBA1006708
 F-HEMBA1006709//ESTs//0.69:60:80//Hs.152752:AA643545
 F-HEMBA1006717//ESTs//2.6e-31:286:78//Hs.55573:W37226
 F-HEMBA1006737//ESTs//1.6e-37:189:99//Hs.97490:AA394105
 F-HEMBA1006744//Human mRNA for KIAA0118 gene, partial cds//1.9e-52:360:84//Hs.154326:D42087
 F-HEMBA1006754//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//2.0e-92:817:78//Hs.129727:AF035587
 F-HEMBA1006758//Human mRNA for KIAA0327 protein, complete cds//4.0e-10:576:56//Hs.149323:AB002325
 F-HEMBA1006767//ESTs//1.7e-18:252:72//Hs.141073:W72720
 F-HEMBA1006779//EST//9.1e-26:395:68//Hs.145366:A1252657
 F-HEMBA1006780//EST//1.0:93:69//Hs.116946:AA680250
 F-HEMBA1006789//ESTs//0.0060:276:59//Hs.144121:A1369798
 F-HEMBA1006795//Human Line-1 repeat mRNA with 2 open reading frame s//4.1e-37:781:64//Hs.23094:M19503
 F-HEMBA1006796//Human clone 23803 mRNA, partial cds//1.4e-07:202:68//Hs.34054:U97298
 F-HEMBA1006807//ESTs, Moderately similar to HYPOTHETICAL 46.4 KD PROTEIN T16H12.5 IN CHROMOSOME III [C.elegans]//4.8e-110:523:98//Hs.125790:AA287723
 F-HEMBA1006821//EST//5.1e-11:246:66//Hs.150542:A1051551

【0854】

【表553】

F-HEMBA1006824//ESTs//1.4e-29:158:98//Hs.127712:AA961624	F-HEMBA1007327//ESTs. Weakly similar to HOST CELL FACTOR C1 [H. sapiens]//3.5e-09:144:76//Hs.20597:W58370
F-HEMBA1006832//EST//3.1e-24:277:74//Hs.139357:AA420970	F-HEMBA1007341//ESTs//7.5e-61:302:98//Hs.154944:AA494130
F-HEMBA1006849//ESTs//0.99:332:57//Hs.128993:AA985327	F-HEMBA1007342//ESTs//2.9e-12:289:64//Hs.135555:AA911006
F-HEMBA1006865	F-HEMBA1007347//EST//0.44:89:70//Hs.65949:Z40561
F-HEMBA1006877//ESTs. Highly similar to HYPOTHETICAL 113.8 KD PROTEIN IN ERG7-KMD2 INTERGENIC REGION [Saccharomyces cerevisiae]//2.4e-61:311:97//Hs.127793:W25938	F-HEMBA1000005//ESTs//1.6e-07:337:60//Hs.126718:AA916568
F-HEMBA1006885//ESTs. Highly similar to HYPOTHETICAL 29.1 KD PROTEIN IN URA7-POL12 INTERGENIC REGION [Saccharomyces cerevisiae]//9.1e-128:805:87//Hs.32376:AA758214	F-HEMBA1000008//H. sapiens mRNA for translin associated protein X//1.1e-43:370:78//Hs.96247:X95073
F-HEMBA1006900//EST//6.8e-05:255:63//Hs.163173:AA781592	F-HEMBA1000018//Nuclear factor of kappa light polypeptide gene enhancer in B-cells 1 (p105)//1.0:108:70//Hs.83428:M58603
F-HEMBA1006914//EST//0.065:366:62//Hs.162914:AA666199	F-HEMBA1000024//EST//5.4e-07:137:70//Hs.125389:AA878307
F-HEMBA1006921//ESTs//2.9e-42:347:82//Hs.159266:AI376989	F-HEMBA1000025//EST//0.99:362:58//Hs.121221:AA757392
F-HEMBA1006926//Human I kappa B mRNA, complete cds//0.90:545:59//Hs.154764:U16258	F-HEMBA1000030//H. sapiens mRNA for cylicin 11//1.3e-10:525:62//Hs.3232:Z46788
F-HEMBA1006929//EST//0.00013:403:61//Hs.162642:AA602539	F-HEMBA1000036
F-HEMBA1006936//EST//0.00014:60:93//Hs.8737:W22712	F-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//6.2e-102:450:98//Hs.20815:AF084928
F-HEMBA1006938//EST//4.7e-51:256:98//Hs.143651:AI150382	F-HEMBA1000039//EST//0.0034:97:73//Hs.141684:W35358
F-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//4.4e-92:437:98//Hs.42644:AJ010841	F-HEMBA1000044//ESTs//0.0048:218:63//Hs.123161:AA807319
F-HEMBA1006949//H. sapiens mRNA for retrotransposon//6.9e-43:385:76//Hs.6940:Z48633	F-HEMBA1000048//EST//0.00025:222:62//Hs.122474:AA765131
F-HEMBA1006973//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//1.8e-144:740:94//Hs.14934:AF004828	F-HEMBA1000050//ESTs//5.6e-28:293:75//Hs.136839:H93717
F-HEMBA1006976//H. sapiens mRNA for Gal-beta(1-3/1-4)GlcNAc alpha-2,3-sialyltransferase//1.9e-79:447:89//Hs.75268:X74570	F-HEMBA1000054//Human Line-1 repeat mRNA with 2 open reading frame s//3.3e-54:259:88//Hs.23094:M19503
F-HEMBA1006993//ESTs//5.4e-19:380:66//Hs.152635:AA600968	F-HEMBA1000055//ESTs//0.0017:289:62//Hs.125755:AA286923
F-HEMBA1006996//ESTs//0.17:242:59//Hs.106879:AA054723	F-HEMBA1000059//Homo sapiens mRNA for KIAA0761 protein, partial cd s//5.9e-59:286:84//Hs.93121:AB018304
F-HEMBA1007002	F-HEMBA1000083
F-HEMBA1007017//EST//1.0:59:72//Hs.113400:R39282	F-HEMBA1000089//EST//0.0016:192:66//Hs.137093:AA917621
F-HEMBA1007018//Homo sapiens dynein light intermediate chain 2 (LIC2) mRNA, complete cds//2.5e-78:827:70//Hs.43003:AF035812	F-HEMBA1000099//ESTs//5.7e-20:213:76//Hs.57883:AA218645
F-HEMBA1007045	F-HEMBA1000103//Human knpi repeat mRNA (cdna clone pcd-kpni-8), 3' end//4.9e-43:418:74//Hs.103948:X00627
F-HEMBA1007051//EST//0.85:65:73//Hs.158641:AI370659	F-HEMBA1000113//EST//4.6e-23:221:76//Hs.142065:AA173763
F-HEMBA1007052	F-HEMBA1000119//Homo sapiens ASMTL gene//2.5e-132:621:98//Hs.6315:Y15521
F-HEMBA1007062	F-HEMBA1000136//ESTs//2.3e-101:507:96//Hs.12659:AA195207
F-HEMBA1007066//ESTs//0.94:160:63//Hs.56071:W52212	F-HEMBA1000141//ESTs//2.1e-15:283:69//Hs.126257:AI279044
F-HEMBA1007073//ESTs//3.6e-50:246:80//Hs.142678:X37845	F-HEMBA1000144//EST//4.5e-52:298:91//Hs.149580:AI281881
F-HEMBA1007078//Human arginine-rich nuclear protein mRNA, complete cds//6.7e-75:417:91//Hs.80510:M74002	F-HEMBA1000173//Zinc finger protein 74 (Cof52)//2.4e-63:285:82//Hs.3057:X92715
F-HEMBA1007080	F-HEMBA1000175//EST//1.0:101:65//Hs.162898:AA659646
F-HEMBA1007085//Guanylate cyclase 2D, membrane (retina-specific)//1.3e-06:568:61//Hs.1974:M92432	F-HEMBA1000198//EST//0.99:179:56//Hs.116880:AA662457
F-HEMBA1007087//Human mevalonate pyrophosphate decarboxylase (MPD) mRNA, complete cds//0.95:541:57//Hs.3828:U49260	F-HEMBA1000215//Homo sapiens mRNA for KIAA0557 protein, partial cd s//1.4e-15:139:82//Hs.101414:AB011129
F-HEMBA1007112//ESTs//3.4e-104:494:98//Hs.19207:AA039595	F-HEMBA1000217//ESTs//3.4e-06:81:88//Hs.121151:T66277
F-HEMBA1007113//ESTs//0.71:246:62//Hs.96235:AA196354	F-HEMBA1000218//EST//0.11:136:63//Hs.134683:AI092013
F-HEMBA1007121//ESTs//3.5e-69:335:98//Hs.140519:AA643182	F-HEMBA1000226//Fragile X mental retardation 1//0.99:126:65//Hs.89764:X69962
F-HEMBA1007129	F-HEMBA1000240//H. sapiens mRNA for Nup88 protein//1.0:334:57//Hs.90734:Y08612
F-HEMBA1007147//ESTs//3.2e-07:235:64//Hs.124813:W46172	F-HEMBA1000244//ESTs//3.2e-15:139:81//Hs.134549:AI078483
F-HEMBA1007149//ESTs//7.2e-08:161:68//Hs.121179:AA757136	F-HEMBA1000250//Homo sapiens protein associated with Myc mRNA, complete cds//2.1e-156:735:98//Hs.151411:AF075587
F-HEMBA1007151	F-HEMBA1000258//EST//0.0091:325:60//Hs.97533:AA435884
F-HEMBA1007174//Homo sapiens epsilon 2b mRNA, complete cds//6.6e-64:318:97//Hs.22396:AF062085	F-HEMBA1000264//Human CHL1 potential helicase (CHL1), complete cd s//1.4e-33:100:100//Hs.27424:U75968
F-HEMBA1007178//ESTs. Moderately similar to !!!! ALU SUBFAMILY J W ARNING ENTRY !!!! [H. sapiens]//4.2e-39:248:90//Hs.157148:AA311921	F-HEMBA1000266//Homo sapiens mRNA for myosin phosphatase target subunit 1 (MYPT1)//0.0019:373:60//Hs.16533:D87930
F-HEMBA1007194//ESTs//2.3e-107:503:99//Hs.100605:AA305965	F-HEMBA1000272//ESTs//1.3e-93:440:99//Hs.109224:N46684
F-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//5.6e-158:478:98//Hs.3363:D86987	F-HEMBA1000274//ESTs//0.41:221:65//Hs.71990:AA151796
F-HEMBA1007206//EST//0.23:119:66//Hs.144402:AA609252	F-HEMBA1000284//EST//0.00024:108:73//Hs.100725:F13689
F-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cd s//1.6e-177:839:98//Hs.27197:AB018340	F-HEMBA1000307//EST//3.6e-10:149:73//Hs.140415:AA778574
F-HEMBA1007243//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Nyhan syndrome)//2.7e-56:647:69//Hs.82314:M31642	F-HEMBA1000312//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.0092:252:65//Hs.41153:AB018326
F-HEMBA1007251//Human plectin (PLEC1) mRNA, complete cds//0.19:210:67//Hs.79706:U53204	F-HEMBA1000317//Thrombospondin 1//7.1e-05:342:59//Hs.87409:X14787
F-HEMBA1007256//Homo sapiens clone 24407 mRNA sequence//1.0:144:64//Hs.12432:AF070575	F-HEMBA1000318//EST//0.014:184:61//Hs.155758:AI311870
F-HEMBA1007267//Human homolog of yeast mutL (hPMW1) gene, complete cds//0.99:239:60//Hs.111749:U13695	F-HEMBA1000335//EST//0.99:187:63//Hs.137424:AA243729
F-HEMBA1007273//ESTs//5.6e-24:271:73//Hs.144951:N34836	F-HEMBA1000336//EST//1.0:209:63//Hs.150410:AI003611
F-HEMBA1007279//ESTs//6.1e-36:185:78//Hs.141022:M06475	F-HEMBA1000337//EST//0.086:133:66//Hs.128207:AA972330
F-HEMBA1007281//ESTs//0.74:94:65//Hs.162533:AA584529	F-HEMBA1000338//EST//7.1e-07:129:72//Hs.140488:AA767127
F-HEMBA1007288//EST//0.83:99:67//Hs.127878:AA968637	F-HEMBA1000339//Small inducible cytokine A5 (RAMSES)//1.2e-36:336:76//Hs.155464:AF088219
F-HEMBA1007300//EST//3.6e-62:355:91//Hs.150139:AI300062	F-HEMBA1000341
F-HEMBA1007301//Collagen, type I, alpha 1(I)5e-09:406:61//Hs.111913:Z74615	F-HEMBA1000343//EST//0.66:163:63//Hs.150822:AI302729
F-HEMBA1007319//EST//0.0068:50:96//Hs.163362:AA890506	F-HEMBA1000354//ESTs//7.1e-61:292:100//Hs.152266:AA926874
F-HEMBA1007320//ESTs//1.0:133:66//Hs.38032:M63634	F-HEMBA1000369//ESTs. Highly similar to t-BOP [M. musculus]//0.013:157:64//Hs.129982:AI420970
F-HEMBA1007322//ESTs//0.0077:187:66//Hs.4852:R84241	F-HEMBA1000374//ESTs//8.7e-53:454:79//Hs.133518:R69934
	F-HEMBA1000376//ESTs//5.9e-14:87:97//Hs.163973:AA744348
	F-HEMBA1000391//ESTs//0.033:237:64//Hs.135289:AI092963
	F-HEMBA1000399//Homo sapiens mRNA for cell cycle checkpoint protei

【0855】

【表554】

n//9.4e-165:762:98//Hs.16184:AJ001642
 F-HEMBB1000402//EST//0.013:291:59//Hs.149191:A1246155
 F-HEMBB1000404//ESTs//3.0e-69:353:96//Hs.135857:AA947194
 F-HEMBB1000420//EST//6.3e-52:258:98//Hs.136434:AA557925
 F-HEMBB1000434//Homo sapiens neuronal thread protein AD7c-NTP mRNA
 A, complete cds//9.4e-73:364:83//Hs.129735:AF010144
 F-HEMBB1000438//ESTs//0.073:446:58//Hs.134632:A1223429
 F-HEMBB1000441//Interleukin 10//1.7e-38:336:77//Hs.2180:M57627
 F-HEMBB1000449//EST//5.5e-21:356:67//Hs.157848:A1362501
 F-HEMBB1000455//ESTs//0.092:147:65//Hs.106446:M93227
 F-HEMBB1000472
 F-HEMBB1000480//EST//0.98:83:71//Hs.146462:A1124898
 F-HEMBB1000487//ESTs//1.4e-59:341:92//Hs.48561:N79206
 F-HEMBB1000490//ESTs//2.5e-27:200:79//Hs.56825:A1057560
 F-HEMBB1000491
 F-HEMBB1000493//ESTs//0.019:103:69//Hs.138358:T66178
 F-HEMBB1000510//Glucocorticoid receptor alpha (alternative product
 s)//1.6e-46:409:77//Hs.102761:U25029
 F-HEMBB1000518//ESTs//3.7e-06:187:64//Hs.140989:R68413
 F-HEMBB1000523//ESTs//0.69:332:59//Hs.106845:W19543
 F-HEMBB1000530//H. sapiens mRNA for extracellular matrix protein co
 llagen type XIV, C-terminus//2.1e-38:138:96//Hs.36131:Y11710
 F-HEMBB1000550//ESTs, Weakly similar to !!!! ALU SUBFAMILY SC WARN
 ING ENTRY !!!! [H.sapiens]//7.7e-31:554:67//Hs.157142:U85996
 F-HEMBB1000554//Homo sapiens mRNA, chromosome 1 specific transcrip
 t KIAA0484//4.0e-27:282:75//Hs.158095:AB007953
 F-HEMBB1000556//Homo sapiens mRNA for KIAA0750 protein, complete c
 ds//2.0e-33:537:65//Hs.5444:AB018293
 F-HEMBB1000564
 F-HEMBB1000573//H. sapiens HCG 11 mRNA//7.5e-27:197:76//Hs.146333:X
 81001
 F-HEMBB1000575//Von Hippel-Lindau syndrome//2.7e-72:255:79//Hs.781
 60:AF010238
 F-HEMBB1000586//Dystrophin (muscular dystrophy, Duchenne and Becke
 r types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268,
 DXS269, DXS270, DXS272//0.011:338:59//Hs.79012:W18533
 F-HEMBB1000589//PLATELET GLYCOPROTEIN V PRECURSOR//2.4e-22:228:79/
 Hs.73734:Z23091
 F-HEMBB1000591//ESTs//1.0e-17:370:64//Hs.58156:W71990
 F-HEMBB1000592//EST//0.0038:51:88//Hs.148022:A1269323
 F-HEMBB1000593//Homo sapiens chromosome 7q22 sequence//4.7e-109:50
 3:99//Hs.3386:AF053356
 F-HEMBB1000598//Ribosomal protein L5//3.5e-29:537:66//Hs.118781:U6
 6589
 F-HEMBB1000623//H. sapiens mRNA for GAP protein//0.89:376:59//Hs.2
 2698:X91809
 F-HEMBB1000630//Homo sapiens KIAA0404 mRNA, partial cds//0.074:16
 8:61//Hs.105850:AB007864
 F-HEMBB1000631//ESTs//1.7e-06:247:64//Hs.156864:A1346481
 F-HEMBB1000632//Human mRNA for KIAA0351 gene, complete cds//5.1e-5
 0:811:65//Hs.29963:AB002349
 F-HEMBB1000637//Sialoporphin (gp115, leukosialin, CD43)//2.4e-79:3
 04:85//Hs.80738:X52075
 F-HEMBB1000638//EST//0.0076:92:75//Hs.125496:AA883735
 F-HEMBB1000643//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.5e-45:477:7
 4//Hs.51048:X68830
 F-HEMBB1000649//Homo sapiens histone H2A.1b mRNA, complete cds//7.
 4e-52:533:75//Hs.51011:L19778
 F-HEMBB1000652//ESTs//1.6e-49:345:84//Hs.132722:AA618531
 F-HEMBB1000665//EST//0.44:152:63//Hs.149534:A1280924
 F-HEMBB1000671//Human Line-1 repeat mRNA with 2 open reading frame
 s//2.2e-79:280:85//Hs.23094:M19503
 F-HEMBB1000673//ESTs//0.99:177:59//Hs.149864:N80474
 F-HEMBB1000684//Protein kinase, interferon-inducible double strand
 ed RNA dependent//2.6e-31:220:87//Hs.73821:M35663
 F-HEMBB1000693//Homo sapiens neuronal mRNA, complete cds//5.3e-12
 0:575:97//Hs.158300:AF040723
 F-HEMBB1000705//ESTs//4.7e-65:350:94//Hs.24610:R33125
 F-HEMBB1000706//EST//8.6e-14:373:61//Hs.138281:R55703
 F-HEMBB1000709//EST//0.99:110:65//Hs.162437:AA577510
 F-HEMBB1000725//RAS-RELATED PROTEIN RAB-8//1.7e-77:635:77//Hs.1231
 09:X56741
 F-HEMBB1000726//EST//1.3e-43:257:84//Hs.162197:AA535216
 F-HEMBB1000738//EST//5.9e-13:259:64//Hs.158699:A1417328
 F-HEMBB1000749//EST//3.1e-42:271:87//Hs.162197:AA535216
 F-HEMBB1000763
 F-HEMBB1000770//ESTs, Weakly similar to MOESIN/EZRIN/RADIXIN HOMOL
 OG [D. melanogaster]//0.021:111:72//Hs.38178:AA921830
 F-HEMBB1000774//ESTs, Weakly similar to mTERF [H. sapiens]//2.5e-11
 6:580:97//Hs.5009:AA081390
 F-HEMBB1000781//Human MEK kinase 3 mRNA, complete cds//5.3e-47:42
 6:74//Hs.86201:U78876
 F-HEMBB1000789//Homo sapiens mRNA for KIAA0677 protein, complete c
 ds//3.0e-65:672:71//Hs.155983:AB014577
 F-HEMBB1000790//ESTs//1.2e-52:344:86//Hs.35254:A1133727
 F-HEMBB1000794//ESTs//0.00098:289:59//Hs.138782:N73572
 F-HEMBB1000807//ESTs//2.1e-91:434:99//Hs.61334:A1298375
 F-HEMBB1000810//ESTs//0.038:92:71//Hs.148763:AA668871
 F-HEMBB1000821//EST//0.94:129:62//Hs.162299:AA555154
 F-HEMBB1000822//ESTs//7.5e-05:199:63//Hs.117018:AA832421
 F-HEMBB1000826//ESTs//4.8e-13:343:65//Hs.153429:A1283069
 F-HEMBB1000827
 F-HEMBB1000831
 F-HEMBB1000835//EST//4.3e-27:201:85//Hs.141451:N29915
 F-HEMBB1000840//EST//6.3e-75:380:96//Hs.142557:AA464948
 F-HEMBB1000848//Human Line-1 repeat mRNA with 2 open reading frame
 s//1.4e-135:875:85//Hs.23094:M19503
 F-HEMBB1000852//Phosphoribosyl pyrophosphate amidotransferase//0.1
 2:292:61//Hs.311:U00238
 F-HEMBB1000870//EST//0.00091:246:62//Hs.126502:AA913831
 F-HEMBB1000876//Homo sapiens ELISC-1 mRNA, partial cds//4.9e-34:20
 0:94//Hs.128434:AF085351
 F-HEMBB1000883//ESTs//0.42:107:67//Hs.154173:A1379823
 F-HEMBB1000887
 F-HEMBB1000888//ESTs//1.0:137:67//Hs.8121:AA521290
 F-HEMBB1000890//ESTs//1.0:116:65//Hs.7105:T23433
 F-HEMBB1000893//EST//0.0079:408:58//Hs.146504:A1129834
 F-HEMBB1000908//EST//9.2e-21:205:79//Hs.132635:A1032875
 F-HEMBB1000910//Human mRNA for KIAA0231 gene, partial cds//0.16:32
 7:60//Hs.7938:D86984
 F-HEMBB1000913//ESTs//1.0e-12:233:68//Hs.137545:AA487049
 F-HEMBB1000915//ESTs//2.5e-90:423:99//Hs.135254:A1095468
 F-HEMBB1000917//EST//2.8e-49:241:100//Hs.162216:AA548089
 F-HEMBB1000927//Hippocalcin//1.2e-31:528:65//Hs.89692:D16593
 F-HEMBB1000947
 F-HEMBB1000959//Cytochrome P450, 51 (lanosterol 14-alpha-demethyla
 se)//9.3e-48:572:72//Hs.2379:U23942
 F-HEMBB1000973//ESTs//4.5e-26:286:76//Hs.137393:AA142938
 F-HEMBB1000975//ESTs//0.78:180:66//Hs.104789:AA417124
 F-HEMBB1000981
 F-HEMBB1000985//Homo sapiens actin binding protein MAYVEN mRNA, co
 mplete cds//6.7e-07:308:62//Hs.122967:AF059569
 F-HEMBB1000991//EST//0.12:125:66//Hs.22945:R43713
 F-HEMBB1000996//ESTs//6.9e-05:273:63//Hs.133116:A1054055
 F-HEMBB1001004//Homo sapiens mRNA for KIAA0565 protein, complete c
 ds//0.62:193:62//Hs.119004:AB014565
 F-HEMBB1001008//EST//4.7e-09:203:65//Hs.105221:AA489025
 F-HEMBB1001011//Human Chromosome 16 BAC clone CIT987SK-A-635H12//
 2.4e-17:384:67//Hs.108604:AC002310
 F-HEMBB1001014//EST, Weakly similar to putative p150 [H. sapiens]//
 0.21:284:60//Hs.161547:W04991
 F-HEMBB1001020//ESTs//9.7e-37:186:76//Hs.138852:AA284247
 F-HEMBB1001024//ESTs, Highly similar to t-BOP [M. musculus]//0.11:2
 42:61//Hs.129982:A1420970
 F-HEMBB1001037//EST//0.0057:192:66//Hs.149987:A1291177
 F-HEMBB1001047//ESTs//1.6e-22:360:70//Hs.120734:W58721
 F-HEMBB1001051//H. sapiens mRNA for FAN protein//3.8e-29:160:98//H
 s.78687:X96586
 F-HEMBB1001056//Homo sapiens mRNA for KIAA0618 protein, complete c
 ds//1.0e-42:149:96//Hs.15832:AB014518
 F-HEMBB1001058//Small inducible cytokine A5 (RANTES)//1.1e-45:349:
 82//Hs.155464:AF088219
 F-HEMBB1001060//ESTs//1.6e-62:464:81//Hs.138663:M24942
 F-HEMBB1001063
 F-HEMBB1001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.9e-
 148:736:95//Hs.12953:AF034803
 F-HEMBB1001096//EST//0.017:154:66//Hs.130403:AA909272
 F-HEMBB1001102//ESTs//2.1e-18:120:95//Hs.163767:R06293
 F-HEMBB1001105//Human BRCA2 region, mRNA sequence CC016//0.30:84:7
 5//Hs.112434:U50529
 F-HEMBB1001112//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN
 SEC61 ALPHA SUBUNIT [Canis familiaris]//9.3e-38:341:77//Hs.14038:
 R06800
 F-HEMBB1001114//EST//6.4e-07:296:62//Hs.128420:AA975062
 F-HEMBB1001117//EST//1.6e-99:464:99//Hs.130493:AA928139
 F-HEMBB1001119
 F-HEMBB1001126
 F-HEMBB1001133//H. sapiens mRNA for translin associated protein X//
 1.2e-28:739:61//Hs.96247:X95073
 F-HEMBB1001137

【0856】

【表555】

F-HEM881001142//Human mRNA for KIAA0331 gene, complete cds//2.1e-23;340:69//Hs.146395:AB002329	F-HEM881001454//ESTs//1.4e-46:279:93//Hs.104866:AA426038
F-HEM881001151//ESTs//2.6e-30:252:79//Hs.6880:W26854	F-HEM881001458//EST//1.7e-09:106:83//Hs.141422:W20920
F-HEM881001153//ESTs//7.6e-16:97:96//Hs.113307:H16716	F-HEM881001463//Homo sapiens mRNA for semaphorin E, complete cds//0.18:387:59//Hs.62705:AB000220
F-HEM881001169//ESTs//1.4e-32:374:71//Hs.161682:AA206863	F-HEM881001464//Homo sapiens Coch-SB2 mRNA, complete cds//0.26:189:67//Hs.21016:AF006740
F-HEM881001175//Human mRNA for ankyrin motif, complete cds//7.1e-36:509:66//Hs.73073:D78334	F-HEM881001482//Homo sapiens mRNA for KIAA0760 protein, partial cds//1.2e-27:292:74//Hs.137168:AB018303
F-HEM881001177//ESTs, Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN HXT14-PHA2 INTERGENIC REGION [S.cerevisiae]//1.5e-65:312:100//Hs.86878:AA599183	F-HEM881001500//ESTs//8.1e-28:312:74//Hs.18498:W52088
F-HEM881001182//Electron-transfer-flavoprotein, beta polypeptide//0.94:199:64//Hs.74047:X71129	F-HEM881001521//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//8.8e-54:359:74//Hs.46328:D87942
F-HEM881001199	F-HEM881001527//Protein tyrosine phosphatase, receptor type, f polypeptide//1.0:198:63//Hs.75216:Y00815
F-HEM881001208//ESTs//0.12:120:69//Hs.130093:AA928802	F-HEM881001531//ESTs//4.3e-33:403:75//Hs.44862:W38735
F-HEM881001209//EST//0.00028:215:65//Hs.118276:W15258	F-HEM881001535//ESTs//0.0029:47:93//Hs.124864:AA663093
F-HEM881001210//EST//2.9e-05:297:60//Hs.88840:AA281452	F-HEM881001536//ESTs//0.0047:120:68//Hs.144858:R67748
F-HEM881001218//Homo sapiens mRNA for KIAA0585 protein, partial cds//8.5e-37:260:76//Hs.72660:AB011157	F-HEM881001537//ESTs, Weakly similar to eukaryotic initiation factor eIF-2 alpha kinase [D.melanogaster]//3.7e-20:297:73//Hs.42457:AA523306
F-HEM881001221//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//0.00046:650:58//Hs.158241:AB007976	F-HEM881001555//Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence//1.1e-35:188:77//Hs.102877:U41315
F-HEM881001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Mus musculus]//6.7e-103:477:100//Hs.127835:A1378790	F-HEM881001562//ESTs//0.95:161:61//Hs.145075:A1028240
F-HEM881001242//Homo sapiens mRNA for LAX-1, complete cds//1.2e-31:458:67//Hs.129918:AB005754	F-HEM881001564//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.4e-49:526:73//Hs.158095:AB007953
F-HEM881001249//EST//0.26:203:63//Hs.140791:AA935909	F-HEM881001565//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.9e-44:324:84//Hs.113283:AF018080
F-HEM881001253//EST//4.0e-91:433:98//Hs.120636:AA325219	F-HEM881001585
F-HEM881001254//ESTs//2.0e-24:180:85//Hs.136391:H04977	F-HEM881001586//EST//0.84:132:64//Hs.145264:A1218708
F-HEM881001267//Ataxia telangiectasia mutated (includes complementation groups A, C and D)//6.1e-24:146:78//Hs.51187:U82828	F-HEM881001588//Human clone 23695 mRNA sequence//6.6e-20:327:67//Hs.90798:U79289
F-HEM881001271//EST//2.5e-05:686:58//Hs.115423:A1359248	F-HEM881001603//ESTs//1.3e-12:84:96//Hs.13380:R60414
F-HEM881001282//CA-binding protein transcription factor, beta subunit 2 (47KD)//0.39:531:57//Hs.78915:U13045	F-HEM881001618//ESTs//4.4e-11:349:63//Hs.132046:AA693680
F-HEM881001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III [Caenorhabditis elegans]//4.9e-10:91:89//Hs.16606:W81021	F-HEM881001619//ESTs//2.1e-06:246:63//Hs.63428:AA058314
F-HEM881001289//ESTs//6.4e-100:467:99//Hs.151720:A1287890	F-HEM881001630//EST//1.4e-07:334:62//Hs.145698:A1266713
F-HEM881001294//ESTs, Highly similar to RAS-LIKE PROTEIN TC10 [Homo sapiens]//1.3e-135:654:98//Hs.124217:AA020848	F-HEM881001635//ESTs//0.92:282:60//Hs.126980:AA934077
F-HEM881001302	F-HEM881001637//ELK1, member of ETS oncogene family//1.1e-27:395:64//Hs.116549:AL009172
F-HEM881001304//ESTs//0.98:109:68//Hs.138972:AA047725	F-HEM881001641//EST//0.11:53:81//Hs.112445:AA594279
F-HEM881001314//ESTs//7.4e-29:285:77//Hs.144749:A1217339	F-HEM881001653//EST//0.91:124:64//Hs.144213:T40480
F-HEM881001315//Small inducible cytokine A5 (RANTES)//1.9e-40:355:78//Hs.155464:AF088219	F-HEM881001665//Human mRNA for apolipoprotein E receptor 2, complete cds//7.0e-13:473:63//Hs.54481:D86407
F-HEM881001317//Human Line-1 repeat mRNA with 2 open reading frames//4.7e-98:625:85//Hs.23094:M19503	F-HEM881001668//ESTs//0.94:83:69//Hs.146202:A1252519
F-HEM881001326//ESTs//0.00030:257:63//Hs.62208:H12380	F-HEM881001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//2.3e-172:803:98//Hs.24439:AB014546
F-HEM881001331//ESTs, Weakly similar to DFS70 [H.sapiens]//1.0e-48:332:87//Hs.43071:AA206222	F-HEM881001684//ESTs, Highly similar to Tbc1 [M.musculus]//5.4e-20:110:100//Hs.106104:AA599496
F-HEM881001335	F-HEM881001685//EST//2.2e-05:112:73//Hs.130984:A1015430
F-HEM881001337//Homo sapiens mRNA for KIAA0563 protein, complete cds//8.5e-56:282:87//Hs.15731:AB011135	F-HEM881001695//Human novel homeobox mRNA for a DNA binding protein//1.6e-08:425:62//Hs.37035:U07664
F-HEM881001339//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.039:161:65//Hs.132206:AF039694	F-HEM881001704//EST//5.8e-20:295:69//Hs.140231:A1054398
F-HEM881001346//Oxytocin receptor//4.2e-42:456:73//Hs.2820:X64878	F-HEM881001706
F-HEM881001348//Homo sapiens mRNA for KIAA0570 protein, complete cds//1.2e-45:176:77//Hs.114293:AB011142	F-HEM881001707//EST//0.091:241:60//Hs.136830:AA692919
F-HEM881001356//EST//0.32:292:59//Hs.135771:A1005648	F-HEM881001717//ESTs//2.9e-06:325:60//Hs.150063:A1298064
F-HEM881001364	F-HEM881001735//Small inducible cytokine A5 (RANTES)//3.2e-46:326:83//Hs.155464:AF088219
F-HEM881001366//EST//7.8e-24:367:69//Hs.138765:W70347	F-HEM881001736//ESTs, Weakly similar to E0405.1 [C.elegans]//5.4e-99:485:97//Hs.120581:W25578
F-HEM881001367//Small inducible cytokine A5 (RANTES)//8.7e-50:326:86//Hs.155464:AF088219	F-HEM881001747//ESTs//8.3e-87:421:98//Hs.137051:AA884244
F-HEM881001369//EST//0.17:211:63//Hs.120066:AA707973	F-HEM881001749//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//3.5e-75:315:83//Hs.129735:AF010144
F-HEM881001380//Homo sapiens mRNA for KIAA0527 protein, partial cds//8.2e-36:225:79//Hs.129748:AB011099	F-HEM881001753//ESTs//0.00013:35:100//Hs.139643:H06263
F-HEM881001384	F-HEM881001756//ESTs//2.3e-89:433:98//Hs.128868:AA931077
F-HEM881001387//ESTs//0.61:215:60//Hs.145915:A1342230	F-HEM881001760//ESTs//6.5e-06:503:58//Hs.21766:A1357639
F-HEM881001394//Human Line-1 repeat mRNA with 2 open reading frames//3.8e-94:568:83//Hs.23094:M19503	F-HEM881001762//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//2.9e-13:498:60//Hs.158241:AB007976
F-HEM881001410//Homo sapiens keratan sulfate proteoglycan mRNA, complete cds//0.021:373:58//Hs.125750:AF065988	F-HEM881001785//EST//0.16:262:60//Hs.162526:AA584102
F-HEM881001424//EST//0.20:307:58//Hs.135336:A1049827	F-HEM881001797//ESTs//0.37:201:63//Hs.91559:AA806370
F-HEM881001426//Homo sapiens clone 23579 mRNA sequence//8.3e-17:205:72//Hs.83466:AF038174	F-HEM881001802//ESTs//1.6e-06:447:58//Hs.134672:A1087951
F-HEM881001429//ESTs, Highly similar to CYTOSOL AMINOPEPTIDASE [Bos taurus]//5.5e-153:729:96//Hs.21679:AF034175	F-HEM881001812//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.3e-54:311:81//Hs.92381:AB007956
F-HEM881001436//Human mRNA for KIAA0347 gene, complete cds//1.2e-44:316:85//Hs.101996:AB002345	F-HEM881001816//ESTs//2.2e-39:302:84//Hs.35985:AA783017
F-HEM881001443	F-HEM881001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds//7.6e-164:763:98//Hs.159396:AF056209
F-HEM881001449//Homo sapiens sodium bicarbonate cotransporter (NBC-C1) mRNA, complete cds//0.033:478:58//Hs.5462:AF007216	F-HEM881001834//TRICHOHYALIN//7.1e-05:548:60//Hs.82276:L09190
	F-HEM881001836//Human mRNA for KIAA0033 gene, partial cds//4.0e-34:272:86//Hs.22271:D26067
	F-HEM881001839//Pyruvate carboxylase//0.050:686:59//Hs.89890:S72370
	F-HEM881001850//EST//0.0035:204:61//Hs.7311:T23858
	F-HEM881001863//Small inducible cytokine A5 (RANTES)//3.0e-48:357:0

【0857】

【表556】

82//Hs.155464:AF088219	F-HEM8B1002249//Homo sapiens haemopoietic progenitor homeobox HPX4
F-HEM8B1001867//ESTs//2.2e-40:265:88//Hs.146323:AI251752	28 (HPX42B) mRNA, complete cds//6.8e-47:418:77//Hs.125231:AF068006
F-HEM8B1001868//ESTs//5.2e-06:131:73//Hs.123362:AA811371	F-HEM8B1002254//Homo sapiens mRNA for KIAA0594 protein, partial cd
F-HEM8B1001869//ESTs//1.0e-86:429:96//Hs.141208:AA825503	s//5.0e-47:437:77//Hs.154872:AB011166
F-HEM8B1001872	F-HEM8B1002255//ESTs//0.017:255:61//Hs.126786:U74314
F-HEM8B1001874//H. sapiens mRNA for CHD5 protein//0.0033:388:60//H	F-HEM8B1002266//Homo sapiens retinoblastoma-associated protein HEC
s.19923:Y12478	mRNA, complete cds//0.17:511:57//Hs.58169:AF017790
F-HEM8B1001875//H. sapiens mRNA for RNA helicase (Myc-regulated dea	F-HEM8B1002280//EST//4.0e-35:182:98//Hs.127701:AA864998
d box protein)//0.32:346:60//Hs.100555:X98743	F-HEM8B1002300
F-HEM8B1001880//EST//4.0e-28:171:92//Hs.151194:AI125868	F-HEM8B1002306//Human G protein-coupled receptor (STRL22) mRNA, co
F-HEM8B1001899//ESTs//0.17:242:62//Hs.136969:AA830918	mplete cds//6.3e-14:228:72//Hs.46468:U45984
F-HEM8B1001905	F-HEM8B1002327//EST//4.3e-21:242:75//Hs.72377:AA161083
F-HEM8B1001906//ESTs//5.6e-49:290:92//Hs.127298:H09155	F-HEM8B1002329//ESTs, Weakly similar to C17G10.1 [C.elegans]//1.7
F-HEM8B1001908//Human monocytic leukaemia zinc finger protein (MO	e-77:399:96//Hs.105837:AA536054
Z) mRNA, complete cds//1.2e-83:672:81//Hs.82210:U47742	F-HEM8B1002340//INSULIN-DEGRADING ENZYME//1.0:319:60//Hs.1508:M211
F-HEM8B1001910//EST, Weakly similar to albumin [H.sapiens]//0.047:	88
206:62//Hs.159777:Z19955	F-HEM8B1002342//Homo sapiens mRNA for putative thioredoxin-like pr
F-HEM8B1001911	otein//1.4e-155:724:98//Hs.42644:AJ010841
F-HEM8B1001915//ESTs//0.92:136:71//Hs.144465:R68882	F-HEM8B1002358//Deoxythymidylate kinase//1.1e-37:192:98//Hs.79006:
F-HEM8B1001921//EST//2.0e-19:398:67//Hs.44789:N36113	L16991
F-HEM8B1001922//ESTs//4.3e-05:370:59//Hs.123669:AA805245	F-HEM8B1002359//Human Rev interacting protein Rip-1 mRNA, complete
F-HEM8B1001925//ESTs//5.7e-27:329:71//Hs.141071:H16398	cds//1.7e-06:66:96//Hs.154762:U00943
F-HEM8B1001930//EST//0.043:157:63//Hs.161927:AA483904	F-HEM8B1002364//EST//4.7e-16:201:73//Hs.149925:AI288838
F-HEM8B1001944//Human mRNA for KIAA0118 gene, partial cds//5.7e-5	F-HEM8B1002371//EST//2.4e-07:319:61//Hs.136459:AA577796
5:444:80//Hs.154326:D42087	F-HEM8B1002381
F-HEM8B1001945//ESTs//1.1e-19:142:88//Hs.7341:N57875	F-HEM8B1002383//vasoactive intestinal peptide receptor 2//0.98:19
F-HEM8B1001947//Human mRNA for KIAA0392 gene, partial cds//1.8e-2	0:63//Hs.2126:L36566
1:333:66//Hs.40100:AB002390	F-HEM8B1002387//EST//2.1e-07:253:61//Hs.145993:AI277784
F-HEM8B1001950//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//	F-HEM8B1002409//ESTs//1.4e-11:94:91//Hs.125958:AI206456
0.020:384:60//Hs.8546:U97669	F-HEM8B1002415//Homo sapiens mRNA, chromosome 1 specific transcrip
F-HEM8B1001952//EST//7.0e-13:302:63//Hs.120089:AA708101	t KIAA0501//2.0e-32:371:73//Hs.159897:AB007970
F-HEM8B1001953//ATL-derived PMA-responsive (APR) peptide//0.97:25	F-HEM8B1002425//Fc fragment of IgA receptor for//2.7e-32:156:82//
2:50//Hs.96:D90070	Hs.54486:X54150
F-HEM8B1001957//ESTs//6.1e-32:446:67//Hs.51305:T47418	F-HEM8B1002442
F-HEM8B1001962//Cytochrome P450, subfamily I (aromatic compound-in	F-HEM8B1002453//Human mRNA for KIAA0118 gene, partial cds//5.6e-5
ducible), polypeptide 2//2.3e-31:390:70//Hs.1361:M55053	3:461:77//Hs.154326:D42087
F-HEM8B1001967//H. sapiens mRNA for urea transporter//9.7e-52:322:8	F-HEM8B1002457//ESTs//3.4e-25:184:70//Hs.140225:AA704101
8//Hs.66710:X96969	F-HEM8B1002458//ESTs//7.0e-10:343:62//Hs.163816:N76274
F-HEM8B1001973//Myelin oligodendrocyte glycoprotein (alternative p	F-HEM8B1002477//Human Grb2-associated binder-1 mRNA, complete cds/
roducts)//2.1e-48:426:78//Hs.53217:Z48051	//6.0e-89:493:92//Hs.159605:U43885
F-HEM8B1001983	F-HEM8B1002489//Homo sapiens 195 kDa cornified envelope precursor
F-HEM8B1001988//ESTs//6.5e-05:237:63//Hs.49760:AA741051	mRNA, complete cds//0.019:228:63//Hs.74304:AF001691
F-HEM8B1001990//ESTs//0.25:171:64//Hs.7961:AA401205	F-HEM8B1002492//EST//0.24:149:62//Hs.146790:AI149051
F-HEM8B1001996//ESTs//1.8e-19:436:65//Hs.125539:AI339103	F-HEM8B1002495//Fc fragment of IgE, high affinity I, receptor for:
F-HEM8B1001997//EST//5.3e-33:294:76//Hs.161041:H82636	beta polypeptide//1.3e-22:331:71//Hs.30:M89796
F-HEM8B1002002//ESTs//1.9e-06:224:67//Hs.110915:AA132964	F-HEM8B1002502//ESTs//1.3e-41:380:78//Hs.61199:AA024494
F-HEM8B1002005//ESTs//5.8e-17:170:78//Hs.141825:AA017093	F-HEM8B1002509//ESTs//0.017:220:63//Hs.155263:AI273725
F-HEM8B1002009//ESTs//0.066:441:58//Hs.125313:AI201685	F-HEM8B1002510//ESTs//6.4e-102:476:99//Hs.152289:AI247354
F-HEM8B1002015//EST//2.3e-18:310:68//Hs.145899:AI274951	F-HEM8B1002520//Human Line-1 repeat mRNA with 2 open reading frame
F-HEM8B1002042//CYTOCHROME P450 1VB1//2.9e-11:446:62//Hs.687:X1669	s//2.4e-50:580:72//Hs.23094:M19503
9	F-HEM8B1002522//EST//0.010:172:62//Hs.147224:AI205719
F-HEM8B1002043//ESTs, Weakly similar to T06E6.d [C.elegans]//1.0:2	F-HEM8B1002531
17:60//Hs.3487:AA425553	F-HEM8B1002534//Small inducible cytokine A5 (RANTES)//3.7e-59:258:
F-HEM8B1002044	88//Hs.155464:AF088219
F-HEM8B1002045	F-HEM8B1002545//ESTs//3.9e-24:181:86//Hs.13753:AI088102
F-HEM8B1002049//Homo sapiens mRNA for KIAA0713 protein, partial cd	F-HEM8B1002550//Syntaxin 5A//0.27:354:59//Hs.154546:U26648
s//0.082:201:61//Hs.88756:AB018256	F-HEM8B1002556//ESTs//1.7e-33:286:79//Hs.146173:AA906191
F-HEM8B1002050//Breakpoint cluster region protein BCR//0.84:267:59	F-HEM8B1002579//EST//1.0:77:68//Hs.147935:AI250286
//Hs.2557:Y00661	F-HEM8B1002582//ESTs//0.00032:178:68//Hs.139163:AA226095
F-HEM8B1002068//Homo sapiens mRNA for KIAA0612 protein, partial cd	F-HEM8B1002590//ESTs//0.64:132:63//Hs.155688:AI003657
s//8.1e-07:402:61//Hs.112499:AB014512	F-HEM8B1002596//ESTs//3.4e-19:462:64//Hs.124399:AA832336
F-HEM8B1002069	F-HEM8B1002600//Homo sapiens tetraspan NET-5 mRNA, complete cds//
F-HEM8B1002092//EST//5.1e-15:180:75//Hs.127928:AA969239	3.0e-152:710:98//Hs.129826:AF089749
F-HEM8B1002094//EST//2.0e-52:264:98//Hs.71763:AA146625	F-HEM8B1002601//EST//9.6e-13:368:62//Hs.137080:AA894817
F-HEM8B1002115//EST//0.0083:244:64//Hs.125353:AA877080	F-HEM8B1002603//EST//0.10:144:63//Hs.158180:AI367945
F-HEM8B1002134//ESTs//1.7e-69:398:91//Hs.157492:AI361027	F-HEM8B1002607//ESTs//0.024:345:62//Hs.143304:AI084058
F-HEM8B1002139//ESTs//0.64:145:71//Hs.157821:AI362013	F-HEM8B1002610//EST//2.1e-14:291:64//Hs.140573:AA826323
F-HEM8B1002142//ESTs//0.013:311:59//Hs.150037:AI292214	F-HEM8B1002613//ESTs//1.9e-17:192:75//Hs.141161:AA210711
F-HEM8B1002152//ESTs//8.4e-12:121:82//Hs.119540:T95254	F-HEM8B1002614//ESTs//0.0048:136:71//Hs.106280:R13901
F-HEM8B1002189//EST//0.26:81:70//Hs.147726:AI220208	F-HEM8B1002617//EST//0.034:320:59//Hs.41223:H89127
F-HEM8B1002190//Alcohol dehydrogenase 2 (class I), beta polypeptid	F-HEM8B1002623//ESTs//0.88:222:60//Hs.129920:AA167217
e//0.16:608:58//Hs.4:X03350	F-HEM8B1002635//Human MAP kinase mRNA, complete cds//3.1e-23:127:1
F-HEM8B1002193//Human sky mRNA for Sky, complete cds//6.6e-35:179:	00//Hs.151051:U07620
100//Hs.301:U18934	F-HEM8B1002664//EST//0.00013:203:61//Hs.117141:AA678811
F-HEM8B1002217//Homo sapiens mRNA for zinc finger protein 10//3.7	F-HEM8B1002677//ESTs//2.4e-22:439:66//Hs.132046:AA693680
e-25:405:67//Hs.104115:X52332	F-HEM8B1002683//ESTs//0.23:224:61//Hs.128883:AI026679
F-HEM8B1002218//EST//0.015:241:61//Hs.105298:AA489813	F-HEM8B1002684//ESTs//7.2e-09:82:87//Hs.140457:H05124
F-HEM8B1002232//Small inducible cytokine A5 (RANTES)//9.0e-31:365:	F-HEM8B1002686//EST//0.25:189:62//Hs.132431:AA909674
71//Hs.155464:AF088219	F-HEM8B1002692//ESTs//0.00020:162:66//Hs.118180:N68504
F-HEM8B1002247	F-HEM8B1002697//EST//7.2e-17:219:74//Hs.100459:T61992

【0858】

【表557】

F-HENBB1002699//Homo sapiens transmembrane activator and CAML interactor (TAC1) mRNA, complete cds//0.059:297:62//Hs.158341:AF023614
 F-HENBB1002702//ESTs//0.26:284:61//Hs.41250:H89588
 F-HENBB1002705//ESTs, Weakly similar to HYPOTHETICAL 38.5 KD PROTEIN IN SU12-TDH2 INTERGENIC REGION [Saccharomyces cerevisiae]//0.0048:84:83//Hs.20814:A1242922
 F-HENBB1002712//ESTs//0.0025:317:58//Hs.7344:AA972729
 F-HAMMA1000009//Human c-yes-1 mRNA//1.0e-48:447:77//Hs.75680:M15990
 F-HAMMA1000019
 F-HAMMA1000020//EST//2.6e-84:431:95//Hs.143333:M51750
 F-HAMMA1000025//EST//1.0:169:59//Hs.130165:AA906945
 F-HAMMA1000043//Human NSCL-1 mRNA sequence//0.94:262:60//Hs.30956:M96739
 F-HAMMA1000045//ESTs//1.7e-48:489:75//Hs.158469:AA897461
 F-HAMMA1000055//ESTs, Highly similar to TESTIN 2 PRECURSOR [Mus musculus]//2.7e-18:330:63//Hs.59906:AA001281
 F-HAMMA1000057//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//1.2e-50:367:75//Hs.133089:AF064019
 F-HAMMA1000069//ESTs//0.58:286:60//Hs.134417:A1336840
 F-HAMMA1000084//Human mRNA for KIAA0033 gene, partial cds//1.1e-48:641:70//Hs.22271:D26067
 F-HAMMA1000085//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.00013:199:69//Hs.37656:AB011174
 F-HAMMA1000092//Homo sapiens telomeric repeat binding factor (TRF1) mRNA, complete cds//1.2e-52:346:77//Hs.90357:U40705
 F-HAMMA1000103//Homo sapiens mRNA for extracellular matrix protein, complete cds//1.0:151:64//Hs.35094:AB011792
 F-HAMMA1000117
 F-HAMMA1000129//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.0015:492:60//Hs.89631:U48508
 F-HAMMA1000133//ESTs//1.0:125:67//Hs.118309:AA653402
 F-HAMMA1000134//EST//1.2e-08:75:92//Hs.160674:A1248319
 F-HAMMA1000139//EST//5.5e-10:139:76//Hs.159121:A1383843
 F-HAMMA1000143//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.2e-26:148:97//Hs.153121:AB014585
 F-HAMMA1000155//Homo sapiens homeobox transcription factor barx2 (BARX2) mRNA, complete cds//3.3e-31:219:87//Hs.129724:AF031924
 F-HAMMA1000163//ESTs//1.2e-59:317:94//Hs.49559:AA401050
 F-HAMMA1000171//ESTs//1.7e-09:161:69//Hs.119070:AA629695
 F-HAMMA1000173//Human drebrin E2 mRNA (DBN1), complete cds//9.2e-40:686:65//Hs.89434:D17530
 F-HAMMA1000175//ESTs//0.65:141:68//Hs.133152:H91657
 F-HAMMA1000183//Human mRNA for KIAA0065 gene, partial cds//1.0e-92:904:72//Hs.70617:D31763
 F-HAMMA1000198//ESTs//0.0092:235:62//Hs.98783:A1091739
 F-HAMMA1000221//EST//3.3e-16:95:98//Hs.128271:AA973035
 F-HAMMA1000227//ESTs//0.010:268:60//Hs.116412:AA506926
 F-HAMMA1000241//ESTs//0.13:140:67//Hs.12328:A1377913
 F-HAMMA1000251//EST//3.7e-07:118:73//Hs.153116:AA856873
 F-HAMMA1000254//ESTs//0.00023:245:59//Hs.150513:A1247587
 F-HAMMA1000257//EST//4.2e-10:155:74//Hs.150409:A1003543
 F-HAMMA1000264//ESTs//2.0e-18:217:75//Hs.152748:N53015
 F-HAMMA1000266//EST//0.14:270:60//Hs.132593:A1031874
 F-HAMMA1000270//Human mRNA for KIAA0118 gene, partial cds//2.5e-54:354:87//Hs.154326:D42087
 F-HAMMA1000277//Hydroxysteroid (11-beta) dehydrogenase 2//1.0e-07:306:65//Hs.1376:U26726
 F-HAMMA1000278//ESTs//4.0e-09:197:67//Hs.157034:A1347361
 F-HAMMA1000279//Complement component 5 receptor 1 (C5a ligand)//8.4e-34:341:68//Hs.2161:M62505
 F-HAMMA1000284
 F-HAMMA1000287//Human mRNA for KIAA0118 gene, partial cds//5.4e-50:245:84//Hs.154326:D42087
 F-HAMMA1000302//EST//5.3e-40:213:98//Hs.122363:AA788641
 F-HAMMA1000307//Polycystic kidney disease 1 (autosomal dominant)//0.55:510:57//Hs.75813:L33243
 F-HAMMA1000309//Apolipoprotein E//9.7e-06:691:58//Hs.76260:M12529
 F-HAMMA1000312//EST//0.042:183:63//Hs.158928:A1379519
 F-HAMMA1000313
 F-HAMMA1000331
 F-HAMMA1000339
 F-HAMMA1000340//ESTs, Highly similar to HYPOTHETICAL 29.4 KD PROTEIN IN STE6-LOS1 INTERGENIC REGION [Saccharomyces cerevisiae]//2.9e-11:87:93//Hs.13096:AA180963
 F-HAMMA1000348//Homo sapiens KIAA0432 mRNA, complete cds//3.6e-23:270:72//Hs.155174:AB007892
 F-HAMMA1000356//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//3.7e-24:233:72//Hs.158095:AB007953
 F-HAMMA1000360//Human Line-1 repeat mRNA with 2 open reading frame s//9.0e-75:498:85//Hs.23094:M19503
 F-HAMMA1000361//Human mRNA for KIAA0118 gene, partial cds//9.1e-50:304:85//Hs.154326:D42087
 F-HAMMA1000372//EST//1.2e-53:376:86//Hs.144295:AA136569
 F-HAMMA1000385//ESTs//1.4e-22:220:76//Hs.142552:AA235344
 F-HAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//1.2e-149:710:98//Hs.32170:AB015132
 F-HAMMA1000395//Acyl-Coenzyme A dehydrogenase, very long chain//0.74:330:60//Hs.82208:L46590
 F-HAMMA1000402//Human Line-1 repeat mRNA with 2 open reading frame s//2.4e-58:834:68//Hs.23094:M19503
 F-HAMMA1000410//Human NADH:ubiquinone oxidoreductase subunit B13 (B13) mRNA, complete cds//1.2e-08:117:84//Hs.83916:U53468
 F-HAMMA1000413//ESTs//3.3e-31:209:88//Hs.146154:A1200725
 F-HAMMA1000414//ESTs//0.82:132:62//Hs.124857:AA687092
 F-HAMMA1000416//ESTs, Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN IN CO9F5.2 IN CHROMOSOME III [C.elegans]//9.8e-33:267:81//Hs.32370:AA521111
 F-HAMMA1000421//ESTs//7.3e-33:320:75//Hs.121659:H02532
 F-HAMMA1000422//Homo sapiens protocadherin (PCDH8) mRNA, complete cds//0.98:553:56//Hs.19492:AF061573
 F-HAMMA1000423//EST//0.0075:179:63//Hs.162974:AA678459
 F-HAMMA1000424//ESTs//1.3e-17:313:67//Hs.139858:A1377641
 F-HAMMA1000429//Homo sapiens sorting nexin 3 (SNX3) mRNA, complete cds//5.1e-48:491:72//Hs.12102:AF034546
 F-HAMMA1000431//ISLET AMYLOID POLYPEPTIDE PRECURSOR//5.1e-39:320:81//Hs.51048:X68830
 F-HAMMA1000444//Homo sapiens mRNA for KIAA0594 protein, partial cds//9.1e-39:342:78//Hs.154872:AB011666
 F-HAMMA1000446
 F-HAMMA1000458//ESTs, Weakly similar to similar to CCAAT/enhancer-binding protein [C.elegans]//5.1e-08:58:93//Hs.9043:M21827
 F-HAMMA1000468//Homo sapiens mRNA for 6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase, complete cds//0.58:311:63//Hs.66721:D49818
 F-HAMMA1000472//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.1e-44:346:80//Hs.51048:X68830
 F-HAMMA1000478//Homo sapiens PYRIN (MEFV) mRNA, complete cds//0.0017:157:73//Hs.113283:AF018080
 F-HAMMA1000483//ISLET AMYLOID POLYPEPTIDE PRECURSOR//4.5e-39:400:75//Hs.51048:X68830
 F-HAMMA1000490//ESTs//3.6e-52:331:88//Hs.163686:AA291948
 F-HAMMA1000500//EST//9.7e-73:346:99//Hs.98812:AA434482
 F-HAMMA1000501//Small inducible cytokine A5 (RANTES)//2.3e-50:325:86//Hs.155464:AF088219
 F-HAMMA1000516//Oxytocin receptor//1.6e-29:660:64//Hs.2820:X64878
 F-HAMMA1000522//ESTs//2.9e-23:328:70//Hs.125142:AA421352
 F-HAMMA1000524//ESTs//1.1e-08:211:65//Hs.33467:R85497
 F-HAMMA1000559//EST//4.7e-17:207:71//Hs.162733:AA614352
 F-HAMMA1000565
 F-HAMMA1000567//Homo sapiens haemopoietic progenitor homeobox HPX4 2B (HPX42B) mRNA, complete cds//5.8e-51:404:80//Hs.125231:AF068006
 F-HAMMA1000576//ESTs//3.8e-32:236:74//Hs.140039:AA047045
 F-HAMMA1000583//ESTs//0.00099:123:70//Hs.135173:A1276780
 F-HAMMA1000585//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//8.8e-45:390:78//Hs.159523:AF001622
 F-HAMMA1000594//ESTs//8.3e-42:322:81//Hs.161660:AA167744
 F-HAMMA1000597//Homo sapiens KIAA0426 mRNA, complete cds//2.6e-37:592:68//Hs.97476:AB007886
 F-HAMMA1000605//Homo sapiens 4F55 mRNA, complete cds//5.1e-26:228:73//Hs.32567:AF073519
 F-HAMMA1000612//Homo sapiens Gx protein (GX) mRNA, complete cds//0.00091:300:60//Hs.29207:AF071494
 F-HAMMA1000616//ESTs//0.41:373:59//Hs.130699:AA621478
 F-HAMMA1000621//EST//0.027:146:62//Hs.148305:AA909605
 F-HAMMA1000623
 F-HAMMA1000625//Homo sapiens ES/130 mRNA, complete cds//0.89:428:56//Hs.98614:AF006751
 F-HAMMA1000643//Homo sapiens nephrocystin (NPHP1) mRNA, partial cds//0.092:365:59//Hs.75474:AF023674
 F-HAMMA1000664//ESTs//7.6e-07:259:64//Hs.140622:AA844353
 F-HAMMA1000669//Human knp1 repeat mRNA (cdna clone pcd-knp1-4), 3' end//9.0e-30:531:64//Hs.139107:X00629
 F-HAMMA1000670//ESTs//6.6e-83:389:100//Hs.148595:A1244490
 F-HAMMA1000672//Homo sapiens CAG32 mRNA, partial cds//0.17:109:73//Hs.4316:U80743
 F-HAMMA1000684//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds//3.3e-07:249:62//Hs.44481:U13220
 F-HAMMA1000696//Interleukin 10//5.6e-47:355:82//Hs.2180:M57627

【0859】

【表558】

F-MAMMA1000707/ESTs//1.4e-09:225:65//Hs.138722:N51081	F-MAMMA1000957/ESTs//1.0:177:59//Hs.149864:N80474
F-MAMMA1000713//Acetylcholinesterase (14-ES domain) [human, tumor cell lines, Genomic, 847 nt]//0.16:84:72//Hs.157124:S71129	F-MAMMA1000962//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.1e-56:310:85//Hs.129735:AF010144
F-MAMMA1000714//Human clone 23947 mRNA, partial cds//0.97:263:61//Hs.27414:U79275	F-MAMMA1000968//ESTs//9.2e-18:128:89//Hs.163980:AA715814
F-MAMMA1000718//ESTs, Weakly similar to putative p150 [H.sapiens]//5.0e-07:210:66//Hs.71148:AA854648	F-MAMMA1000975//ESTs//3.8e-08:219:66//Hs.110937:AA137096
F-MAMMA1000720//ESTs//1.4e-50:301:83//Hs.138852:AA284247	F-MAMMA1000979//EST//0.00022:155:65//Hs.101379:Z39802
F-MAMMA1000723//ESTs, Weakly similar to ORF2-like protein [H.sapiens]//8.1e-22:288:72//Hs.114685:AA700024	F-MAMMA1000987//EST//1.1e-48:373:81//Hs.139034:W27062
F-MAMMA1000731//Homo sapiens CHD1 mRNA, complete cds//1.5e-23:292:66//Hs.22670:AF006513	F-MAMMA1000998//EST//2.0e-07:356:62//Hs.132467:AA922007
F-MAMMA1000732//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//4.8e-40:288:78//Hs.158095:AB007953	F-MAMMA1001003//ESTs//0.47:129:67//Hs.164016:A1003724
F-MAMMA1000733//RAS GTPASE-ACTIVATING-LIKE PROTEIN IQGAP1//0.25:467:58//Hs.1742:L33075	F-MAMMA1001008//ESTs//1.9e-17:153:82//Hs.141161:AA210711
F-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.3e-169:802:98//Hs.31575:AF100141	F-MAMMA1001021//Homo sapiens beta-dystrobrevin (BDTN) mRNA, complete cds//4.7e-17:100:100//Hs.13451:Y15718
F-MAMMA1000738//EST//1.0:149:63//Hs.136928:AA812580	F-MAMMA1001024//ESTs//0.97:251:62//Hs.59389:R93968
F-MAMMA1000744//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.3e-51:323:88//Hs.153468:AB011147	F-MAMMA1001030//Homo sapiens orphan G protein-coupled receptor HG38 mRNA, complete cds//3.6e-32:753:61//Hs.98384:AF062006
F-MAMMA1000746//EST//2.3e-42:409:76//Hs.61199:AA024494	F-MAMMA1001035//ESTs//6.9e-28:268:77//Hs.139536:AA180857
F-MAMMA1000752//EST, Weakly similar to putative p150 [H.sapiens]//1.1e-14:285:68//Hs.162011:AA513663	F-MAMMA1001038
F-MAMMA1000760//Myelin oligodendrocyte glycoprotein [alternative products]//6.2e-47:341:82//Hs.53217:Z48051	F-MAMMA1001041//ALPHA-ACTININ 1, CYTOSKELETAL ISOFORM//2.7e-10:357:65//Hs.119000:M95178
F-MAMMA1000761//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H.sapiens]//9.8e-19:131:76//Hs.118972:AA761369	F-MAMMA1001050//EST//1.8e-29:321:74//Hs.161240:A1419882
F-MAMMA1000775//EST//6.9e-32:424:69//Hs.44554:N34288	F-MAMMA1001059//ESTs, Weakly similar to protein synthesis initiation factor 4A-II homolog//7.9e-87:415:99//Hs.135623:AA134719
F-MAMMA1000776//EST//5.5e-43:154:84//Hs.141581:AA315361	F-MAMMA1001067//EST//0.30:166:60//Hs.148441:A1198503
F-MAMMA1000778//EST//4.4e-28:226:80//Hs.128952:AA984114	F-MAMMA1001073//ESTs//1.0e-98:476:98//Hs.98321:AA455585
F-MAMMA1000782//ESTs//0.35:270:60//Hs.29153:AA551137	F-MAMMA1001074//ESTs//1.6e-82:396:98//Hs.118923:AA252116
F-MAMMA1000798//Homo sapiens clone 24407 mRNA sequence//1.6e-23:531:65//Hs.12432:AF070575	F-MAMMA1001075//Homo sapiens (clone F4) transmembrane protein mRNA sequence//3.7e-29:559:65//Hs.135251:L09749
F-MAMMA1000802//EST//3.1e-67:340:97//Hs.126081:AA459849	F-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frames//2.7e-99:689:83//Hs.23094:M19503
F-MAMMA1000824//ESTs//0.98:44:90//Hs.42802:N20130	F-MAMMA1001080//IG ALPHA-2 CHAIN C REGION//5.8e-43:319:81//Hs.32225:AF067420
F-MAMMA1000831//ESTs//0.0081:194:60//Hs.150400:A1298089	F-MAMMA1001082//ESTs//6.2e-28:275:77//Hs.152685:AA613896
F-MAMMA1000839//Small inducible cytokine A5 (RANTES)//4.7e-48:241:74//Hs.155464:AF088219	F-MAMMA1001091//Homo sapiens mRNA for KIAA0711 protein, complete cds//0.0081:586:57//Hs.5333:AB018254
F-MAMMA1000841	F-MAMMA1001092//Human kpni repeat mRNA (cdna clone pcd-kpni-8), 3' end//5.1e-24:328:72//Hs.103948:X00627
F-MAMMA1000842//Human monocytic leukaemia zinc finger protein (MOZ) mRNA, complete cds//0.18:483:59//Hs.82210:U47742	F-MAMMA1001105//Homo sapiens OVO-like 1 binding protein (OVOL1) mRNA, complete cds//2.1e-24:507:66//Hs.97905:AF016045
F-MAMMA1000843//EST//0.34:113:68//Hs.58415:W74696	F-MAMMA1001110//Human mRNA for KIAA0125 gene, complete cds//0.94:448:57//Hs.38365:D50915
F-MAMMA1000845//EST//2.9e-06:56:80//Hs.123243:AA804877	F-MAMMA1001126//Small inducible cytokine A5 (RANTES)//4.6e-18:123:85//Hs.155464:AF088219
F-MAMMA1000851//EST//0.78:103:65//Hs.135656:AA907022	F-MAMMA1001133
F-MAMMA1000855	F-MAMMA1001139
F-MAMMA1000856//Homo sapiens preprocathepsin P mRNA, partial cds//0.14:320:59//Hs.71388:AF032906	F-MAMMA1001143//ESTs//2.6e-18:121:82//Hs.135117:A1091534
F-MAMMA1000859//SOX-3 PROTEIN//0.014:474:57//Hs.157429:X71135	F-MAMMA1001145//ESTs//1.5e-36:442:69//Hs.124712:H90217
F-MAMMA1000862//EST//1.0:92:66//Hs.157599:A1357342	F-MAMMA1001154//EST//0.054:208:61//Hs.162088:AA505741
F-MAMMA1000863//ELK1, member of ETS oncogene family//1.2e-30:214:75//Hs.116549:AL009172	F-MAMMA1001161//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.6e-38:337:77//Hs.153468:AB011147
F-MAMMA1000865//ESTs//0.99:127:66//Hs.125230:AA873812	F-MAMMA1001162//EST//4.7e-16:117:90//Hs.130894:A1014299
F-MAMMA1000867//EST//0.027:236:60//Hs.147156:A1191777	F-MAMMA1001181
F-MAMMA1000875//Human mRNA for KIAA0269 gene, complete cds//0.96:245:59//Hs.75850:D87459	F-MAMMA1001186//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//6.5e-47:313:81//Hs.97203:U83171
F-MAMMA1000876//ESTs//1.5e-39:192:90//Hs.132020:AA704147	F-MAMMA1001191//ESTs//5.8e-34:197:94//Hs.121575:AA758083
F-MAMMA1000877//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.4e-91:484:94//Hs.138938:AA012894	F-MAMMA1001198
F-MAMMA1000880//EST//0.014:142:66//Hs.137044:AA878812	F-MAMMA1001202//ESTs//1.5e-37:210:83//Hs.79788:AA527348
F-MAMMA1000883//EST//1.0:166:62//Hs.126352:AA894465	F-MAMMA1001203//ESTs//1.2e-29:199:76//Hs.141605:H92974
F-MAMMA1000897//H.sapiens mRNA for inter-alpha-trypsin inhibitor heavy chain H3//2.6e-06:211:63//Hs.76716:X67055	F-MAMMA1001206//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.5e-25:275:75//Hs.105292:AA504776
F-MAMMA1000905//Cartilage matrix protein//0.97:190:64//Hs.150366:M55683	F-MAMMA1001215//ESTs//1.9e-06:300:63//Hs.113566:T03200
F-MAMMA1000906//ESTs//3.0e-07:145:72//Hs.133556:AA702506	F-MAMMA1001220//Human mRNA for KIAA0118 gene, partial cds//2.7e-53:367:84//Hs.154326:D42087
F-MAMMA1000908//ESTs//1.1e-70:484:84//Hs.142497:AA189081	F-MAMMA1001222//Homo sapiens mRNA for KIAA0634 protein, partial cds//1.8e-05:435:59//Hs.30898:AB014534
F-MAMMA1000914//Angiopoietin 1//0.14:450:59//Hs.2463:D13628	F-MAMMA1001243//ESTs//5.2e-19:118:94//Hs.122830:AA765587
F-MAMMA1000921//ESTs//6.8e-96:448:99//Hs.135721:A1125239	F-MAMMA1001244
F-MAMMA1000931//CD4 receptor (exons 1 and 2) [human, T-lymphocyte, mRNA, 3429 nt]//1.0e-25:312:66//Hs.116007:S79267	F-MAMMA1001249//ESTs//1.3e-89:420:99//Hs.147744:A1220476
F-MAMMA1000940//EST//2.9e-42:209:76//Hs.140567:AA825968	F-MAMMA1001256//ESTs//2.1e-34:282:80//Hs.46158:A1160121
F-MAMMA1000941//Dihydrolipoamide branched chain transacylase (E2 component of branched chain keto acid dehydrogenase complex)//1.8e-38:395:71//Hs.89479:X66785	F-MAMMA1001259//ESTs//2.9e-07:68:95//Hs.6193:AA045149
F-MAMMA1000942//ESTs//1.9e-19:252:71//Hs.141575:AA211734	F-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete cds//2.8e-41:659:64//Hs.65238:AB014561
F-MAMMA1000943//Human mRNA for KIAA0305 gene, complete cds//0.077:236:63//Hs.83790:AB002303	F-MAMMA1001268//Human Line-1 repeat mRNA with 2 open reading frames//1.7e-33:336:74//Hs.23094:M19503
F-MAMMA1000956//Homo sapiens hRVP1 mRNA for RVP1, complete cds//8.8e-33:566:64//Hs.25640:AB000714	F-MAMMA1001271//Homo sapiens CAGH3 mRNA, complete cds//3.4e-06:487:59//Hs.21858:U80747
	F-MAMMA1001274//Human mRNA for KIAA0080 gene, partial cds//5.1e-62:396:76//Hs.74554:D38522
	F-MAMMA1001280//ESTs//7.3e-14:273:67//Hs.126503:AA913832
	F-MAMMA1001292//Human mRNA for KIAA0176 gene, partial cds//5.6e-54:616:71//Hs.4935:D79998

【0860】

【表559】

F-MAMMA1001296//ESTs//4.8e-34:136:85//Hs.70279:AA57426	complete cds//8.0e-45:323:83//Hs.46468:U45984
F-MAMMA1001298//ESTs//0.021:73:80//Hs.114233:N91305	F-MAMMA1001715//ESTs//1.3e-14:188:72//Hs.130815:AA936548
F-MAMMA1001305//Human DNA sequence from PAC 127B20 on chromosome 2	F-MAMMA1001730//ESTs//0.048:198:65//Hs.116412:AA506926
2q11.2-pter, contains gene for GTPase-activating protein similar to	F-MAMMA1001735//Human beta-tubulin class III isotype (beta-3) mRNA
rhoGAP protein, ribosomal protein L6 pseudogene, ESTs and CA rep	A, complete cds//1.5e-111:725:84//Hs.159154:U47634
eat//1.9e-58:295:97//Hs.102336:Z83838	F-MAMMA1001740//EST//0.77:119:65//Hs.148140:AA887098
F-MAMMA1001322//ESTs//9.4e-18:221:74//Hs.139132:AA211087	F-MAMMA1001743//ESTs//6.5e-27:195:72//Hs.163688:H48768
F-MAMMA1001324//Human endogenous retrovirus pHE.1 (ERV9)//6.7e-75:	F-MAMMA1001744//EST//0.00019:134:70//Hs.146863:AI161245
745:73//Hs.93174:X57147	F-MAMMA1001745//Human Line-1 repeat mRNA with 2 open reading frame
F-MAMMA1001330//ESTs//2.6e-26:169:91//Hs.4209:AA205806	s//4.7e-67:822:69//Hs.23094:M19503
F-MAMMA1001341//ESTs//0.10:267:62//Hs.155922:AI147197	F-MAMMA1001751//Homo sapiens two P domain potassium channel subuni
F-MAMMA1001343//ESTs//0.0024:323:62//Hs.119238:AA476267	t (HOH01) mRNA, complete cds//1.0e-36:583:65//Hs.79351:U33632
F-MAMMA1001346//Homo sapiens mRNA for KIAA0715 protein, partial cd	F-MAMMA1001754//ESTs//5.1e-97:456:99//Hs.157928:AA775822
s//0.84:89:75//Hs.109358:AB018258	F-MAMMA1001757//EST//0.042:177:63//Hs.144436:R07109
F-MAMMA1001383//Putative mismatch repair/binding protein hMSH3//7.	F-MAMMA1001760//Homo sapiens RET finger protein-like 1 antisense t
3e-49:273:80//Hs.42674:U61981	ranscript, partial//6.6e-41:309:84//Hs.102576:AJ010230
F-MAMMA1001386//INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN COMPLEX	F-MAMMA1001764//ESTs//0.057:290:60//Hs.68647:AA524072
ACID LABILE CHAIN PRECURSOR//4.6e-09:415:58//Hs.839:M86826	F-MAMMA1001768//Human transcription factor, forkhead related activ
F-MAMMA1001397//Prostaglandin 12 (prostaglandin) synthase //1.3e-2	ator 4 (FREAC-4) mRNA, complete cds//2.2e-05:504:60//Hs.96028:AF04
6:358:67//Hs.61333:D83402	2832
F-MAMMA1001408//ESTs//7.2e-06:123:72//Hs.26753:R60763	F-MAMMA1001769//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1
F-MAMMA1001411//Autosomal dominant polycystic kidney disease type	e-85:686:79//Hs.113283:AF018080
1//1.0:176:64//Hs.82001:U50928	F-MAMMA1001771//Human semaphorin III family homolog mRNA, complete
F-MAMMA1001419//Homo sapiens KIAA0395 mRNA, partial cds//4.1e-45:4	cds//0.00071:392:60//Hs.32981:U38276
09:80//Hs.43681:AL022394	F-MAMMA1001783//ESTs//8.8e-23:206:79//Hs.142524:H02940
F-MAMMA1001420//Homo sapiens mRNA for alpha(1,2)fucosyltransferas	F-MAMMA1001785//ESTs//1.3e-52:270:97//Hs.61809:AA503549
e, complete cds//0.00042:125:75//Hs.46328:D87942	F-MAMMA1001788//Human kpni repeat mRNA (cdna clone pcd-kpni-8), 3'
F-MAMMA1001435//Human HsLIM15 mRNA for HsLIM15, complete cds//8.2	end//6.7e-21:212:77//Hs.103948:K00627
e-43:543:71//Hs.37181:D64108	F-MAMMA1001790//Homo sapiens KIAA0409 mRNA, partial cds//2.2e-06:1
F-MAMMA1001442//ESTs//7.9e-15:103:92//Hs.25780:R51321	39:72//Hs.5158:AB007869
F-MAMMA1001446//ESTs//3.5e-44:292:73//Hs.111583:AA463590	F-MAMMA1001806//ESTs//6.4e-44:373:79//Hs.105665:H78987
F-MAMMA1001452//ESTs//0.73:152:65//Hs.163766:AI424040	F-MAMMA1001812//ESTs//4.8e-83:407:97//Hs.98613:D83884
F-MAMMA1001465//ESTs//1.0e-15:201:75//Hs.8836:AA181053	F-MAMMA1001815//EST//2.1e-56:374:85//Hs.141488:H47096
F-MAMMA1001476//Human mRNA for 5'-terminal region of UBRK, complete	F-MAMMA1001817//EST//8.6e-39:336:78//Hs.162236:AA551582
cds//2.0e-24:273:72//Hs.75939:D78335	F-MAMMA1001818//EST//0.32:375:58//Hs.72729:AA167589
F-MAMMA1001487//ESTs, Weakly similar to ORF2-like protein [H.sapie	F-MAMMA1001820//Homo sapiens cytokine-like factor-1 precursor (CL
ns)]//3.2e-25:397:68//Hs.116874:AA524909	F-1) mRNA, complete cds//0.082:153:66//Hs.114948:AF059293
F-MAMMA1001501//CALPAIN 1, LARGE//3.1e-53:438:81//Hs.2575:X04366	F-MAMMA1001824//EST//0.0013:195:63//Hs.129275:AA929742
F-MAMMA1001502//Human p12OE4F transcription factor mRNA, complete	F-MAMMA1001836//ESTs//7.4e-52:283:95//Hs.92290:R76691
cds//0.99:258:61//Hs.154196:U87269	F-MAMMA1001837//Homo sapiens mRNA for zinc finger protein FPM315,
F-MAMMA1001510//ESTs//8.7e-09:380:61//Hs.118701:AA420795	complete cds//2.0e-29:641:62//Hs.56808:D88827
F-MAMMA1001522//ESTs//7.1e-44:321:80//Hs.120170:AI018506	F-MAMMA1001848//ESTs//3.5e-53:264:99//Hs.116430:AA644665
F-MAMMA1001547	F-MAMMA1001851//ESTs//0.00050:251:64//Hs.163776:AI393028
F-MAMMA1001551//Homo sapiens mRNA for KIAA0462 protein, partial cd	F-MAMMA1001854
s//7.5e-130:614:98//Hs.129937:AB007931	F-MAMMA1001858//EST//1.0:113:68//Hs.132482:AA922218
F-MAMMA1001575//ESTs, Weakly similar to zinc finger protein C2H2-1	F-MAMMA1001864//EST//1.3e-06:399:60//Hs.161500:N68060
71 [H.sapiens]]//0.71:181:62//Hs.118866:AI017072	F-MAMMA1001868//Homo sapiens nuclear receptor co-repressor N-CoR m
F-MAMMA1001576//Tubulin, gamma polypeptide//5.7e-97:529:91//Hs.150	RNA, complete cds//0.084:672:58//Hs.152455:AF044209
785:M61764	F-MAMMA1001874//ESTs//0.97:292:58//Hs.24553:AI150687
F-MAMMA1001590//EST//1.7e-13:94:92//Hs.95900:AA160339	F-MAMMA1001878
F-MAMMA1001600//EST//1.0e-08:81:87//Hs.149220:AI247132	F-MAMMA1001880//ESTs//9.2e-09:277:62//Hs.15776:T91944
F-MAMMA1001604//EST//0.0070:157:62//Hs.162516:AA583375	F-MAMMA1001890//EST//1.7e-85:440:97//Hs.128842:AA977576
F-MAMMA1001606//Human clone 23627 mRNA, complete cds//0.64:336:58/	F-MAMMA1001907//EST//2.7e-26:294:74//Hs.98794:AA434078
/Hs.23642:U79266	F-MAMMA1001908//ESTs//3.2e-109:505:100//Hs.146145:AI391521
F-MAMMA1001620//ESTs//6.8e-16:99:79//Hs.164052:AA836152	F-MAMMA1001931//ESTs//1.0:108:67//Hs.126624:AA768874
F-MAMMA1001627//Pregnancy-associated plasma protein A//0.27:379:58	F-MAMMA1001956//Apolipoprotein E//1.0:322:59//Hs.76260:M12529
//Hs.158229:U28727	F-MAMMA1001963//ESTs//0.84:320:60//Hs.6523:AA218859
F-MAMMA1001630//Human DNA sequence from clone 71L16 on chromosome	F-MAMMA1001969//Homo sapiens clone 23892 mRNA sequence//3.6e-79:42
Xp11. Contains a probable Zinc Finger protein (pseudo) gene, an unk	3:81//Hs.91916:AF035317
nown putative gene, a pseudogene with high similarity to part of a	F-MAMMA1001970//Oxytocin receptor//9.7e-31:626:64//Hs.2820:X64878
ntigen KI-67, a putative Chondroitin 6-Sulfotransferase LIKE gene	F-MAMMA1001992//EST, Weakly similar to reverse transcriptase [H.sa
and a KIAA0267 LIKE putative Na(+)/H(+) exchanger protein gene. Co	piens)]//7.9e-09:150:72//Hs.118222:N91115
ntains a predicted CpG island, ESTs, STSs and GSSs and genomic mar	F-MAMMA1002009//ESTs//2.2e-18:234:69//Hs.21978:AA009633
kers DXS1003 and DXS1055//1.4e-40:447:73//Hs.154353:AL022165	F-MAMMA1002011//ESTs//0.91:276:59//Hs.141196:AA704826
F-MAMMA1001633//Human zinc finger protein (LD5-1) mRNA, complete c	F-MAMMA1002032//ESTs//7.8e-40:344:77//Hs.141658:N77915
ds//3.6e-44:611:67//Hs.57679:U57796	F-MAMMA1002033//ESTs//2.5e-30:293:76//Hs.139158:AA226159
F-MAMMA1001635	F-MAMMA1002041//Homo sapiens mRNA, chromosome 1 specific transcrip
F-MAMMA1001649//ESTs//1.4e-47:238:99//Hs.124063:T75524	t KIAA0484//1.2e-54:455:70//Hs.158095:AB007953
F-MAMMA1001654//Homo sapiens retinal rod Na-Ca/K exchanger (NCKX1)	F-MAMMA1002042//ESTs//1.4e-20:199:79//Hs.140913:R44580
mRNA, complete cds//0.00069:140:68//Hs.59829:AB014602	F-MAMMA1002047//EST//4.2e-14:170:75//Hs.124348:AA830225
F-MAMMA1001663//Homo sapiens mRNA for KIAA0448 protein, complete c	F-MAMMA1002056//EST//2.1e-49:414:80//Hs.162335:AA564256
ds//0.015:135:71//Hs.27349:AB007917	F-MAMMA1002058//EST//4.7e-26:268:78//Hs.140520:AA809305
F-MAMMA1001670//ESTs, Highly similar to 52 KD RO PROTEIN [Homo sa	F-MAMMA1002068//Human Line-1 repeat mRNA with 2 open reading frame
piens]]//0.064:472:60//Hs.110819:AI027548	s//8.5e-36:382:75//Hs.23094:M19503
F-MAMMA1001671	F-MAMMA1002078
F-MAMMA1001679//ESTs//0.94:55:83//Hs.152506:AA573317	F-MAMMA1002082
F-MAMMA1001683//ESTs//1.6e-92:480:96//Hs.118496:AA036889	F-MAMMA1002084//EST//0.37:351:59//Hs.46576:N46012
F-MAMMA1001686//ESTs//0.00019:171:66//Hs.140402:AI138765	F-MAMMA1002093//Homo sapiens mRNA for ATP-dependent RNA helicase,
F-MAMMA1001692//ESTs//0.97:104:70//Hs.27596:AI188549	partial//0.54:388:57//Hs.99423:AJ010840
F-MAMMA1001711//Human G protein-coupled receptor (STRL22) mRNA, co	F-MAMMA1002108//Loricrin//0.00066:410:56//Hs.155657:M61120

【0861】

【表560】

F-MAMMA1002118//EST//0.50:262:64//Hs.126872:AA932932
 F-MAMMA1002125//Small inducible cytokine A5 (RANTES)//2.4e-39:272:86//Hs.155464:AF088219
 F-MAMMA1002132//EST//6.4e-05:245:60//Hs.149361:A1272963
 F-MAMMA1002140//ESTs//5.8e-33:212:71//Hs.141203:H52638
 F-MAMMA1002143//SERUM PROTEIN M5E55//1.9e-12:192:70//Hs.148101:M88338
 F-MAMMA1002145//EST//0.12:204:60//Hs.160983:A1392837
 F-MAMMA1002153
 F-MAMMA1002155//ESTs. Weakly similar to p40 [H.sapiens]//3.6e-67:335:97//Hs.88424:AA281385
 F-MAMMA1002156//Integrin, beta 3 (platelet glycoprotein IIb, anti gen CD61)//0.99:310:58//Hs.87149:M35999
 F-MAMMA1002158//EST//0.015:278:58//Hs.162666:AA605196
 F-MAMMA1002170//40S RIBOSOMAL PROTEIN S2//6.9e-82:573:82//Hs.119389:X17206
 F-MAMMA1002174//Human NOF1 mRNA, complete cds//2.2e-42:375:78//Hs.75859:U39400
 F-MAMMA1002198//H.sapiens mRNA for thiol-specific antioxidant//3.3e-36:121:98//Hs.146354:Z22548
 F-MAMMA1002209//ESTs//1.1e-84:409:98//Hs.139235:AA278362
 F-MAMMA1002215//Loricrin//0.0024:369:57//Hs.155657:M61120
 F-MAMMA1002219//ESTs. Weakly similar to coded for by C. elegans CD HA yk52b10.3 [C.elegans]//9.5e-41:202:100//Hs.118849:AA215645
 F-MAMMA1002230//ESTs//0.92:253:60//Hs.4222:A1024063
 F-MAMMA1002236//ESTs. Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]//4.6e-69:344:90//Hs.76822:A1359536
 F-MAMMA1002243//Homo sapiens serine threonine kinase II (STK11) mRNA, complete cds//0.99:454:56//Hs.122755:AF032986
 F-MAMMA1002250//Human involucrin mRNA//0.0037:396:62//Hs.157091:M13903
 F-MAMMA1002267//ESTs//2.0e-12:296:62//Hs.155686:A1308841
 F-MAMMA1002268//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//1.2e-06:427:61//Hs.69949:M94172
 F-MAMMA1002269
 F-MAMMA1002282//ESTs//5.9e-65:342:95//Hs.13962:T72715
 F-MAMMA1002292//EST//0.0050:346:58//Hs.97639:AA398440
 F-MAMMA1002293//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//2.8e-60:387:75//Hs.133089:AF064019
 F-MAMMA1002294//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//4.3e-07:349:64//Hs.92614:M62302
 F-MAMMA1002297//EST//0.98:98:68//Hs.148207:AA897460
 F-MAMMA1002298//Paired basic amino acid cleaving system 4//0.0061:471:57//Hs.77234:AB001914
 F-MAMMA1002299//ESTs//1.0:162:68//Hs.134132:AA205935
 F-MAMMA1002308//ESTs. Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.9e-41:293:83//Hs.105292:AA504776
 F-MAMMA1002310//Homo sapiens serine protease-like protease (nesl) mRNA, complete cds//0.0037:173:67//Hs.69423:AF055481
 F-MAMMA1002311//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.8e-41:473:65//Hs.92381:AB007956
 F-MAMMA1002312//ESTs//0.0017:279:60//Hs.163773:AA066291
 F-MAMMA1002317//ESTs//1.0:131:64//Hs.66075:F08908
 F-MAMMA1002319//Homo sapiens clone 24566 mRNA sequence//1.2e-28:410:68//Hs.133342:AF070536
 F-MAMMA1002322//ESTs//1.2e-47:356:82//Hs.152413:AA780515
 F-MAMMA1002329//Homo sapiens clone 24444 Rap2 interacting protein 8 (RPI8) mRNA, complete cds//0.0079:143:67//Hs.6755:AF055026
 F-MAMMA1002332//Human kpni repeat mRNA (cdna clone pcd-kpni-8), 3' end//1.2e-26:342:72//Hs.103948:K00627
 F-MAMMA1002333//Homo sapiens mRNA for KIAA0711 protein, complete cds//6.8e-07:669:58//Hs.5333:AB018254
 F-MAMMA1002339//H.sapiens mRNA for retrotransposon//3.2e-40:348:73//Hs.6940:Z48633
 F-MAMMA1002347//EST. Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.9e-14:146:81//Hs.163073:R02591
 F-MAMMA1002351//ESTs//1.2e-74:371:96//Hs.111429:W28907
 F-MAMMA1002352//EST//1.1e-44:264:77//Hs.141095:H23818
 F-MAMMA1002360//ESTs//7.6e-15:200:70//Hs.19770:AA447830
 F-MAMMA1002361//ESTs//2.5e-29:277:79//Hs.155115:AA669923
 F-MAMMA1002362//EST//0.25:304:58//Hs.162427:AA576345
 F-MAMMA1002380//FACTOR VIII INTRON 22 PROTEIN//0.29:485:59//Hs.83363:M34677
 F-MAMMA1002384//ESTs//1.1e-05:220:65//Hs.141388:R52022
 F-MAMMA1002385//ESTs. Moderately similar to T11G6.8 [C.elegans]//

8.4e-118:578:97//Hs.25516:A1086362
 F-MAMMA1002392//EST//0.85:319:57//Hs.126484:AA913624
 F-MAMMA1002411//ESTs//0.00044:89:76//Hs.141685:A1142632
 F-MAMMA1002413//ESTs//0.0020:303:61//Hs.94903:W85737
 F-MAMMA1002417//ESTs//1.4e-06:223:65//Hs.143695:AA662745
 F-MAMMA1002427//ESTs//5.4e-48:356:82//Hs.146811:AA410788
 F-MAMMA1002428//EST//1.0:96:71//Hs.105130:AA482030
 F-MAMMA1002434//Human mRNA for KIAA0118 gene, partial cds//2.2e-52:370:83//Hs.154326:D42087
 F-MAMMA1002446
 F-MAMMA1002454//ESTs//9.1e-50:163:100//Hs.80162:AA534809
 F-MAMMA1002461//Human diacylglycerol kinase (DAGK) mRNA, complete cds//6.3e-06:595:59//Hs.99932:L38707
 F-MAMMA1002470
 F-MAMMA1002475//Human MAP kinase activated protein kinase 2 mRNA, complete cds//0.018:417:58//Hs.75074:U12779
 F-MAMMA1002480//ESTs//0.0015:258:62//Hs.132082:M67059
 F-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//9.4e-120:560:98//Hs.155223:AF055460
 F-MAMMA1002494//ESTs//2.4e-68:359:95//Hs.124652:AA857628
 F-MAMMA1002498//ESTs. Weakly similar to hypothetical protein [H.sapiens]//4.0e-07:257:63//Hs.133013:AA604920
 F-MAMMA1002524//Huntingtin (Huntington disease)//0.0085:215:65//Hs.79391:L12392
 F-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds//4.5e-162:775:97//Hs.18858:AF065214
 F-MAMMA1002545//ESTs//6.4e-46:351:81//Hs.146811:AA410788
 F-MAMMA1002554
 F-MAMMA1002556//Human beige-like protein (BGL) mRNA, partial cds//0.96:187:62//Hs.62354:M83822
 F-MAMMA1002566//ESTs//0.0033:130:68//Hs.117018:AA832421
 F-MAMMA1002571//EST//0.28:115:66//Hs.156768:A1351368
 F-MAMMA1002573//ESTs//2.1e-48:265:94//Hs.155128:A1224516
 F-MAMMA1002585
 F-MAMMA1002590//ESTs//3.2e-11:280:63//Hs.36049:AA436831
 F-MAMMA1002597//ESTs//4.8e-10:118:77//Hs.156166:A1334107
 F-MAMMA1002598//Ribosomal protein L7//3.6e-23:123:100//Hs.153:X57958
 F-MAMMA1002603//EST//0.070:99:71//Hs.122387:AA789220
 F-MAMMA1002612//ESTs. Moderately similar to hCDC10 protein [H.sapiens]//8.3e-18:353:65//Hs.60895:AA428463
 F-MAMMA1002617//B94 PROTEIN//0.0097:229:62//Hs.75522:M92357
 F-MAMMA1002618
 F-MAMMA1002622//Homo sapiens advillin mRNA, complete cds//4.7e-22:157:90//Hs.47344:AF041449
 F-MAMMA1002623//EST//1.5e-33:168:81//Hs.141526:M52300
 F-MAMMA1002625
 F-MAMMA1002629//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0507//1.1e-35:355:76//Hs.158241:AB007976
 F-MAMMA1002636//Homo sapiens mRNA for KIAA0288 gene, complete cds//1.9e-05:439:61//Hs.91400:AB006626
 F-MAMMA1002637//KINESIN LIGHT CHAIN//2.0e-47:367:72//Hs.117977:L04733
 F-MAMMA1002646//EST//1.2e-32:302:78//Hs.112540:AA601385
 F-MAMMA1002650//TRICHOHYALIN//1.2e-08:570:63//Hs.82276:L09190
 F-MAMMA1002655//EST//8.8e-40:198:100//Hs.159724:A1393335
 F-MAMMA1002662//EST//0.99:95:63//Hs.144074:A1005489
 F-MAMMA1002665//Lysosomal-associated membrane protein 2//1.8e-35:722:64//Hs.8262:U36336
 F-MAMMA1002671//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//8.6e-06:272:64//Hs.106070:U22398
 F-MAMMA1002673
 F-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.2e-162:752:99//Hs.3363:D86987
 F-MAMMA1002685//ESTs//7.5e-40:373:78//Hs.163937:M69915
 F-MAMMA1002698//ESTs//2.5e-09:190:68//Hs.138292:A1220397
 F-MAMMA1002699//Homo sapiens epsin 2b mRNA, complete cds//4.7e-56:398:81//Hs.22396:AF062085
 F-MAMMA1002701//ESTs//4.3e-10:110:80//Hs.156041:A1274697
 F-MAMMA1002708//Homo sapiens mRNA for alpha(1,2) fucosyltransferase, complete cds//1.1e-51:307:79//Hs.46328:D87942
 F-MAMMA1002711//EST//3.6e-38:186:77//Hs.139715:M25041
 F-MAMMA1002721//EST//3.9e-06:110:71//Hs.136758:AA714692
 F-MAMMA1002727//EST//0.97:137:63//Hs.145153:A1150165
 F-MAMMA1002728//ESTs. Highly similar to PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE [Saccharomyces cerevisiae]//2.6e-12:129:81//Hs.154181:AA193502
 F-MAMMA1002744//ESTs//0.0026:420:58//Hs.95793:AA617853
 F-MAMMA1002746//ESTs//0.28:117:69//Hs.12925:T66312

【0862】

【表561】

F-MAMMA1002748	F-MAMMA1003055//ESTs//0.00011:130:70//Hs.130539:R68518
F-MAMMA1002754//ESTs//1.1e-34:340:77//Hs.163641:R61848	F-MAMMA1003056
F-MAMMA1002758//Homo sapiens KIAA0442 mRNA, partial cds//1.1e-27:151:98//Hs.32168:AB007902	F-MAMMA1003057//ESTs, Moderately similar to hypothetical protein M D6 [M.musculus]//1.3e-88:334:97//Hs.96500:A1206781
F-MAMMA1002764//ESTs//1.7e-45:323:84//Hs.155243:N70293	F-MAMMA1003066//ESTs//0.77:88:71//Hs.143618:A1022618
F-MAMMA1002765//EST//3.2e-11:145:73//Hs.162551:AA584782	F-MAMMA1003089//Homo sapiens mRNA for KIAA0631 protein, partial cds//4.5e-51:329:71//Hs.75154:AB014531
F-MAMMA1002769	F-MAMMA1003099//Homo sapiens actin-binding protein homolog ABP-278 mRNA, complete cds//8.5e-44:288:88//Hs.81008:AF043045
F-MAMMA1002775//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene//7.6e-84:417:97//Hs.77705:U07563	F-MAMMA1003104//H.sapiens mRNA for ASM-like phosphodiesterase 3a//1.0:213:60//Hs.42945:Y08136
F-MAMMA1002780//EST//0.78:210:63//Hs.149413:A1273988	F-MAMMA1003113//Homo sapiens mRNA for hair keratin acidic 3-II//0.99:200:64//Hs.32950:X82634
F-MAMMA1002782	F-MAMMA1003127//Homo sapiens brush border myosin I (BBMI) mRNA, complete cds//5.4e-27:421:66//Hs.5394:AF105424
F-MAMMA1002796//ESTs//0.021:122:65//Hs.132221:A1380710	F-MAMMA1003135//Envoplakin//0.56:250:62//Hs.25482:U53786
F-MAMMA1002807//EST//1.0e-31:184:71//Hs.161497:N66919	F-MAMMA1003140
F-MAMMA1002820//ESTs//0.21:292:59//Hs.132513:A1378514	F-MAMMA1003146//Homo sapiens mRNA for GalT3 protein//7.2e-82:397:97//Hs.151344:Y15062
F-MAMMA1002830//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.4e-57:286:88//Hs.15731:AB011135	F-MAMMA1003150//Homo sapiens mRNA for KIAA0515 protein, partial cds//0.00019:297:61//Hs.108945:AB011087
F-MAMMA1002833//Human mRNA for KIAA0033 gene, partial cds//9.1e-52:583:72//Hs.22271:D25067	F-MAMMA1003166//Glycoprotein Ib (platelet), beta polypeptide//1.2e-31:487:65//Hs.3847:U59632
F-MAMMA1002835	F-MAMMA1000001//Human plectin (PLEC1) mRNA, complete cds//0.16:244:63//Hs.79706:U53204
F-MAMMA1002838//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 1 [Locusta migratoria]//7.7e-38:179:78//Hs.141344:H29951	F-MAMMA10000018//Human mRNA for KIAA0066 gene, partial cds//1.5e-63:385:92//Hs.82510:D31886
F-MAMMA1002842//ESTs//1.7e-19:134:89//Hs.111583:AA463590	F-MAMMA10000032
F-MAMMA1002843//Homo sapiens mRNA for KIAA0810 protein, partial cds//5.4e-137:635:99//Hs.7531:AB018353	F-MAMMA10000035//Human mRNA for KIAA0199 gene, partial cds//4.1e-110:849:81//Hs.78442:D83782
F-MAMMA1002844//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//1.6e-07:329:58//Hs.107747:A1357868	F-MAMMA10000037//Homo sapiens mRNA for KIAA0690 protein, partial cds//3.5e-108:542:95//Hs.60103:AB014590
F-MAMMA1002858	F-MAMMA10000039//Human plectin (PLEC1) mRNA, complete cds//0.11:545:57//Hs.79706:U53204
F-MAMMA1002868//EST//4.1e-23:180:77//Hs.163196:AA767643	F-MAMMA10000055//ESTs, Highly similar to TIP120 [R.norvegicus]//3.2e-69:353:96//Hs.154980:AA948067
F-MAMMA1002869//Human PINCH protein mRNA, complete cds//7.0e-88:696:78//Hs.83987:U09284	F-MAMMA10000059//Homo sapiens T cell immune response cDNA7 (TIRC7) mRNA, complete cds//0.029:281:59//Hs.46465:U45285
F-MAMMA1002871//ESTs//3.4e-93:466:96//Hs.11873:T68423	F-MAMMA10000062//ESTs//0.30:368:59//Hs.131675:AA843210
F-MAMMA1002880//EST//2.0e-09:364:59//Hs.145181:A1183632	F-MAMMA10000080//Homo sapiens chromosome 9, Pl clone 11659//2.8e-102:493:97//Hs.3439:AC004472
F-MAMMA1002881//Homo sapiens mRNA for 25 kDa trypsin inhibitor, complete cds//3.8e-30:680:61//Hs.129732:D45027	F-MAMMA10000086//Homo sapiens mRNA for KIAA0661 protein, complete cds//5.8e-116:550:97//Hs.65238:AB014561
F-MAMMA1002886//Long (electrocardiographic) QT syndrome 2//0.00075:504:60//Hs.19944:U04270	F-MAMMA10000092//Murine leukemia viral (bmi-1) oncogene homolog//0.42:190:63//Hs.431:L13689
F-MAMMA1002887//ESTs//0.044:144:68//Hs.133152:H91657	F-MAMMA10000118//Homo sapiens clone 23763 unknown mRNA, partial cds//0.00086:126:70//Hs.92693:AF007155
F-MAMMA1002890//EST//1.7e-05:74:86//Hs.116013:AA612666	F-MAMMA10000119//Peroxisome receptor 1//0.00055:458:58//Hs.158084:Z48054
F-MAMMA1002892//EST//2.1e-67:383:93//Hs.22815:R44265	F-MAMMA1000127
F-MAMMA1002895//Human transcription factor ERF-1 mRNA, complete cds//0.00053:382:57//Hs.61796:U85658	F-MAMMA1000131
F-MAMMA1002908//EST//0.0022:132:68//Hs.161697:AA224952	F-MAMMA1000132//Homo sapiens NADH:ubiquinone oxidoreductase NDUF56 subunit mRNA, nuclear gene encoding mitochondrial protein, complete cds//3.7e-92:448:97//Hs.49767:AF044959
F-MAMMA1002909//ESTs//9.1e-21:343:70//Hs.142068:AA176125	F-MAMMA1000153//Homo sapiens mRNA for MTC8-related protein MTC16a, complete cds//1.0:546:58//Hs.110099:AB010419
F-MAMMA1002930//ESTs//0.55:72:72//Hs.132440:AA923730	F-MAMMA1000186//Homo sapiens clone 23763 unknown mRNA, partial cds//0.00081:126:70//Hs.92693:AF007155
F-MAMMA1002937//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//7.9e-103:485:99//Hs.102928:A136344	F-MAMMA1000187//ESTs//3.4e-79:400:96//Hs.54971:A1424382
F-MAMMA1002938//Homo sapiens mRNA for KIAA0698 protein, complete cds//1.6e-194:910:98//Hs.31720:AB014598	F-MAMMA1000199//Homo sapiens mRNA for KIAA0722 protein, complete cds//0.87:454:59//Hs.47061:AF045458
F-MAMMA1002941//ESTs//9.5e-19:196:67//Hs.137945:A1423389	F-MAMMA1000242
F-MAMMA1002947//ESTs//1.2e-96:460:99//Hs.156001:A1313418	F-MAMMA1000244//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.97:135:66//Hs.27910:AF049105
F-MAMMA1002964//Homo sapiens KIAA0424 mRNA, partial cds//0.48:250:60//Hs.54697:AB007884	F-MAMMA1000252//TRICHOHYALIN//0.030:273:58//Hs.82276:L09190
F-MAMMA1002970//EST//2.0e-16:132:84//Hs.136518:AA601400	F-MAMMA1000256//Glutamine-fructose-6-phosphate transaminase//1.5e-13:248:69//Hs.1674:M90516
F-MAMMA1002972	F-MAMMA1000257//ESTs, Highly similar to mago nashi [H.sapiens]//2.9e-98:530:93//Hs.104650:A1037879
F-MAMMA1002973//ESTs//3.2e-43:225:74//Hs.155179:AA223932	F-MAMMA1000260//Human mRNA for KIAA0130 gene, complete cds//2.1e-58:460:80//Hs.23106:D50920
F-MAMMA1002982//ESTs//0.0017:162:66//Hs.152669:AA604944	F-MAMMA1000271//ESTs//0.93:224:60//Hs.91226:AA649047
F-MAMMA1002987//EST//0.044:254:59//Hs.135014:A1095645	F-MAMMA1000272
F-MAMMA1003003//Coagulation factor III (thromboplastin, tissue factor)//3.9e-22:185:83//Hs.62192:J02931	F-MAMMA1000280//ESTs, Highly similar to VACUOLAR ATP SYNTHASE SUBUNIT D [Bos taurus]//1.3e-21:308:73//Hs.15071:AA781144
F-MAMMA1003004//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.0e-16:343:61//Hs.159897:AB007970	F-MAMMA1000300
F-MAMMA1003007//EST//6.6e-10:265:66//Hs.144389:AA530979	F-MAMMA1000314//Human mRNA for KIAA0159 gene, complete cds//2.6e-128:708:92//Hs.5719:D63880
F-MAMMA1003011//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.2e-51:620:69//Hs.75258:AF054174	F-MAMMA1000318//Human mRNA for ribosomal protein L39, complete cds//1.8e-35:182:99//Hs.9837:D79205
F-MAMMA1003013//Human HMX4C mRNA for a homeobox protein//0.73:347:58//Hs.74061:X59372	
F-MAMMA1003015//EST//2.5e-11:137:77//Hs.141312:H73062	
F-MAMMA1003019//ESTs//0.0099:182:65//Hs.60787:A1374951	
F-MAMMA1003026//EST//1.0:136:67//Hs.9123:Y50137	
F-MAMMA1003031//EST//1.3e-11:244:67//Hs.136611:AA669549	
F-MAMMA1003035	
F-MAMMA1003039//ESTs//1.4e-23:265:74//Hs.33393:R83391	
F-MAMMA1003040//Homo sapiens tapasin (NCS-17) mRNA, complete cds//1.5e-93:339:85//Hs.5247:AF029750	
F-MAMMA1003044//Cyclin D2//1.0:234:61//Hs.75586:D13639	
F-MAMMA1003047//H.sapiens mRNA for F2583.3 kinase like protein from C.elegans//1.0:209:60//Hs.99491:Y12336	
F-MAMMA1003049//EST//0.99:126:67//Hs.162634:AA601742	

【0863】

【表562】

F-NT2RM1000341//ESTs//2.3e-72:381:95//Hs.23070:AA631976	s//0.084:386:58//Hs.101474:AB018350
F-NT2RM1000354//EST//5.2e-27:202:84//Hs.151186:AI125798	F-NT2RM1000962//Human mRNA for KIAA0252 gene, partial cds//0.98:29
F-NT2RM1000355//ESTs, Weakly similar to putative [M.musculus]//7.7	9:59//Hs.83419:D87440
e-75:387:95//Hs.108619:W28608	F-NT2RM1000978
F-NT2RM1000365//ESTs//1.7e-99:495:97//Hs.103926:AA165691	F-NT2RM1001003//Homo sapiens alpha-catenin related protein (ACRP)
F-NT2RM1000377//ESTs, Weakly similar to protein-tyrosine-phosphatase [H.sapiens]//7.4e-91:481:95//Hs.163707:AA137181	mRNA, complete cds//1.3e-161:760:98//Hs.58488:U97067
F-NT2RM1000388//65 KD YES-ASSOCIATED PROTEIN//0.36:340:57//Hs.893	F-NT2RM1001008//ESTs//1.3e-12:144:75//Hs.133122:AI025200
9:X80507	F-NT2RM1001043//EST//0.24:117:64//Hs.161536:N80395
F-NT2RM1000394//HISTONE H3.3//8.5e-91:474:93//Hs.118838:M11353	F-NT2RM1001044//ESTs, Weakly similar to C43E11.9 [C.elegans]//3.0
F-NT2RM1000399	e-98:491:96//Hs.102173:AA045270
F-NT2RM1000421	F-NT2RM1001059//Human plectin (PLEC1) mRNA, complete cds//0.52:53
F-NT2RM1000430//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//1.2e-85:418:97//Hs.20815:AF084928	3:57//Hs.79706:U53204
F-NT2RM1000499//ESTs, Weakly similar to KIAA0167 protein [H.sapiens]	F-NT2RM1001066//ESTs//1.2e-114:538:99//Hs.129020:AI380703
s//1.6e-38:201:97//Hs.106262:AI052382	F-NT2RM1001072//Human beige-like protein (BGL) mRNA, partial cds//
F-NT2RM1000539//EST//0.070:145:62//Hs.149711:A1284660	0.69:586:56//Hs.62354:M83822
F-NT2RM1000553//EST//2.2e-48:265:95//Hs.99230:AA449847	F-NT2RM1001074//Macrophage stimulating 1 (hepatocyte growth factor-like)//0.0019:294:64//Hs.30223:X90846
F-NT2RM1000555//EST//0.82:193:61//Hs.96944:AI359957	F-NT2RM1001082//Archain//3.9e-37:290:81//Hs.33642:X81198
F-NT2RM1000563//Human plectin (PLEC1) mRNA, complete cds//1.0:336:	F-NT2RM1001085
58//Hs.79706:U53204	F-NT2RM1001092//Zinc finger protein 43 (HTF6)//1.9e-57:770:68//Hs.
F-NT2RM1000623//Homo sapiens mRNA for KIAA0287 gene, partial cds//	74107:X59244
0.98:226:61//Hs.17931:AB006625	F-NT2RM1001102//ESTs//1.2e-35:638:63//Hs.131737:AI343331
F-NT2RM1000648//ESTs, Weakly similar to similar to M. musculus MER	F-NT2RM1001105//WEE1-LIKE PROTEIN KINASE//0.0024:246:63//Hs.75188:
5 and other AHP/C-TSA proteins [C.elegans]//6.2e-51:254:98//Hs.1320	U10564
96:AA314601	F-NT2RM1001112//ESTs//8.9e-82:437:93//Hs.6330:H38495
F-NT2RM1000661//Homo sapiens translation initiation factor 4e mRNA	F-NT2RM1001115
A, complete cds//8.5e-55:276:97//Hs.19122:AF038957	F-NT2RM1001139//Keratin 9//1.5e-05:518:59//Hs.2783:Z29074
F-NT2RM1000666//Homo sapiens BAI 1 mRNA, complete cds//0.87:274:60	F-NT2RM2000006//ESTs//3.9e-16:96:98//Hs.101117:AA576113
//Hs.113936:AB005297	F-NT2RM2000013//RNA polymerase II polypeptide B (140 kD)//6.3e-13:
F-NT2RM1000669//ESTs//5.5e-63:481:85//Hs.90527:AI188279	640:59//Hs.148027:X63563
F-NT2RM1000672	F-NT2RM2000030
F-NT2RM1000691//Homo sapiens mRNA for HRIHFB2060, partial cds//7.0	F-NT2RM2000032//ESTs//7.1e-18:138:68//Hs.114031:AA700958
e-121:582:98//Hs.146282:AB015348	F-NT2RM2000042//ESTs//0.0091:241:61//Hs.147895:AI286243
F-NT2RM1000699//ESTs//1.1e-89:435:97//Hs.28964:AA715101	F-NT2RM2000092
F-NT2RM1000702//ESTs//5.4e-90:429:99//Hs.151001:AA564706	F-NT2RM2000093//ESTs//2.6e-40:226:94//Hs.163521:H42085
F-NT2RM1000725//Homo sapiens mRNA for neuropathy target esterase//	F-NT2RM2000101//ESTs//1.0:235:61//Hs.48860:N27428
1.5e-66:435:85//Hs.5038:AJ004832	F-NT2RM2000124//Protein kinase, cAMP-dependent, catalytic, alpha//
F-NT2RM1000741//Homo sapiens mRNA for KIAA0567 protein, partial cd	5.8e-46:287:88//Hs.77271:X07767
s//2.6e-127:690:92//Hs.147946:AB011139	F-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA,
F-NT2RM1000742//Homo sapiens AC133 antigen mRNA, complete cds//8.2	A, complete cds//3.0e-139:566:97//Hs.18953:AF067223
e-68:524:83//Hs.112360:AF027208	F-NT2RM2000192//EST//3.5e-07:168:65//Hs.163122:AA756999
F-NT2RM1000746//ESTs//2.6e-37:231:89//Hs.94446:AA845465	F-NT2RM2000239//ESTs, Weakly similar to K04G2.6 [C.elegans]//3.6e-
F-NT2RM1000770//Homo sapiens KIAA0425 mRNA, complete cds//3.3e-09:	93:489:95//Hs.143499:R72672
321:63//Hs.150390:AB007885	F-NT2RM2000250//Homo sapiens mRNA for KIAA0590 protein, complete c
F-NT2RM1000772//Eukaryotic translation initiation factor 3 (eIF-3)	ds//1.0e-129:615:98//Hs.111862:AB011162
p36 subunit//0.053:271:60//Hs.139745:U39067	F-NT2RM2000259//ESTs//6.1e-30:172:85//Hs.116406:AA209520
F-NT2RM1000780//Human Line-1 repeat mRNA with 2 open reading frame	F-NT2RM2000260//ESTs//2.5e-25:133:93//Hs.14169:AA203500
s//6.9e-20:128:94//Hs.23094:M19503	F-NT2RM2000287//ESTs//6.2e-13:97:83//Hs.118523:H98981
F-NT2RM1000781//ESTs//4.4e-60:346:92//Hs.35089:N50845	F-NT2RM2000322//Interferon regulatory factor 5//0.84:208:61//Hs.54
F-NT2RM1000800	434:U51127
F-NT2RM1000802	F-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete c
F-NT2RM1000811//Homo sapiens AC133 antigen mRNA, complete cds//1.2	ds//2.8e-176:805:99//Hs.129952:AB011132
e-64:490:84//Hs.112360:AF027208	F-NT2RM2000363//ESTs//1.2e-24:139:96//Hs.48818:N63543
F-NT2RM1000826//ESTs//0.82:193:61//Hs.96944:AI359957	F-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK
F-NT2RM1000829//Mannose-binding lectin, soluble (opsonic defect)//	7 mRNA, partial cds//3.7e-96:599:86//Hs.75871:U48251
0.92:263:58//Hs.2314:X15422	F-NT2RM2000371
F-NT2RM1000833//Hydroxysteroid (11-beta) dehydrogenase 2//0.022:17	F-NT2RM2000374//ESTs//3.2e-13:98:91//Hs.65853:AI050866
8:67//Hs.1376:U26726	F-NT2RM2000395//Growth arrest-specific 1//0.80:129:67//Hs.65029:L1
F-NT2RM1000850//Human protein tyrosine kinase related mRNA sequenc	3698
e//3.8e-06:384:59//Hs.90314:L05148	F-NT2RM2000402//Human p76 mRNA, complete cds//7.2e-23:714:59//Hs.2
F-NT2RM1000852//Homo sapiens mRNA for ATP-dependent RNA helicase,	8757:U81006
partial//3.0e-149:726:97//Hs.99423:AJ010840	F-NT2RM2000407//ESTs//9.4e-92:458:96//Hs.148873:T33582
F-NT2RM1000857//ESTs//0.52:274:60//Hs.112095:AA447643	F-NT2RM2000420//EST//1.8e-61:296:99//Hs.147186:AI193053
F-NT2RM1000867//ESTs, Highly similar to signal peptidase:SUBUNIT//	F-NT2RM2000422//Solute carrier family 6 (neurotransmitter transpor
5.3e-54:277:96//Hs.11125:AI015619	ter, serotonin), member 4//1.5e-06:260:61//Hs.553:L05568
F-NT2RM1000874//ESTs//0.032:185:64//Hs.97713:AA442239	F-NT2RM2000452//ESTs//1.0:132:62//Hs.110004:AI097379
F-NT2RM1000882//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC2	F-NT2RM2000469//ESTs//0.34:249:60//Hs.149575:AI281807
69730) containing the NFEN1 gene//4.0e-155:750:97//Hs.132898:AC004	F-NT2RM2000490//Homo sapiens mRNA for KIAA0747 protein, partial cd
770	s//2.4e-16:386:63//Hs.8309:AB018290
F-NT2RM1000883//Homo sapiens l-1 receptor candidate protein mRNA,	F-NT2RM2000502//Human nicotinamide N-methyltransferase (NNMT) mRNA,
complete cds//8.8e-158:762:97//Hs.26285:AF082516	A, complete cds//0.99:272:61//Hs.76669:U08021
F-NT2RM1000885//Homo sapiens mRNA for KIAA0661 protein, complete c	F-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complet
ds//6.3e-19:310:67//Hs.65238:AB014561	e cds//1.6e-172:824:97//Hs.4812:AF061243
F-NT2RM1000894	F-NT2RM2000522//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.1
F-NT2RM1000898	8:313:60//Hs.129725:AF047487
F-NT2RM1000905//EST//4.8e-07:77:84//Hs.148017:AI268701	F-NT2RM2000540//ESTs, Weakly similar to C27F2.7 gene product [C.el
F-NT2RM1000924//HOMEOBOX PROTEIN HOX-A5//0.00051:458:59//Hs.37034:	egans]//2.7e-41:231:94//Hs.7049:AI141736
W26679	F-NT2RM2000556//ESTs//3.1e-33:183:96//Hs.136990:AA769220
F-NT2RM1000927//Homo sapiens mRNA for KIAA0807 protein, partial cd	F-NT2RM2000566//Integrin, alpha 7B//2.0e-155:751:97//Hs.74369:AF03

【0864】

【表563】

2108 F-NT2RM2000567//RYANODINE RECEPTOR, SKELETAL MUSCLE//6.3e-09:689:59//Hs.89631:U48508 F-NT2RM2000569//ESTs//5.4e-17:170:77//Hs.158277:H09128 F-NT2RM2000577//ESTs, Highly similar to ISOLEUCYL-TRNA SYNTHETAS E, MITOCHONDRIAL [Saccharomyces cerevisiae]//1.4e-33:214:92//Hs.55609:W37993 F-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.8e-175:820:98//Hs.3363:D85987 F-NT2RM2000588//ESTs//1.5e-33:183:97//Hs.136990:AA769220 F-NT2RM2000594 F-NT2RM2000599//Homo sapiens Mad4 homolog (Mad4) mRNA, complete cds//0.017:253:65//Hs.102402:AF040963 F-NT2RM2000609//ESTs//1.0:220:59//Hs.110155:AA007313 F-NT2RM2000612//ESTs//0.97:208:59//Hs.73217:AA846548 F-NT2RM2000623//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.024:326:59//Hs.6150:AB011093 F-NT2RM2000624//ESTs//2.3e-118:557:99//Hs.145904:AA203258 F-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds//2.0e-143:664:98//Hs.19542:AB018272 F-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds//2.4e-139:664:98//Hs.7278:AB014558 F-NT2RM2000639//ESTs//0.98:144:65//Hs.154364:A1189702 F-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds//3.4e-169:518:99//Hs.115763:AB014576 F-NT2RM2000669//ESTs//1.3e-56:283:98//Hs.156342:A1337371 F-NT2RM2000691//Homo sapiens actin-related protein Arp3 (ARP3) mRNA, complete cds//6.7e-86:746:74//Hs.5321:AF006083 F-NT2RM2000714//Human mRNA for KIAA0231 gene, partial cds//2.2e-50:748:64//Hs.7938:D85984 F-NT2RM2000718//Homo sapiens mRNA for HRIHFB2436, partial cds//7.6e-126:594:98//Hs.136058:AB015342 F-NT2RM2000735//Zinc finger protein 43 (ZFP43) //2.7e-112:756:82//Hs.74107:K59244 F-NT2RM2000740//ESTs, Highly similar to HYPOTHETICAL 132.7 KD HELICASE IN ALG7-ENP1 INTERGENIC REGION [Saccharomyces cerevisiae]//4.2e-85:464:91//Hs.161551:W24286 F-NT2RM2000795//Homo sapiens tapasin (NCS-17) mRNA, complete cds//1.0e-82:640:81//Hs.5247:AF029750 F-NT2RM2000821//Human mRNA for KIAA0340 gene, partial cds//0.32:67:95//Hs.105919:AB002338 F-NT2RM2000837//ESTs//2.3e-105:501:98//Hs.101514:A1346701 F-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds//2.8e-185:847:99//Hs.137580:AB015046 F-NT2RM2000952//ESTs, Weakly similar to lethal(2)denticleless [D.melanogaster]//6.2e-94:441:99//Hs.59075:A1023761 F-NT2RM2000984//Human mRNA for KIAA0246 gene, partial cds//0.94:35:1:62//Hs.84753:D87433 F-NT2RM2001004//ESTs//5.0e-10:247:64//Hs.36049:AA436831 F-NT2RM2001035//ESTs, Highly similar to POP2 PROTEIN [Saccharomyces cerevisiae]//2.9e-48:282:93//Hs.17035:A1080471 F-NT2RM2001065 F-NT2RM2001100//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//1.7e-08:449:62//Hs.75111:D87258 F-NT2RM2001105//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.00079:274:59//Hs.102732:U88153 F-NT2RM2001131//TRICHOHYALIN//2.5e-20:684:62//Hs.82276:L09190 F-NT2RM2001141 F-NT2RM2001152//ESTs//0.53:333:58//Hs.153087:AA649042 F-NT2RM2001177 F-NT2RM2001194//ESTs, Weakly similar to T28H10.2 [C.elegans]//2.4e-23:149:93//Hs.10618:A1288739 F-NT2RM2001196//ESTs//4.0e-98:486:97//Hs.59628:W91959 F-NT2RM2001201//Human mRNA for KIAA0005 gene, complete cds//2.8e-44:554:69//Hs.155291:D13630 F-NT2RM2001221//Homo sapiens mRNA for KIAA0806 protein, complete cds//0.97:165:64//Hs.24279:AB018349 F-NT2RM2001238//EST//6.8e-67:420:89//Hs.130586:A1004766 F-NT2RM2001243//V-jun avian sarcoma virus 17 oncogene homolog//0.87:125:64//Hs.75889:U85928 F-NT2RM2001247//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.0066:321:61//Hs.132206:AF039694 F-NT2RM2001256 F-NT2RM2001291//ESTs//1.1e-86:459:93//Hs.10267:W27845 F-NT2RM2001306//Homo sapiens paraoxonase (PON2) mRNA, complete cds//1.0:182:65//Hs.75221:AF001601 F-NT2RM2001312//ESTs//2.0e-35:338:70//Hs.141440:N21615 F-NT2RM2001319//ESTs, Weakly similar to No definition line found [C.elegans]//5.2e-30:277:77//Hs.25347:A1136605 F-NT2RM2001324//Homo sapiens mRNA for beta-spectrin III, complete cds//0.031:245:62//Hs.26915:AB008567 F-NT2RM2001345//ESTs//9.2e-91:428:99//Hs.151001:AA564706 F-NT2RM2001360//ESTs//0.98:45:80//Hs.133520:AA878905 F-NT2RM2001370//Human transportin (TRN) mRNA, complete cds//0.72:24:61//Hs.82925:U70322 F-NT2RM2001393//Mannosidase, alpha B, lysosomal//0.42:383:57//Hs.108969:U68382 F-NT2RM2001420//EST//1.0:287:62//Hs.125285:AA830378 F-NT2RM2001424//Homo sapiens mRNA for E1B-55kDa-associated protein //2.3e-97:453:99//Hs.155218:AJ007509 F-NT2RM2001499//Ecotropic retroviral receptor//5.4e-47:589:68//Hs.2928:X57303 F-NT2RM2001504//Homo sapiens agrin precursor mRNA, partial cds//0.25:328:60//Hs.68900:AF016903 F-NT2RM2001524//ESTs//1.0e-11:93:90//Hs.33687:R85969 F-NT2RM2001544//ESTs//1.0e-25:157:92//Hs.137451:AA351459 F-NT2RM2001547//ESTs//2.0e-29:168:96//Hs.116392:AA936262 F-NT2RM2001575//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro) //6.9e-28:582:64//Hs.1042:W62800 F-NT2RM2001582//ESTs, Moderately similar to red-1 [M.musculus]//0.0032:57:89//Hs.114722:AA448077 F-NT2RM2001588//Homo sapiens KIAA0442 mRNA, partial cds//2.3e-11:282:65//Hs.32168:AB007902 F-NT2RM2001592//ESTs//4.8e-73:372:95//Hs.163801:A1391729 F-NT2RM2001605//Homo sapiens clone 23592 mRNA sequence//7.3e-87:74:9:75//Hs.76272:S66431 F-NT2RM2001613//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.13184:0:A1016073 F-NT2RM2001632//EST//8.7e-18:222:76//Hs.160402:A1393918 F-NT2RM2001635//Homo sapiens mRNA for KIAA0618 protein, complete cds//3.0e-154:740:98//Hs.15832:AB014518 F-NT2RM2001637//ESTs//2.2e-06:386:61//Hs.145198:A1276952 F-NT2RM2001641//ESTs, Highly similar to NADH-CYTOCHROME B5 REDUCTASE [Bos taurus]//3.5e-13:94:92//Hs.22142:AA814725 F-NT2RM2001648//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.13184:0:A1016073 F-NT2RM2001652//ESTs//2.5e-06:82:80//Hs.128203:AA972301 F-NT2RM2001659//ESTs//2.8e-15:92:98//Hs.123321:AA810287 F-NT2RM2001664//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//1.2e-173:802:99//Hs.31323:AF044195 F-NT2RM2001668//ESTs, Weakly similar to DNA MISMATCH REPAIR PROTEIN MSH6 [H.sapiens]//1.1e-136:671:97//Hs.27721:U17907 F-NT2RM2001670//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.1e-25:352:70//Hs.101414:AB011129 F-NT2RM2001671//ESTs//1.8e-08:63:98//Hs.158069:A1365356 F-NT2RM2001675 F-NT2RM2001681//ESTs//0.16:197:63//Hs.20585:R10305 F-NT2RM2001688//ESTs//1.8e-24:130:100//Hs.162504:AA668211 F-NT2RM2001695//EST//5.6e-51:189:89//Hs.162197:AA535216 F-NT2RM2001696//ESTs, Highly similar to gene ERCC5 protein [H.sapiens]//5.8e-16:144:84//Hs.14671:T79937 F-NT2RM2001698//ESTs//0.14:184:63//Hs.148080:A1277415 F-NT2RM2001699//ESTs//6.5e-14:136:79//Hs.127790:A1003817 F-NT2RM2001700//Homo sapiens putative seven pass transmembrane protein (TM7SF1) mRNA, complete cds//0.95:270:61//Hs.15791:AF027826 F-NT2RM2001706//ESTs//2.8e-47:304:86//Hs.146811:AA410788 F-NT2RM2001716//Semenogelin I//0.98:153:64//Hs.1968:M81650 F-NT2RM2001718 F-NT2RM2001723//Homo sapiens clone 23770 mRNA sequence//4.4e-28:16:3:95//Hs.12457:AF052123 F-NT2RM2001727//Homo sapiens mRNA for KIAA0462 protein, partial cds//2.0e-112:530:98//Hs.129937:AB007931 F-NT2RM2001730//Homo sapiens mRNA for KIAA0560 protein, complete cds//0.95:269:58//Hs.129952:AB011132 F-NT2RM2001743 F-NT2RM2001753//Human AF-6 mRNA, complete cds//0.095:350:59//Hs.100469:AB011399 F-NT2RM2001760//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.3e-17:181:75//Hs.13184:0:A1016073 F-NT2RM2001768//ESTs//0.61:189:62//Hs.144847:A1222742 F-NT2RM2001771//Zinc finger protein 10 (KIX) //1.1e-66:669:71//Hs.2479:X78933 F-NT2RM2001782//YY1 transcription factor//0.094:149:65//Hs.97496:M77698 F-NT2RM2001784//ESTs//8.2e-31:190:92//Hs.144587:A1193595 F-NT2RM2001785//Homo sapiens chromosome 11, BAC CIT-HSP-311a8 (BC2

【0865】

【表564】

69730) containing the hFEN1 gene//1.6e-48:476:74//Hs.132898:AC004770	F-NT2RM4000155
F-NT2RM2001797//Human mRNA for KIAA0065 gene, partial cds//6.1e-6	F-NT2RM4000156//ESTs//5.9e-73:345:100//Hs.155958:AA573632
6:481:72//Hs.70617:D31763	F-NT2RM4000167//Homo sapiens kinesin family member protein KIF3A mRNA, complete cds//9.8e-30:676:61//Hs.159228:AF041853
F-NT2RM2001800//Human mRNA for transcriptional activator hSNF2b, c	F-NT2RM4000169//ESTs//2.0e-103:483:99//Hs.43729:AA497044
omplete cds//0.49:142:66//Hs.78202:U29175	F-NT2RM4000191//TRICHODIALIN//0.011:324:60//Hs.82276:L09190
F-NT2RM2001803//Homo sapiens IkappaB kinase complex associated pro	F-NT2RM4000197//ESTs//1.5e-48:311:88//Hs.136144:W27744
tein (IKAP) mRNA, complete cds//2.7e-179:827:99//Hs.31323:AF044195	F-NT2RM4000199//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARM1
F-NT2RM2001805//EST//1.0:45:80//Hs.159007:AI381341	NG ENTRY !!!! [H.sapiens]//0.13:322:61//Hs.145088:AI221147
F-NT2RM2001813//EST//0.41:268:58//Hs.150031:AI292068	F-NT2RM4000200
F-NT2RM2001823//H.sapiens mRNA for 218kD Mi-2 protein//9.7e-21:55	F-NT2RM4000202//Homo sapiens mRNA for KIAA0288 gene, complete cds//
4:60//Hs.74441:X86691	0.0027:424:60//Hs.91400:AB006626
F-NT2RM2001839//Homo sapiens calumein (Calu) mRNA, complete cds//	F-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete c
1.2e-132:738:90//Hs.7753:AF013759	ds//4.4e-184:856:98//Hs.111138:AB018255
F-NT2RM2001840//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.8	F-NT2RM4000215//SET translocation (myeloid leukemia-associated)//
e-58:329:86//Hs.113283:AF018080	0.0013:358:60//Hs.75055:M93651
F-NT2RM2001855//ADP-ribosylation factor 5//1.0:301:60//Hs.77541:MS	F-NT2RM4000229//Homo sapiens mRNA for KIAA0722 protein, complete c
7567	ds//0.65:572:60//Hs.47061:AF045458
F-NT2RM2001867//ESTs, Weakly similar to ZK792.1 [C.elegans]//3.0e-	F-NT2RM4000233//ESTs//2.0e-37:269:85//Hs.148873:T33582
28:421:66//Hs.8763:W30741	F-NT2RM4000244//EST//0.83:319:57//Hs.162412:AA573439
F-NT2RM2001879//ESTs//6.3e-43:234:94//Hs.122546:AA186723	F-NT2RM4000251//ESTs, Weakly similar to CUT1 PROTEIN [Schizosaccha
F-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete c	romyces pombe]//1.1e-16:112:92//Hs.93841:AA442297
ds//6.1e-189:866:97//Hs.4198:AB014610	F-NT2RM4000265//Homo sapiens mRNA for alpha(1,2)fucosyltransferas
F-NT2RM2001896//Homo sapiens mRNA for JM23 protein, complete codin	e, complete cds//1.8e-48:229:83//Hs.46328:D87942
g sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLC101133Q7	F-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRN
(RZPD Berlin))//3.0e-13:606:57//Hs.23170:AJ005892	A, complete cds//2.5e-154:609:93//Hs.31305:M99438
F-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cd	F-NT2RM4000324//Homo sapiens hCPE-R mRNA for CPE-receptor, complet
s//9.4e-178:859:97//Hs.129937:AB007931	e cds//0.070:460:59//Hs.5372:AB000712
F-NT2RM2001930//Homo sapiens semaphorin F homolog mRNA, complete c	F-NT2RM4000327//ESTs//0.019:269:60//Hs.153697:A1240707
ds//4.2e-08:481:59//Hs.27621:U52840	F-NT2RM4000344//ESTs, Highly similar to YME1 PROTEIN [Saccharomyc
F-NT2RM2001935//ESTs, Highly similar to MULTIDRUG RESISTANCE PROT	es cerevisiae]//2.7e-83:432:95//Hs.12796:W27884
EIN HOMOLOG 50 [Drosophila melanogaster]//0.37:424:60//Hs.118634:U	F-NT2RM4000349//Human mRNA for KIAA0005 gene, complete cds//5.2e-5
66688	3:666:68//Hs.155291:D13630
F-NT2RM2001936//Homo sapiens clone 614 unknown mRNA, complete sequ	F-NT2RM4000354//ESTs, Weakly similar to lethal(2)denticleless [D.m
ence//2.2e-139:653:98//Hs.21811:AF091080	elanogaster]//0.0078:55:92//Hs.59075:A1023761
F-NT2RM2001950//ESTs//0.12:91:76//Hs.107295:W80392	F-NT2RM4000356//ESTs//1.0:225:60//Hs.161175:A1418425
F-NT2RM2001982	F-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cd
F-NT2RM2001983//Homo sapiens Tax interaction protein 2 mRNA, parti	s//5.3e-135:628:99//Hs.8152:AB014542
al cds//1.2e-21:123:98//Hs.6454:AF089816	F-NT2RM4000368//ESTs//4.9e-13:323:63//Hs.143695:AA662745
F-NT2RM2001989//Homo sapiens mRNA for DRIM protein//0.71:319:59//H	F-NT2RM4000386//Human DNA sequence from clone 1052M9 on chromosome
s.104135:AJ006778	Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's
F-NT2RM2001997//ESTs//1.7e-25:135:100//Hs.126894:AA932538	s disease (lymphoproliferative syndrome) (DSHP), part of a 60S Aci
F-NT2RM2001998//ESTs, Weakly similar to Mi-2 protein [H.sapiens]//	dic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DDC4
0.99:271:60//Hs.63888:AA203398	LIKE gene. Contains ESTs and GSSs//2.0e-72:843:68//Hs.23796:AL022
F-NT2RM2002004//Homo sapiens mRNA for KIAA0731 protein, partial cd	718
s//3.5e-37:509:65//Hs.6214:AB018274	F-NT2RM4000395//Nitric oxide synthase 2A (inducible, hepatocytes)/
F-NT2RM2002014//Homo sapiens mRNA for CRM1 protein, complete cds//	0.63:166:65//Hs.946:X73029
0.79:429:58//Hs.79090:D89729	F-NT2RM4000414//Homo sapiens XYLB mRNA for xylulokinase, complete
F-NT2RM2002030//Glutamine-fructose-6-phosphate transaminase//9.0e-	cds//4.9e-17:114:94//Hs.137580:AB015046
89:822:73//Hs.1674:M90516	F-NT2RM4000421
F-NT2RM2002049//ESTs//0.99:109:71//Hs.19303:AA928427	F-NT2RM4000425//Homo sapiens mRNA for KIAA0594 protein, partial cd
F-NT2RM2002055//ESTs//1.1e-91:453:98//Hs.158370:AI382154	s//1.1e-42:432:74//Hs.154872:AB011166
F-NT2RM2002080//ESTs//6.1e-75:302:96//Hs.153471:AI198377	F-NT2RM4000433//Colony stimulating factor 3 receptor (granulocyte)
F-NT2RM2002091//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.69:293:58//	//0.023:543:58//Hs.2175:M59820
Hs.89631:U48508	F-NT2RM4000457
F-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase,	F-NT2RM4000471//Human transcriptional corepressor hKAP1/TIF1B mRN
partial//2.5e-165:776:98//Hs.99423:AJ010840	A, complete cds//0.060:178:63//Hs.66369:U95040
F-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 prot	F-NT2RM4000486//ESTs//9.2e-48:237:99//Hs.160685:A1280004
ein (GAC1) mRNA, complete cds//7.6e-145:684:98//Hs.26312:AF030435	F-NT2RM4000496//ESTs//0.069:252:61//Hs.155958:AA573632
F-NT2RM2002128	F-NT2RM4000511//EST//0.92:191:58//Hs.61517:AA028915
F-NT2RM2002142//ESTs//0.0031:183:66//Hs.144505:AA757274	F-NT2RM4000514
F-NT2RM2002145//Homo sapiens erythroblast macrophage protein EMP m	F-NT2RM4000515//ESTs//7.3e-93:450:98//Hs.120975:AA034409
RNA, complete cds//1.4e-144:800:92//Hs.20815:AF084928	F-NT2RM4000520//ESTs//0.13:183:65//Hs.144828:A121305
F-NT2RM2002178//Homo sapiens mRNA for KIAA0467 protein, partial cd	F-NT2RM4000531//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4
s//1.7e-165:787:97//Hs.11147:AB007936	[Mus musculus]//1.8e-153:756:96//Hs.125870:A1364967
F-NT2RM2002580//Keratin 10 (epidermolytic hyperkeratosis; keratosis	F-NT2RM4000532//ESTs//7.7e-43:388:78//Hs.105665:H78907
s palmaris et plantaris)//0.064:291:61//Hs.99936:X14487	F-NT2RM4000534
F-NT2RM4000024//RNA polymerase II polypeptide B (140 kD)//8.0e-10:	F-NT2RM4000585
610:59//Hs.148027:X63563	F-NT2RM4000590//Homo sapiens mRNA for KIAA0469 protein, complete c
F-NT2RM4000027//ESTs//1.6e-64:352:94//Hs.21331:H93074	ds//1.2e-19:593:62//Hs.7764:AB007938
F-NT2RM4000030//ESTs//1.0:115:63//Hs.131055:AI391464	F-NT2RM4000595//ESTs, Highly similar to HYPOTHETICAL 54.9 KD PROT
F-NT2RM4000046//ESTs//2.6e-09:207:65//Hs.143533:AI094674	EIN CO2F5.7 IN CHROMOSOME III [Caenorhabditis elegans]//3.1e-104:5
F-NT2RM4000061//EST//0.89:207:60//Hs.98445:AI038511	32:96//Hs.6092:T75227
F-NT2RM4000085//ESTs, Weakly similar to The KIAA0134 gene product	F-NT2RM4000603//Human mRNA for KIAA0392 gene, partial cds//1.7e-1
is related to human RNA helicase A. [H.sapiens]//1.6e-30:369:70//H	5:305:68//Hs.40100:AB002390
s.114623:AI204280	F-NT2RM4000611//EST//0.76:268:58//Hs.150031:AI292068
F-NT2RM4000086	F-NT2RM4000616
F-NT2RM4000104//Homo sapiens chromosome 16 zinc finger protein ZNF	F-NT2RM4000674
210 (ZNF210) mRNA, complete cds//1.3e-24:345:69//Hs.13128:AF060865	F-NT2RM4000689
F-NT2RM4000139	F-NT2RM4000698//Apolipoprotein E//1.0:290:59//Hs.76260:M12529

【0866】

【表565】

F-NT2RM4000700	9:356:59//Hs.26971:AC003003
F-NT2RM4000712//Homo sapiens ubiquitin hydrolyzing enzyme 1 (UBH1) mRNA, partial cds//3.5e-91:744:77//Hs.42400:AF022789	F-NT2RM4001313//H. sapiens mRNA for phosphatidylinositol 3-kinase//8.0e-79:474:89//Hs.32971:Z46973
F-NT2RM4000717//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//2.6e-163:771:97//Hs.6823:W18181	F-NT2RM4001316//ESTs//1.2e-14:126:84//Hs.154344:AA258335
F-NT2RM4000733//PUTATIVE TACHYKININ RECEPTOR//0.70:257:60//Hs.957:W84605	F-NT2RM4001320//Human mRNA for Neuroblastoma, complete cds//3.6e-4:3:642:66//Hs.87435:D89016
F-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cd s//1.2e-159:743:98//Hs.137168:AB018303	F-NT2RM4001340//EST//0.40:135:70//Hs.161198:A1418988
F-NT2RM4000741	F-NT2RM4001344//ESTs, Highly similar to HYPOTHETICAL GTP-BINDING PROTEIN IN PM140-PAC2 INTERGENIC REGION [Saccharomyces cerevisiae]//0.0096:284:58//Hs.120997:R56714
F-NT2RM4000751//ESTs, Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//1.1e-75:388:96//Hs.112361:R99396	F-NT2RM4001347//ESTs, Weakly similar to weakly similar to ANK repe at region of Fowlpox virus BamHI-orf7 protein [C.elegans]//3.7e-5:2:252:100//Hs.15301:AA167818
F-NT2RM4000764//ESTs//3.8e-104:539:95//Hs.24739:H67815	F-NT2RM4001371//EST//0.52:262:59//Hs.145991:A1277656
F-NT2RM4000778//ESTs//1.5e-85:419:97//Hs.99838:AA204731	F-NT2RM4001382//Homo sapiens RanBP7/importin 7 mRNA, complete cds//7.2e-169:790:98//Hs.5151:AF098799
F-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete c ds//1.8e-173:810:98//Hs.18586:AB007920	F-NT2RM4001384
F-NT2RM4000787//EST//0.011:182:65//Hs.159928:AA969186	F-NT2RM4001410//ESTs//1.1e-47:290:91//Hs.72447:AA160575
F-NT2RM4000790//Homo sapiens chromosome 19, cosmid R27216//4.5e-15:6:736:98//Hs.25817:ACD05306	F-NT2RM4001411//Homo sapiens mRNA for APS, complete cds//2.5e-23:4:75:64//Hs.105052:AB000520
F-NT2RM4000795//ESTs, Highly similar to LIVER CARBOXYLESTERASE PR ECURSOR [Homo sapiens]//6.7e-19:160:80//Hs.124902:A1337820	F-NT2RM4001412
F-NT2RM4000796//Human K+ channel subunit gene, complete cds//0.96:292:62//Hs.124212:M64676	F-NT2RM4001414//ESTs, Moderately similar to F18547_1 [H.sapiens]//5.2e-18:133:87//Hs.28209:A1073817
F-NT2RM4000798//ESTs//1.9e-34:271:82//Hs.128203:AA972301	F-NT2RM4001437//Human mRNA for KIAA0118 gene, partial cds//2.5e-4:2:611:70//Hs.154326:D42087
F-NT2RM4000813//Homo sapiens snRNA activating protein complex 190k D subunit (SNAP190) mRNA, complete cds//0.052:238:64//Hs.113265:AF 032387	F-NT2RM4001444
F-NT2RM4000820//ESTs//0.053:274:61//Hs.23748:H16568	F-NT2RM4001454//ESTs//3.9e-31:169:96//Hs.117982:AA644658
F-NT2RM4000833	F-NT2RM4001455//ESTs//0.0054:48:100//Hs.14920:AA910914
F-NT2RM4000848//Human mRNA for KIAA0324 gene, partial cds//0.97:37:4:61//Hs.7841:AB002322	F-NT2RM4001483//ESTs, Weakly similar to ZINC FINGER PROTEIN ZFP-36 [H.sapiens]//1.1e-71:313:99//Hs.163754:AA587784
F-NT2RM4000852//EST//1.0:222:60//Hs.120354:AA718934	F-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete c ds//3.9e-157:724:99//Hs.153121:AB014585
F-NT2RM4000855//ESTs, Highly similar to RAS-RELATED C3 BOTULINUM TOXIN SUBSTRATE 2 [Homo sapiens]//4.4e-29:164:95//Hs.115095:A13929 43	F-NT2RM4001519//ESTs//0.66:264:59//Hs.139891:AA553619
F-NT2RM4000887	F-NT2RM4001522//ESTs, Weakly similar to D9481.12 gene product [S.c erevisiae]//1.3e-114:536:99//Hs.88820:AA456247
F-NT2RM4000895//Homo sapiens HuUAP1 mRNA for UDP-N-acetylglucosami ne pyrophosphorylase, complete cds//6.8e-22:407:64//Hs.21293:AB011 004	F-NT2RM4001557
F-NT2RM4000950	F-NT2RM4001565//ESTs//1.7e-107:509:99//Hs.146139:AA731487
F-NT2RM4000971//ESTs//3.6e-27:142:100//Hs.130912:A1014546	F-NT2RM4001566//Human phosphatidylinositol 3-kinase catalytic subu nit p110delta mRNA, complete cds//1.0:255:60//Hs.14207:U86453
F-NT2RM4000979//Homo sapiens KIAA0415 mRNA, complete cds//3.7e-53: 571:77//Hs.7289:AB007875	F-NT2RM4001569//ESTs//1.4e-86:417:98//Hs.153044:A1198859
F-NT2RM4000996//Zinc finger protein 3 (A8-51)//8.7e-34:381:67//Hs. 2481:X78926	F-NT2RM4001582
F-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cd s//1.6e-171:803:98//Hs.19542:AB018272	F-NT2RM4001592//EST//0.61:142:64//Hs.162900:AA664566
F-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cd s//1.1e-126:584:99//Hs.15711:AB014539	F-NT2RM4001594//Homo sapiens mRNA for KIAA0522 protein, partial cd s//0.0072:484:60//Hs.129892:AB011094
F-NT2RM4001032//Homo sapiens mRNA for KIAA0711 protein, complete c ds//4.8e-05:469:58//Hs.5333:AB018254	F-NT2RM4001597//ESTs, Moderately similar to red-1 [M.musculus]//2. 3e-72:387:95//Hs.114722:AA448077
F-NT2RM4001047//ESTs, Moderately similar to M025 PROTEIN [M.muscul us]//7.0e-56:340:92//Hs.87310:A1247543	F-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete c ds//1.1e-163:750:99//Hs.23255:AB018334
F-NT2RM4001054//HIGH AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR I " A FORM" PRECURSOR//0.79:142:69//Hs.77424:M63835	F-NT2RM4001611//ESTs, Weakly similar to F25H9.6 [C.elegans]//8.6e- 05:91:79//Hs.24647:W19739
F-NT2RM4001084	F-NT2RM4001629//ESTs, Moderately similar to 55 KD ERYTHROCYTE MEM BRANE PROTEIN [Homo sapiens]//0.0042:153:68//Hs.114832:A1147946
F-NT2RM4001092//Human mRNA for KIAA0050 gene, complete cds//0.045: 235:62//Hs.108947:D30758	F-NT2RM4001650//Human mRNA for KIAA0341 gene, partial cds//0.95:32 8:60//Hs.101761:AB002339
F-NT2RM4001116	F-NT2RM4001662//Human mRNA for KIAA0322 gene, partial cds//8.3e-8 3:449:93//Hs.153685:AB002320
F-NT2RM4001140//Human engrailed protein (EN2) gene, 5' end//0.0002 9:225:61//Hs.134989:L12701	F-NT2RM4001666//ESTs//2.1e-11:78:96//Hs.152446:AA555323
F-NT2RM4001151//ESTs//1.1e-07:190:65//Hs.151691:AA443730	F-NT2RM4001682//EST//0.027:145:70//Hs.133253:A1052638
F-NT2RM4001155//ESTs//2.2e-12:181:74//Hs.128826:A1004145	F-NT2RM4001710//ESTs//0.098:140:62//Hs.5796:AA767384
F-NT2RM4001160//EST//0.83:166:61//Hs.117051:AA677351	F-NT2RM4001714//Human mRNA for KIAA0202 gene, partial cds//2.2e-8 6:748:74//Hs.80712:D86957
F-NT2RM4001187	F-NT2RM4001715//ESTs//1.3e-104:490:99//Hs.127336:A1332905
F-NT2RM4001191//ESTs//1.3e-42:248:93//Hs.13475:R18220	F-NT2RM4001731//Human involucrin mRNA//0.23:432:59//Hs.157091:M139 03
F-NT2RM4001200//Zinc finger protein 10 (K0X 1)//4.0e-68:799:69//H s.2479:X78933	F-NT2RM4001741//Human mRNA for KIAA0320 gene, partial cds//6.9e-8 0:737:73//Hs.150443:AB002318
F-NT2RM4001203//Homo sapiens rab3-GAP regulatory domain mRNA, comp late cds//1.4e-153:707:99//Hs.14934:AF004828	F-NT2RM4001746//H. sapiens NF-H gene, exon 1 (and joined CDS)//2.1 e-07:418:61//Hs.75735:X15306
F-NT2RM4001204//ESTs, Moderately similar to HYPOTHETICAL 59.1 KD PROTEIN ZK637.1 IN CHROMOSOME III [Caenorhabditis elegans]//0.19:2 91:62//Hs.31582:AA877205	F-NT2RM4001754//ESTs, Weakly similar to RETROVIRUS-RELATED POL POL YPROTEIN [Mus musculus]//2.0e-27:205:83//Hs.110601:AA206719
F-NT2RM4001217//Homo sapiens nuclear matrix protein NRP/B (NRPB) m RNA, complete cds//7.0e-63:715:70//Hs.104925:AF059611	F-NT2RM4001758//H. sapiens mRNA for serine/threonine protein kinase ENK//2.1e-86:729:75//Hs.157199:X97630
F-NT2RM4001256//ESTs, Weakly similar to probable CBP3 protein homo log [C.elegans]//1.1e-67:208:96//Hs.26676:AA033997	F-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cd s//7.4e-175:803:99//Hs.39871:AB018270
F-NT2RM4001258//Homo sapiens mRNA for KIAA0481 protein, complete c ds//0.0019:435:59//Hs.6360:AB007950	F-NT2RM4001783//ESTs, Weakly similar to T1208.1 [C.elegans]//3.1e- 71:376:95//Hs.108396:AA160677
F-NT2RM4001309//Human Chromosome 16 BAC clone C17987SK-254P9//0.01	F-NT2RM4001810//Homo sapiens centrosomal Nek2-associated protein 1 (C-NAP1) mRNA, complete cds//0.99:446:58//Hs.27910:AF049105
	F-NT2RM4001813//Homo sapiens clone 24820 mRNA sequence//6.6e-14:24 9:70//Hs.146312:AF070547

【0867】

【表566】

F-NT2RM4001819//Cell division cycle 2-like 1 (PITSLRE proteins)//1.4e-35:195:95//Hs.963:M37712	F-NT2RM4002256//ESTs//7.5e-28:358:74//Hs.13356:A1205764
F-NT2RM4001823//ESTs. Weakly similar to ZINC FINGER PROTEIN 91 [H. sapiens]//2.3e-40:252:90//Hs.119294:A1379442	F-NT2RM4002266//Human kinase Myt1 (Myt1) mRNA, complete cds//0.73:502:57//Hs.77783:AF014118
F-NT2RM4001828//Zinc finger protein 157 (H2F22)//1.8e-75:688:72//Hs.89897:U28687	F-NT2RM4002278//EST//0.33:138:63//Hs.144096:A1032180
F-NT2RM4001835//NUCLEOBINDIN PRECURSOR//0.0022:588:59//Hs.953:M96824	F-NT2RM4002281
F-NT2RM4001841//ESTs//0.86:156:67//Hs.146276:A1214204	F-NT2RM4002287//ESTs//0.00037:55:98//Hs.11134:T62979
F-NT2RM4001842//ESTs//0.20:191:62//Hs.107657:AA126814	F-NT2RM4002294//Human mRNA for KIAA0281 gene, complete cds//6.7e-50:511:72//Hs.31463:D87457
F-NT2RM4001856	F-NT2RM4002301
F-NT2RM4001858//Human putative cerebral cortex transcriptional regulator T-Brain-1 (Tbr-1) mRNA, complete cds//8.0e-10:244:66//Hs.22138:U49250	F-NT2RM4002323//ESTs//3.6e-09:105:87//Hs.131737:A1343331
F-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CA LC//2.3e-150:704:98//Hs.61628:Y17711	F-NT2RM4002339
F-NT2RM4001876//Human mRNA for KIAA0231 gene, partial cds//9.1e-44:621:66//Hs.7938:D86984	F-NT2RM4002344//EST//0.16:166:64//Hs.128600:AA906454
F-NT2RM4001880	F-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//9.1e-151:708:98//Hs.26163:AB014549
F-NT2RM4001905//ESTs//7.5e-11:137:75//Hs.86950:A1204212	F-NT2RM4002374//Homo sapiens mRNA for KIAA0720 protein, partial cds//0.0040:303:63//Hs.23741:AB018263
F-NT2RM4001922//ESTs//2.5e-51:291:93//Hs.26660:A1312633	F-NT2RM4002383//ESTs//8.0e-16:153:78//Hs.155243:N70293
F-NT2RM4001930//Homo sapiens mRNA for putative glucosyltransferase, partial cds//0.98:359:57//Hs.155356:AJ224875	F-NT2RM4002390
F-NT2RM4001938	F-NT2RM4002398
F-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//3.6e-172:808:98//Hs.118631:AF098162	F-NT2RM4002409
F-NT2RM4001953//Human mRNA for KIAA0118 gene, partial cds//5.0e-54:362:83//Hs.154326:D42087	F-NT2RM4002438//ESTs. Weakly similar to probable CBP3 protein homolog [C. elegans]//1.1e-55:282:96//Hs.26676:AA033997
F-NT2RM4001965//ESTs. Weakly similar to KIAA0157 gene product is novel. [H. sapiens]//1.8e-65:337:96//Hs.130135:AA905493	F-NT2RM4002446//Homo sapiens clone 24574 mRNA sequence//0.59:339:60//Hs.18686:AF052151
F-NT2RM4001969//ESTs//0.00024:261:63//Hs.157579:A1312862	F-NT2RM4002452
F-NT2RM4001979//Homo sapiens mRNA for KIAA0798 protein, complete cds//3.2e-63:527:76//Hs.159277:AB018341	F-NT2RM4002457//Homo sapiens mRNA for epiregulin, complete cds//3.2e-25:228:81//Hs.115263:D30783
F-NT2RM4001984//EST//7.1e-05:235:61//Hs.105444:AA508082	F-NT2RM4002460//EST//1.0:142:65//Hs.145370:A1252780
F-NT2RM4001987//Homo sapiens mRNA for KIAA0467 protein, partial cds//0.73:181:65//Hs.11147:AB007936	F-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds//8.9e-165:777:98//Hs.8765:AF083255
F-NT2RM4002013//ESTs//0.97:185:63//Hs.103345:A1302271	F-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//7.3e-95:464:97//Hs.94781:AB014591
F-NT2RM4002018//ESTs//2.5e-76:398:94//Hs.119544:T95601	F-NT2RM4002493
F-NT2RM4002034	F-NT2RM4002499//ESTs//1.3e-44:653:67//Hs.23790:N99347
F-NT2RM4002044//ESTs//9.6e-83:410:97//Hs.128162:AA815048	F-NT2RM4002504//Small inducible cytokine A5 (RANTES)//4.3e-30:225:83//Hs.155464:AF088219
F-NT2RM4002054//EST//8.5e-12:176:71//Hs.137181:R56912	F-NT2RM4002527//Human pre-B cell enhancing factor (PBEF) mRNA, complete cds//0.99:290:60//Hs.154968:U02020
F-NT2RM4002055//Homo sapiens mRNA for KIAA0640 protein, partial cds//3.3e-173:803:98//Hs.153026:AB014540	F-NT2RM4002532//Human mRNA for KIAA0238 gene, partial cds//1.0:232:61//Hs.82042:D87075
F-NT2RM4002062//ESTs. Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]//7.0e-94:396:94//Hs.59346:A1126802	F-NT2RM4002534//Homo sapiens angiotensin/vasopressin receptor AII/AVP mRNA, complete cds//1.0:100:70//Hs.159483:AF054176
F-NT2RM4002063	F-NT2RM4002558//Homo sapiens amphiphysin II mRNA, complete cds//0.17:393:61//Hs.6619:U84004
F-NT2RM4002066//Homo sapiens OPA-containing protein mRNA, complete cds//1.1e-74:889:69//Hs.85313:AF071309	F-NT2RM4002565//Homo sapiens mRNA for Asparaginyl tRNA Synthetase, complete cds//1.0:226:60//Hs.84043:D84273
F-NT2RM4002067//ESTs//2.3e-34:455:69//Hs.118273:AA626040	F-NT2RM4002567//ESTs. Weakly similar to C17G10.1 [C. elegans]//3.3e-88:484:93//Hs.105837:AA536054
F-NT2RM4002073//Insulin-like growth factor binding protein 2//3.2e-10:470:61//Hs.162:X16302	F-NT2RM4002571//ESTs. Weakly similar to UDP-GalNAc:polypeptide N-acetylglucosaminyltransferase [H. sapiens]//0.059:121:70//Hs.155413:AA429394
F-NT2RM4002075//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//2.9e-24:588:61//Hs.122967:AF059569	F-NT2RM4002593//ESTs//1.0e-15:103:95//Hs.108920:W28151
F-NT2RM4002093//Polypyrimidine tract binding protein (hnRNP I) (alternative products)//9.2e-34:532:65//Hs.146459:X66975	F-NT2RM4002594//Homo sapiens 26S proteasome regulatory subunit (SU G2) mRNA, complete cds//1.0e-06:499:59//Hs.79357:D78275
F-NT2RM4002109//Homo sapiens mitotic centromere-associated kinesin mRNA, complete cds//0.99:408:62//Hs.69360:U63743	F-NT2RM4002623//ESTs//1.2e-11:92:92//Hs.164046:T97402
F-NT2RM4002128//Homo sapiens mRNA for KIAA0642 protein, partial cds//0.93:202:63//Hs.8152:AB014542	F-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds//2.0e-102:746:81//Hs.3628:AB014587
F-NT2RM4002140//Human p300 protein mRNA, complete cds//0.99:320:59//Hs.25272:U01877	F-NT2RP1000035//Homo sapiens mRNA for NS1-binding protein (NS1-BP)//3.7e-155:747:96//Hs.159597:AJ012449
F-NT2RM4002145//CARBOXYPEPTIDASE N 83 KD CHAIN//2.7e-06:388:59//Hs.73858:J05158	F-NT2RP1000040//ESTs//1.3e-58:338:92//Hs.17534:H16907
F-NT2RM4002146//ESTs. Highly similar to similar to mago nashi [H. sapiens]//1.6e-135:646:97//Hs.104650:A1037879	F-NT2RP1000063//ESTs//0.0013:72:83//Hs.108196:W81647
F-NT2RM4002161//Homo sapiens laforin (EPN2A) mRNA, partial cds//1.4e-150:763:95//Hs.22464:AF084535	F-NT2RP1000086//Human mRNA for KIAA0360 gene, partial cds//5.4e-185:548:91//Hs.79971:X98834
F-NT2RM4002174	F-NT2RP1000101//Homo sapiens hook2 protein (HOOK2) mRNA, complete cds//0.33:247:61//Hs.30792:AF044924
F-NT2RM4002189//Mucin 2, intestinal/tracheal//0.087:298:61//Hs.315:L21998	F-NT2RP1000111
F-NT2RM4002194//Human semaphorin III family homolog mRNA, complete cds//7.3e-11:454:60//Hs.32981:U38276	F-NT2RP1000112//TTK protein kinase//3.2e-40:324:81//Hs.2052:M86699
F-NT2RM4002205//EST//2.6e-21:270:71//Hs.120013:AA707454	F-NT2RP1000124//ESTs//2.4e-42:268:89//Hs.146078:A1084025
F-NT2RM4002213//Homo sapiens mRNA for KIAA0610 protein, partial cds//0.52:313:61//Hs.118087:AB011182	F-NT2RP1000130//ESTs. Moderately similar to HEPATOMA-DERIVED GROWTH FACTOR [H. sapiens]//1.4e-71:382:94//Hs.127842:W38901
F-NT2RM4002226//ESTs. Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]//8.4e-125:588:98//Hs.23900:U82984	F-NT2RP1000163//Homo sapiens cell cycle progression 2 protein (CPR 2) mRNA, complete cds//2.1e-06:77:90//Hs.3760:AF011792
F-NT2RM4002251//ESTs//1.0:77:74//Hs.155135:AA910966	F-NT2RP1000170//EST//0.68:130:63//Hs.146994:A1184430
	F-NT2RP1000174//Homo sapiens clone 24432 mRNA sequence//8.3e-140:679:97//Hs.78019:AF070535
	F-NT2RP1000191//ESTs//1.3e-71:405:93//Hs.24054:N46499
	F-NT2RP1000202//H. sapiens mRNA for cytokine inducible nuclear protein//2.0e-05:591:58//Hs.74019:X83703
	F-NT2RP1000243
	F-NT2RP1000259

【0868】

【表567】

F-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//5.4e-109:528:97//Hs.4214:AF067730
 F-NT2RP1000324//ESTs//3.4e-98:499:96//Hs.42530:N41661
 F-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds//1.3e-148:693:98//Hs.31584:AF053551
 F-NT2RP1000333//Homo sapiens monocyte/macrophage Ig-related receptor MIR-10 (MIR ci-10) mRNA, complete cds//0.28:328:60//Hs.22405:AF004231
 F-NT2RP1000348//Human plectin (PLEC1) mRNA, complete cds//0.018:337:62//Hs.79706:U53204
 F-NT2RP1000357
 F-NT2RP1000358//DYNAMIN-1//0.96:273:59//Hs.126:L07807
 F-NT2RP1000363//Homo sapiens mRNA for KIAA0638 protein, partial cds//3.2e-126:497:86//Hs.77864:AB014538
 F-NT2RP1000376//Homo sapiens calcium-independent phospholipase A2 mRNA, complete cds//5.9e-178:877:96//Hs.120360:AF064594
 F-NT2RP1000409//ESTs//5.4e-59:415:83//Hs.140578:AA828031
 F-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds//3.0e-179:710:98//Hs.21862:AB011159
 F-NT2RP1000416//ESTs. Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//7.3e-177:857:97//Hs.6823:W18181
 F-NT2RP1000418//Homo sapiens calcium-activated potassium channel (KCNK3) mRNA, complete cds//0.46:222:60//Hs.89230:AF031815
 F-NT2RP1000439//EST//0.98:339:56//Hs.137377:AA101603
 F-NT2RP1000443//Human SLP-76 associated protein mRNA, complete cds//1.0:356:59//Hs.58435:AF001862
 F-NT2RP1000460
 F-NT2RP1000470//Human DNA from chromosome 19-specific cosmid R2709 0, genomic sequence//3.7e-134:665:96//Hs.143187:AC002985
 F-NT2RP1000478//Human beta-tubulin class III isotype (beta-3) mRNA, complete cds//6.2e-57:440:80//Hs.159154:U47634
 F-NT2RP1000481//ESTs//4.8e-21:154:87//Hs.17392:AA535102
 F-NT2RP1000493
 F-NT2RP1000513//ESTs//2.2e-71:409:91//Hs.121029:AA480977
 F-NT2RP1000522//Homo sapiens clone DTIP1A11 mRNA, CAG repeat region//0.21:255:62//Hs.98834:U92992
 F-NT2RP1000547//H. sapiens mRNA for transmembrane protein rnp24//1.9e-06:337:63//Hs.75914:X92098
 F-NT2RP1000574//Homo sapiens homeobox protein MEIS2 (MEIS2) mRNA, partial cds//1.4e-82:295:92//Hs.104105:AF017418
 F-NT2RP1000577//Human sialoprotein mRNA, complete cds//0.014:235:65//Hs.121552:J05213
 F-NT2RP1000581//VON WILLEBRAND FACTOR PRECURSOR//1.6e-33:223:89//Hs.110802:X04385
 F-NT2RP1000609//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC2 69730) containing the hFEN1 gene//2.2e-49:506:73//Hs.132898:AC004770
 F-NT2RP1000629//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//3.6e-19:556:62//Hs.152936:D63475
 F-NT2RP1000630
 F-NT2RP1000677//Human breast tumor autoantigen mRNA, complete sequence//2.4e-05:189:59//Hs.3844:U24576
 F-NT2RP1000688//ESTs. Weakly similar to T06E6.d [C.elegans]//2.5e-43:232:95//Hs.3487:AA425553
 F-NT2RP1000695//ESTs. Weakly similar to C27F2.7 gene product [C.elegans]//9.2e-53:312:90//Hs.7049:A1141736
 F-NT2RP1000701//Myogenic factor 3//0.81:186:63//Hs.2834:AF027148
 F-NT2RP1000721//Homo sapiens mRNA for repressor protein, partial cds//4.0e-33:278:78//Hs.58167:D30612
 F-NT2RP1000730//ESTs. Weakly similar to putative p150 [H.sapiens]//6.2e-40:297:84//Hs.18122:A1338045
 F-NT2RP1000733//G1 to S phase transition 1//1.4e-31:286:78//Hs.2707:X17644
 F-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds//2.6e-123:604:96//Hs.21771:AF101434
 F-NT2RP1000746
 F-NT2RP1000767
 F-NT2RP1000782//Human globin gene//3.6e-21:140:91//Hs.100090:M69023
 F-NT2RP1000796//H. sapiens mRNA for ROX protein//0.17:404:57//Hs.25497:X96401
 F-NT2RP1000825//Human DNA sequence from PAC 127B20 on chromosome 2 2q11.2-qter, contains gene for GTPase-activating protein similar to rhoGAP protein, ribosomal protein L6 pseudogene, ESTs and CA repeat//2.7e-23:147:91//Hs.102336:Z83838
 F-NT2RP1000833//Homo sapiens cAMP phosphodiesterase A1 (PDE9A) mRNA, complete cds//5.4e-143:424:96//Hs.18953:AF067223
 F-NT2RP1000834//ESTs//0.18:280:60//Hs.157215:A1332903
 F-NT2RP1000836//EST//0.60:103:66//Hs.145708:A1267990
 F-NT2RP1000846//EST//1.2e-15:322:65//Hs.149925:A1288838
 F-NT2RP1000851//ESTs//6.1e-96:459:98//Hs.121586:AA423875
 F-NT2RP1000856//Human globin gene//6.7e-22:140:91//Hs.100090:M69023
 F-NT2RP1000860//Homo sapiens KL04P mRNA, complete cds//2.2e-107:551:95//Hs.125156:AF064094
 F-NT2RP1000902//EST//1.8e-28:218:85//Hs.145258:A1218683
 F-NT2RP1000915//ESTs//0.8e-11:102:81//Hs.163740:A1248847
 F-NT2RP1000916//ESTs. Weakly similar to coded for by C. elegans CD NA cm04e9 [C.elegans]//2.2e-27:159:94//Hs.122153:AA780270
 F-NT2RP1000943//Human hSIAH2 mRNA, complete cds//0.45:130:68//Hs.20191:U76248
 F-NT2RP1000944//EST//0.99:116:63//Hs.116633:AA668400
 F-NT2RP1000947//Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds//2.7e-26:185:87//Hs.108332:U39317
 F-NT2RP1000954//Homo sapiens BACH1 mRNA, complete cds//0.81:329:56//Hs.154276:AB002803
 F-NT2RP1000958//ESTs//1.3e-20:129:92//Hs.163740:A1248847
 F-NT2RP1000959//Ribosomal protein, large, P0//0.36:76:73//Hs.73742:M17885
 F-NT2RP1000966//NUCLEOLIN//1.2e-72:353:98//Hs.79110:M08058
 F-NT2RP1000980//ESTs//1.6e-109:555:96//Hs.84429:M28866
 F-NT2RP1000988//Human chromosome 3p21.1 gene sequence//2.6e-73:665:80//Hs.82837:L13435
 F-NT2RP1001011
 F-NT2RP1001013//ESTs//3.4e-40:393:74//Hs.120206:A1089163
 F-NT2RP1001014
 F-NT2RP1001033//Tubulin, gamma polypeptide//0.00041:313:59//Hs.150785:M61764
 F-NT2RP1001073//Glucocorticoid receptor//1.0:204:61//Hs.75772:M10901
 F-NT2RP1001079//ESTs//1.0:174:62//Hs.158209:A1360531
 F-NT2RP1001080//Homo sapiens forkhead protein (FKHL1) mRNA, complete cds//0.57:215:64//Hs.14845:AF032886
 F-NT2RP1001113//ESTs. Weakly similar to coded for by C. elegans CD NA CEES82F [C.elegans]//1.4e-65:293:95//Hs.32751:H38087
 F-NT2RP1001173
 F-NT2RP1001177//Homo sapiens histone macroH2A1.2 mRNA, complete cds//6.1e-26:259:74//Hs.75258:AF054174
 F-NT2RP1001185//EST//1.4e-27:266:77//Hs.122245:AA781524
 F-NT2RP1001199//ESTs//0.97:75:73//Hs.131498:A1022150
 F-NT2RP1001247//Human endometrial bleeding associated factor mRNA, complete cds//1.6e-19:120:95//Hs.25195:U81523
 F-NT2RP1001248//ESTs//3.0e-21:143:93//Hs.157243:A1337094
 F-NT2RP1001253//PUTATIVE GLUCOSAMINE-6-PHOSPHATE ISOMERASE//1.2e-89:344:93//Hs.3090:AJ002231
 F-NT2RP1001286//H. sapiens mRNA for adenosine triphosphatase, calcium//0.026:392:57//Hs.5541:Y15724
 F-NT2RP1001294
 F-NT2RP1001302
 F-NT2RP1001310//Homo sapiens creatine transporter mRNA, complete cds//3.6e-07:379:61//Hs.154503:U36341
 F-NT2RP1001311//ESTs//9.5e-73:403:93//Hs.24739:M67815
 F-NT2RP1001313//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC2 69730) containing the hFEN1 gene//3.1e-87:437:97//Hs.132898:AC004770
 F-NT2RP1001361//ESTs. Highly similar to NADH-UBIQUINONE OXIDOREDUCTASE SUBUNIT B14.5B [Bos taurus]//6.8e-101:480:94//Hs.75017:AA166853
 F-NT2RP1001385//EST//0.86:127:65//Hs.156304:A1336859
 F-NT2RP1001395//Homo sapiens stannin mRNA, complete cds//0.75:355:58//Hs.76691:AF070673
 F-NT2RP1001410//Thromboxane A2 receptor//1.0:157:63//Hs.89887:D38081
 F-NT2RP1001424//ESTs//5.3e-20:118:95//Hs.159792:R60700
 F-NT2RP1001432//ESTs//5.3e-20:118:95//Hs.159792:R60700
 F-NT2RP1001449//Homo sapiens clone 24733 mRNA sequence//5.7e-86:422:97//Hs.21970:AF052149
 F-NT2RP1001457//H. sapiens DAP-kinase mRNA//0.40:231:61//Hs.153924:X76104
 F-NT2RP1001466
 F-NT2RP1001475//ESTs//1.2e-98:495:97//Hs.14347:AA287742
 F-NT2RP1001482
 F-NT2RP1001494
 F-NT2RP1001543//ESTs//1.2e-38:207:98//Hs.131063:A1016400
 F-NT2RP1001546//Homo sapiens mRNA for DAP-1 beta, complete cds//0.00077:254:64//Hs.75814:AB000277
 F-NT2RP1001569
 F-NT2RP1001616//Homo sapiens Tax interaction protein 1 mRNA, parti

【0869】

【表568】

al cds//2.5e-41:496:74//Hs.12956:U90913	F-NT2RP2000289
F-NT2RP1001665//ESTs//9.4e-58:311:96//Hs.127391:AA954420	F-NT2RP2000297//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//4.2e-60:744:70//Hs.37138:U35376
F-NT2RP2000001//Homo sapiens clone 617 unknown mRNA, complete sequence//4.7e-137:685:96//Hs.93677:AF091081	F-NT2RP2000298//ESTs//6.1e-46:322:85//Hs.159490:A1123467
F-NT2RP2000006//ESTs. Weakly similar to 80035.14 [C.elegans]//8.2e-47:300:89//Hs.6473:AA853955	F-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds//4.3e-13:140:80//Hs.58218:U82381
F-NT2RP2000007//Human mRNA for KIAA0392 gene, partial cds//1.1e-15:241:68//Hs.40100:AB002390	F-NT2RP2000327//ESTs//4.3e-18:108:98//Hs.126212:A1417006
F-NT2RP2000008//Human mRNA for KIAA0065 gene, partial cds//1.5e-29:526:66//Hs.70617:D31763	F-NT2RP2000328//ESTs//6.3e-88:437:96//Hs.127336:A1332905
F-NT2RP2000027//ESTs. Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//2.0e-26:214:82//Hs.140385:AA773359	F-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//6.6e-41:607:66//Hs.101642:X60673
F-NT2RP2000032//ESTs//0.91:368:57//Hs.131209:A1038867	F-NT2RP2000337//Homo sapiens neurocan (CSPG3) mRNA, complete cds//0.96:126:69//Hs.153706:AF026547
F-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//6.1e-78:383:97//Hs.8309:AB018290	F-NT2RP2000346//Homo sapiens apoptosis associated protein (CADD34) mRNA, complete cds//1.2e-130:627:97//Hs.76556:U83981
F-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//7.8e-97:467:97//Hs.6216:AF061749	F-NT2RP2000369//Homo sapiens mRNA for KIAA0630 protein, partial cds//0.56:464:57//Hs.12259:AB014530
F-NT2RP2000054//HOMEOBOX/POU DOMAIN PROTEIN RDC-1//1.0:110:70//Hs.74095:L20433	F-NT2RP2000412//ESTs//1.0:214:60//Hs.91226:AA649047
F-NT2RP2000056//Human HPT epsilon mRNA for protein tyrosine phosphatase epsilon//1.2e-27:146:100//Hs.155991:X54134	F-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds//1.6e-67:375:93//Hs.808:L28010
F-NT2RP2000067//Human DNA sequence from clone 1052M9 on chromosome Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome) (DSHP), part of a 60S Acid Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DDC4 LIKE gene. Contains ESTs and GSSs//8.1e-41:767:61//Hs.23796:AL022718	F-NT2RP2000420//ESTs. Moderately similar to zinc finger protein [H. sapiens]//3.9e-75:413:92//Hs.36779:AA626790
F-NT2RP2000070//Homo sapiens chromosome 5, BAC clone 203o13 (LBNLH155), complete sequence//6.5e-08:344:58//Hs.159402:AC005609	F-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//6.7e-128:609:96//Hs.5819:AF102265
F-NT2RP2000076//H. sapiens mRNA for TFIIA//0.00023:356:62//Hs.121686:D14887	F-NT2RP2000438//ESTs//1.3e-05:50:98//Hs.156532:AA913381
F-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds//6.8e-79:278:97//Hs.54877:AF050078	F-NT2RP2000448//EST//1.1e-24:136:98//Hs.160402:A1393918
F-NT2RP2000079//ESTs//1.2e-36:202:94//Hs.17606:A1279879	F-NT2RP2000459//H. sapiens mRNA for imogen 38//1.9e-22:158:87//Hs.154655:Z68747
F-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//7.1e-160:752:98//Hs.22926:AB018338	F-NT2RP2000498//ESTs//1.0e-17:181:79//Hs.155243:N70293
F-NT2RP2000091	F-NT2RP2000503//ESTs//4.5e-41:205:100//Hs.62751:AA765702
F-NT2RP2000097	F-NT2RP2000510
F-NT2RP2000098//ESTs//0.086:92:69//Hs.159389:A1371963	F-NT2RP2000516
F-NT2RP2000108//Human mRNA for KIAA0392 gene, partial cds//1.4e-18:200:77//Hs.40100:AB002390	F-NT2RP2000523//ESTs. Highly similar to APOLIPROTEIN B mRNA EDITING PROTEIN [Rattus norvegicus]//3.2e-15:167:75//Hs.10984:AA806768
F-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//1.6e-115:551:97//Hs.17706:AB018356	F-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cds//5.6e-38:196:98//Hs.14409:AB011144
F-NT2RP2000120//ESTs. Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [C.elegans]//0.019:72:81//Hs.5268:W22670	F-NT2RP2000617//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)//1.0:242:57//Hs.114001:Z20656
F-NT2RP2000126//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//1.4e-120:607:96//Hs.159273:AF054177	F-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds//4.2e-151:732:97//Hs.7314:AB014514
F-NT2RP2000133//Neuronal pentraxin II//0.00014:401:61//Hs.3281:U29195	F-NT2RP2000644//ESTs//0.035:276:60//Hs.43660:N33174
F-NT2RP2000147//Human clathrin assembly protein 50 (AP50) mRNA, complete cds//2.2e-18:559:60//Hs.152936:D63475	F-NT2RP2000656
F-NT2RP2000153//Homo sapiens splicing factor (CC1.3) mRNA, complete cds//0.33:85:70//Hs.256:L10910	F-NT2RP2000658//ESTs//0.032:281:59//Hs.124853:AA420602
F-NT2RP2000157//ESTs//0.53:75:81//Hs.24885:R49291	F-NT2RP2000668
F-NT2RP2000161//ESTs//2.6e-06:89:84//Hs.21738:A1188190	F-NT2RP2000678//ESTs//2.9e-16:310:65//Hs.126867:A1093453
F-NT2RP2000173	F-NT2RP2000704//ESTs. Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C4.4 IN CHROMOSOME II PRECURSOR [Caenorhabditis elegans]//2.4e-31:233:78//Hs.114905:AA088442
F-NT2RP2000175	F-NT2RP2000710
F-NT2RP2000183//Homo sapiens mRNA for dihydropyrimidinase related protein 4, complete cds//0.0018:324:58//Hs.100058:AB006713	F-NT2RP2000715
F-NT2RP2000195//ESTs. Weakly similar to C37E2.2 [C.elegans]//3.6e-37:233:90//Hs.56750:A1148761	F-NT2RP2000731
F-NT2RP2000205//ESTs//5.6e-58:317:93//Hs.49559:AA401050	F-NT2RP2000758//EST//1.0e-14:199:71//Hs.162409:AA573242
F-NT2RP2000208	F-NT2RP2000764//ESTs. Weakly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//1.6e-74:445:89//Hs.21421:AA911739
F-NT2RP2000224//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds//0.0071:243:61//Hs.143641:AB009462	F-NT2RP2000809//ESTs//1.2e-36:235:89//Hs.154580:N34101
F-NT2RP2000232//EST//0.0087:187:62//Hs.151024:Z39990	F-NT2RP2000812//Homo sapiens pendrin (PDS) mRNA, complete cds//0.22:351:58//Hs.159275:AF030880
F-NT2RP2000233//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.17:342:59//Hs.8546:U97669	F-NT2RP2000814
F-NT2RP2000239//Human mRNA for KIAA0380 gene, complete cds//1.0:227:60//Hs.47822:AB002378	F-NT2RP2000816//Homo sapiens mRNA for KIAA0610 protein, partial cds//1.0:311:61//Hs.118087:AB011182
F-NT2RP2000248//EST//0.49:117:70//Hs.61016:AA019719	F-NT2RP2000819
F-NT2RP2000257//Macrophage stimulating 1 (hepatocyte growth factor-like)//0.51:227:60//Hs.30223:X90846	F-NT2RP2000841//Human mRNA for KIAA0294 gene, complete cds//3.4e-28:390:70//Hs.20695:AB002292
F-NT2RP2000258//ESTs//3.1e-48:261:94//Hs.128230:AA972691	F-NT2RP2000842//Human lysophosphatidic acid receptor homolog mRNA, complete cds//9.5e-29:167:94//Hs.75794:U80811
F-NT2RP2000270//ESTs//2.9e-38:357:75//Hs.140329:AA714011	F-NT2RP2000845//ESTs//1.0e-83:403:98//Hs.156828:A1336850
F-NT2RP2000274//ESTs//1.1e-106:508:98//Hs.47646:AA307599	F-NT2RP2000863//ESTs. Highly similar to HYPOTHETICAL 36.7 KD PROTEIN C2F7.02C IN CHROMOSOME I [Schizosaccharomyces pombe]//6.4e-34:207:92//Hs.135235:A1081880
F-NT2RP2000283//EST//1.0:139:63//Hs.128256:AA972910	F-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete cds//7.7e-142:732:94//Hs.3615:AB018284
F-NT2RP2000288	F-NT2RP2000892//ESTs. Weakly similar to mitogen-activated kinase kinase 5 [H. sapiens]//0.50:189:65//Hs.46146:AA418097
	F-NT2RP2000931//MATRIN 3//1.1e-130:610:98//Hs.78825:AB018266
	F-NT2RP2000932//Homo sapiens BAC clone CS166A23 from Tg21//5.5e-66:326:97//Hs.15144:AC005014
	F-NT2RP2000938//ESTs//1.8e-28:296:75//Hs.22822:H06408
	F-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds//1.9e-113:533:98//Hs.19822:AB018298
	F-NT2RP2000965//ESTs//5.3e-59:328:94//Hs.35575:R96494

【0870】

【表569】

F-NT2RP2000970	5:65//Hs.82201:M55268
F-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 96.8 KD PROTEIN IN S152-MTD1 INTERGENIC REGION [Saccharomyces cerevisiae]//7.3 e-76:385:96//Hs.21875:AA243700	F-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds//2.3e-138:647:98//Hs.27197:AB018340
F-NT2RP2000987//ESTs//5.6e-11:177:72//Hs.15776:T91944	F-NT2RP2001613
F-NT2RP2001036//ESTs//2.0e-55:352:88//Hs.122131:AA789292	F-NT2RP2001628//ESTs//4.9e-45:238:96//Hs.135222:A1082229
F-NT2RP2001044//EST//0.069:267:60//Hs.102808:N67117	F-NT2RP2001634//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//4.9e-124:604:96//Hs.58488:U97067
F-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-145:696:97//Hs.67619:AB007957	F-NT2RP2001660//Homo sapiens putative 13 S Golgi transport complex 90kD subunit brain-specific isoform mRNA, complete cds//1.3e-145:687:97//Hs.159558:AF058718
F-NT2RP2001065	F-NT2RP2001663//Enolase 1, (alpha)//4.2e-38:372:74//Hs.675:M14328
F-NT2RP2001070//Human mRNA for KIAA0315 gene, partial cds//1.0:310:60//Hs.3989:AB002313	F-NT2RP2001675//X-LINKED HELICASE 1//0.040:454:58//Hs.96264:U72936
F-NT2RP2001081	F-NT2RP2001677//Homo sapiens mRNA for KIAA0771 protein, partial cds//0.028:285:63//Hs.6162:AB018314
F-NT2RP2001094//ESTs//0.0071:262:64//Hs.128115:A1356560	F-NT2RP2001678//Homo sapiens semaphorin F homolog mRNA, complete cds//1.7e-34:328:76//Hs.27621:U52840
F-NT2RP2001119//Small inducible cytokine A5 (RANTES)//2.2e-34:311:78//Hs.155464:AF088219	F-NT2RP2001699//EST//0.029:94:68//Hs.125936:AA889091
F-NT2RP2001127//Human mRNA for KIAA0234 gene, complete cds//3.5e-33:519:63//Hs.80358:U52191	F-NT2RP2001720//ESTs, Highly similar to Rap2 interacting protein 8 [M.musculus]//1.0:173:62//Hs.107361:A197870
F-NT2RP2001137//ESTs, Highly similar to RAB GDP DISSOCIATION INHIBITOR ALPHA [Bos taurus]//6.4e-34:201:91//Hs.118470:A1336362	F-NT2RP2001721
F-NT2RP2001149//EST//3.9e-27:244:78//Hs.162236:AA551582	F-NT2RP2001740//Homo sapiens Rigui (RIGU1) mRNA, complete cds//0.58:403:57//Hs.8114:AF022991
F-NT2RP2001168//ESTs//0.0023:216:62//Hs.134938:A1091361	F-NT2RP2001748//Farnesyl diphosphate synthase (farnesyl pyrophosphate synthetase, dimethylallyltransferase, geranyltransferase)//1.2e-19:151:86//Hs.77393:D14697
F-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete cds//7.4e-114:567:96//Hs.26247:AB007949	F-NT2RP2001762//Homo sapiens exonuclease 1a (EXO1a) mRNA, complete cds//5.2e-34:191:96//Hs.47504:AF091754
F-NT2RP2001174//H. sapiens ZNF81 gene//0.21:256:59//Hs.104020:X68011	F-NT2RP2001813//EST//0.46:183:57//Hs.144096:A1032180
F-NT2RP2001196	F-NT2RP2001839//EST//2.5e-12:86:94//Hs.133226:A1052250
F-NT2RP2001218//ESTs//1.1e-65:337:96//Hs.115710:AA524598	F-NT2RP2001861//Homo sapiens mRNA for paraplegin//0.068:146:71//Hs.78497:Y16610
F-NT2RP2001226//Guanylate cyclase 1, soluble, alpha 2//0.030:395:59//Hs.2685:Z50053	F-NT2RP2001869//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//0.0013:174:62//Hs.9443:AF027219
F-NT2RP2001233//Zinc finger protein 136 (clone pHZ-20)//4.4e-58:65:67//Hs.69740:U09367	F-NT2RP2001876//Allograft inflammatory factor 1//2.2e-08:162:67//Hs.76364:Y14768
F-NT2RP2001245//EST//0.018:228:62//Hs.116798:AA633813	F-NT2RP2001883
F-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cds//8.1e-108:514:97//Hs.7531:AB018353	F-NT2RP2001898//75 KD INOSITOL-1,4,5-TRISPHOSPHATE 5-PHOSPHATASE P RECURSOR//3.0e-113:633:90//Hs.142189:M74161
F-NT2RP2001277//EST//0.42:127:66//Hs.42834:N20277	F-NT2RP2001900//EST//1.9e-14:132:84//Hs.130049:AA902650
F-NT2RP2001290//Homo sapiens alpha SNAP mRNA, complete cds//1.8e-52:527:76//Hs.75848:U39412	F-NT2RP2001907//ESTs, Weakly similar to ankyrin 3, long form [H.sapiens]//0.37:263:62//Hs.106377:H29757
F-NT2RP2001295//ESTs//3.4e-29:90:100//Hs.123321:AA810287	F-NT2RP2001926//ESTs//1.1e-87:430:97//Hs.133487:A1393754
F-NT2RP2001312//ESTs//1.0:121:61//Hs.160261:A1145387	F-NT2RP2001936
F-NT2RP2001327//Human B12 protein mRNA, complete cds//1.9e-30:359:71//Hs.76090:M80783	F-NT2RP2001943
F-NT2RP2001328//ESTs//5.2e-103:532:94//Hs.69476:AA628522	F-NT2RP2001946//ESTs//1.0:110:69//Hs.7941:AA894797
F-NT2RP2001347//ESTs//4.3e-28:217:82//Hs.31775:HA1883	F-NT2RP2001947
F-NT2RP2001366//ESTs, Weakly similar to ZK1058.5 [C.elegans]//1.8e-72:418:91//Hs.107039:W27244	F-NT2RP2001969//ESTs//3.3e-93:433:93//Hs.9622:W44489
F-NT2RP2001378	F-NT2RP2001976//Homo sapiens KIAA0432 mRNA, complete cds//0.20:238:63//Hs.155174:AB007892
F-NT2RP2001381//ESTs//0.59:235:62//Hs.118569:A1377558	F-NT2RP2001985//Homo sapiens mRNA for KIAA0545 protein, partial cds//7.4e-05:235:62//Hs.129943:AB011117
F-NT2RP2001392//Homo sapiens chromosome 5, BAC clone 203o13 (LBNL H155), complete sequence//0.28:225:62//Hs.159402:AC005609	F-NT2RP2001991//EST//0.0027:163:68//Hs.162458:AA579196
F-NT2RP2001394//ESTs//8.3e-22:133:78//Hs.109655:A1189767	F-NT2RP2002025//Homo sapiens mRNA for KIAA0756 protein, partial cds//3.2e-62:314:97//Hs.116604:AB018299
F-NT2RP2001397//ESTs//0.090:265:60//Hs.152775:AA633088	F-NT2RP2002032
F-NT2RP2001420	F-NT2RP2002033//EST//1.2e-16:224:74//Hs.150409:A1003543
F-NT2RP2001423//ESTs, Weakly similar to hypothetical protein [H.sapiens]//0.030:443:59//Hs.140506:AA308018	F-NT2RP2002041//EST//0.022:139:69//Hs.127219:AA939336
F-NT2RP2001427//EST//1.9e-19:174:79//Hs.132635:A1032875	F-NT2RP2002046//ESTs//1.1e-35:218:92//Hs.130678:R51509
F-NT2RP2001436//EST//0.16:132:66//Hs.128265:AA972966	F-NT2RP2002047//ESTs//0.43:131:64//Hs.153939:A1284198
F-NT2RP2001440//Tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide//9.8e-56:603:72//Hs.75544:Z82248	F-NT2RP2002058//Homo sapiens mRNA for KIAA0741 protein, complete cds//0.96:137:71//Hs.3615:AB018284
F-NT2RP2001445//ESTs//2.2e-26:193:86//Hs.128610:AA504218	F-NT2RP2002066//Homo sapiens transmembrane receptor UNC5C (UNC5C) mRNA, complete cds//3.1e-36:509:66//Hs.44553:AF055634
F-NT2RP2001449	F-NT2RP2002070//ESTs//0.00027:107:72//Hs.4852:R84241
F-NT2RP2001450	F-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//3.4e-129:643:96//Hs.11039:AF052183
F-NT2RP2001457	F-NT2RP2002078//EST//1.0:83:65//Hs.115996:AA609014
F-NT2RP2001506	F-NT2RP2002079//ESTs//6.2e-06:326:60//Hs.134202:A1313156
F-NT2RP2001511//ESTs, Weakly similar to F48F.1 [C.elegans]//3.2e-83:409:98//Hs.156161:A1333779	F-NT2RP2002099//Homo sapiens mRNA for E18-55kDa-associated protein//3.2e-112:533:97//Hs.155218:AJ007509
F-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protein ARALARI//6.4e-138:657:97//Hs.4277:Y14494	F-NT2RP2002105//Homo sapiens serine threonine kinase 11 (STK11) mRNA, complete cds//6.1e-07:408:60//Hs.122755:AF032986
F-NT2RP2001526//EST//1.0:180:61//Hs.136311:AA437134	F-NT2RP2002124//ESTs//1.3e-90:459:96//Hs.142053:AA224286
F-NT2RP2001536//Homo sapiens X-ray repair cross-complementing protein 3 (XRCC3) mRNA, complete cds//5.2e-105:384:94//Hs.99742:AF035586	F-NT2RP2002137//ATPase, Ca++ transporting, plasma membrane 4//0.0032:319:59//Hs.995:M83363
F-NT2RP2001560	F-NT2RP2002154//Homo sapiens mRNA for C17orf1 protein//1.0:149:65//Hs.100217:AJ008112
F-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.4e-124:590:98//Hs.67619:AB007957	F-NT2RP2002172//EST//4.4e-14:276:67//Hs.148392:A1085314
F-NT2RP2001576//Erythrocyte membrane protein band 4.9 (dematin)//0.046:521:60//Hs.75936:U28389	F-NT2RP2002185//ESTs, Weakly similar to ubiquitin S6(1) [D.melanog
F-NT2RP2001581//EST//1.0:28:96//Hs.148002:A1264876	
F-NT2RP2001597//Casein kinase 2, alpha prime polypeptide//0.069:16	

【0871】

【表570】

aster)/6.8e-61:354:91//Hs.109966:C06057	0:628:62//Hs.87435:D89016
F-NT2RP2002192//Human 75-kD autoantigen (PM-Scl) mRNA, complete cds	F-NT2RP2002750//Human mRNA for KIAA0331 gene, complete cds//2.1e-2
s//3.7e-37:194:97//Hs.91728:M58460	9:285:75//Hs.146395:AB002329
F-NT2RP2002193//Homo sapiens protein inhibitor of activated STAT p	F-NT2RP2002752//EST//2.2e-06:126:74//Hs.159913:AA862709
rotein PIASx-alpha mRNA, complete cds//6.8e-15:228:67//Hs.111323:A	F-NT2RP2002753//ESTs//4.3e-14:137:81//Hs.133478:T79705
F077954	F-NT2RP2002769//Human plectin (PLEC1) mRNA, complete cds//0.017:50
F-NT2RP2002208	7:57//Hs.79706:U53204
F-NT2RP2002219//ESTs//0.0059:247:61//Hs.36495:AA151628	F-NT2RP2002778//EST//1.6e-57:319:93//Hs.147519:A1216407
F-NT2RP2002231//ESTs//0.29:167:63//Hs.112013:A1394318	F-NT2RP2002800
F-NT2RP2002235//H.sapiens mRNA for PHAP2b protein//0.86:67:82//H	F-NT2RP2002839//ESTs//0.075:177:62//Hs.132445:AA921763
s.84264:U70439	F-NT2RP2002857//ESTs//0.99:88:69//Hs.132104:A1382142
F-NT2RP2002252//Homo sapiens mRNA for KIAA0527 protein, partial cd	F-NT2RP2002862
s//0.79:264:59//Hs.129748:AB011099	F-NT2RP2002880
F-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, compl	F-NT2RP2002891//Homo sapiens mRNA for KIAA0673 protein, partial cd
ete cds//2.1e-51:315:89//Hs.150595:AF005418	s//1.0:237:62//Hs.106487:AB014573
F-NT2RP2002259//Human L-myc protein gene, complete cds//1.2e-26:34	F-NT2RP2002925//ESTs//1.6e-33:318:77//Hs.16808:M22606
3:71//Hs.92137:M19720	F-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRN
F-NT2RP2002270//ESTs. Weakly similar to AF-9 PROTEIN [H.sapiens]//	A. complete cds//3.9e-136:623:99//Hs.116674:AF038392
1.3e-31:206:88//Hs.4029:Z78373	F-NT2RP2002929//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//
F-NT2RP2002292//ESTs//1.3e-07:153:67//Hs.13533:M23079	0.24:158:65//Hs.108447:AJ000517
F-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2)	F-NT2RP2002939
mRNA, partial cds//5.0e-95:467:96//Hs.24812:AF069532	F-NT2RP2002954
F-NT2RP2002316//ESTs//0.95:194:63//Hs.157214:AA805445	F-NT2RP2002959//Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH
F-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11	5B) mRNA, complete cds//6.4e-21:135:91//Hs.108332:U39317
a) mRNA, complete cds//1.3e-124:640:95//Hs.31034:AB015594	F-NT2RP2002979
F-NT2RP2002333//Protein-tyrosine kinase tyk2 (non-receptor)//1.0:2	F-NT2RP2002980
57:60//Hs.75516:X54637	F-NT2RP2002986//Homo sapiens actin binding protein MAYVEN mRNA, co
F-NT2RP2002373	mplete cds//7.8e-11:272:61//Hs.122967:AF059569
F-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced var	F-NT2RP2002987//ESTs//8.2e-20:99:82//Hs.138965:A1004740
iant mRNA, complete cds//3.1e-139:673:97//Hs.109051:AF038958	F-NT2RP2002993
F-NT2RP2002394//Human clone 23695 mRNA sequence//0.16:456:59//Hs.9	F-NT2RP2003000//Small inducible cytokine A5 (RANTES)//2.1e-46:353:
0798:U79289	81//Hs.155464:AF088219
F-NT2RP2002408//HOMEOBOX/POU DOMAIN PROTEIN RDC-1//0.00069:265:65/	F-NT2RP2003034//ESTs//1.6e-08:263:66//Hs.164048:AA811741
/Hs.74095:L20433	F-NT2RP2003073//Human clone 230971 defective mariner transposon Hs
F-NT2RP2002426//EST//4.3e-33:271:79//Hs.145743:A1269098	mar2 mRNA sequence//4.6e-43:381:78//Hs.159176:U92019
F-NT2RP2002439//ESTs//0.0041:129:68//Hs.146064:AA714326	F-NT2RP2003099//TRICHOHYALIN//0.98:183:62//Hs.82276:L09190
F-NT2RP2002442//ESTs. Weakly similar to similar to molybdopter bi	F-NT2RP2003108//H.sapiens nek2 mRNA for protein kinase//0.025:185:
osynthesis MCEB proteins [C.elegans]//5.6e-26:169:89//Hs.25198:AA9	67//Hs.153704:U11050
04265	F-NT2RP2003117//ESTs//7.6e-30:219:88//Hs.153408:AA416633
F-NT2RP2002457//ESTs//0.00031:121:71//Hs.134860:A1091436	F-NT2RP2003121//ESTs//1.9e-13:158:73//Hs.129998:A1291379
F-NT2RP2002464//Human mRNA for KIAA0086 gene, complete cds//0.001	F-NT2RP2003125//Serum response factor (c-fos serum response elemen
3:207:63//Hs.1560:D42045	t-binding transcription factor)//4.5e-06:556:57//Hs.155321:J03161
F-NT2RP2002475//ESTs//1.0:85:75//Hs.155371:A1139929	F-NT2RP2003129//ESTs//0.095:218:63//Hs.70836:AA121544
F-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, c	F-NT2RP2003137
omplete cds//7.6e-125:607:96//Hs.125856:AB005289	F-NT2RP2003157//Homo sapiens mRNA for KIAA0620 protein, partial cd
F-NT2RP2002498	s//0.40:227:61//Hs.105958:AB014520
F-NT2RP2002503//Human zinc finger protein (FDZF2) mRNA, complete c	F-NT2RP2003158//Homo sapiens mRNA for proteasome subunit p58, comp
ds//2.2e-89:314:87//Hs.102681:U95044	lete cds//5.7e-113:581:93//Hs.9736:067025
F-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete c	F-NT2RP2003161//ESTs//0.0095:120:65//Hs.163532:A1424170
ds//3.8e-159:761:97//Hs.23255:AB018334	F-NT2RP2003164//EST//0.11:179:63//Hs.163299:AA853944
F-NT2RP2002520//RAB5, member RAS oncogene family//0.99:216:59//Hs.	F-NT2RP2003165//Human mRNA for KIAA0355 gene, complete cds//1.0e-3
107563:M28212	9:342:79//Hs.153014:AB002353
F-NT2RP2002537	F-NT2RP2003177//ESTs//3.6e-80:414:96//Hs.4767:M91123
F-NT2RP2002546//EST//0.81:161:65//Hs.120562:AA741096	F-NT2RP2003194//ESTs//5.4e-20:119:95//Hs.149531:A1393223
F-NT2RP2002549//ESTs//0.76:228:61//Hs.146313:AA594979	F-NT2RP2003206//EST//0.095:182:60//Hs.88461:AA278594
F-NT2RP2002591//Homo sapiens mRNA for KIAA0798 protein, complete c	F-NT2RP2003228//CDC21 HOMOLOG//9.3e-138:726:93//Hs.154443:X74794
ds//2.9e-33:285:78//Hs.159277:AB018341	F-NT2RP2003230//ESTs//3.0e-10:239:62//Hs.163720:AA526947
F-NT2RP2002595//Adenylate cyclase 8 (brain)//0.39:377:59//Hs.2522:	F-NT2RP2003237//Human 53K isoform of Type II phosphatidylinositol-
235309	4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.3e-62:543:77//H
F-NT2RP2002606//Human Line-1 repeat mRNA with 2 open reading frame	s.108956:U48696
s//6.4e-24:144:95//Hs.23094:M19503	F-NT2RP2003243//Homo sapiens proline and glutamic acid rich nuclea
F-NT2RP2002609//Human guanine nucleotide regulatory protein (tim1)	r protein isoform mRNA, partial cds//0.52:200:62//Hs.102732:U88153
mRNA, complete cds//1.0:120:68//Hs.334:U02082	F-NT2RP2003265
F-NT2RP2002618//H.sapiens mRNA for arginine methyltransferase, spl	F-NT2RP2003272//ESTs. Weakly similar to ubiquitin S6(1) [D.melanog
ice variant, 1262 bp//4.3e-28:460:63//Hs.20521:Y10805	aster]//5.8e-57:313:93//Hs.109966:C06057
F-NT2RP2002621	F-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cd
F-NT2RP2002643//Human p300/CBP-associated factor (P/CAF) mRNA, com	s//4.9e-147:714:96//Hs.154919:AB014525
plete cds//0.0022:210:64//Hs.155302:U57317	F-NT2RP2003280
F-NT2RP2002672//ESTs//1.4e-30:226:84//Hs.94694:M52493	F-NT2RP2003286//Homo sapiens mRNA for KIAA0587 protein, complete c
F-NT2RP2002701//ESTs. Highly similar to HYPOTHETICAL 68.7 KD PROT	ds//0.0097:243:65//Hs.21862:AB011159
EIN ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]//8.3e-56:27	F-NT2RP2003293//ESTs//5.5e-28:418:70//Hs.146227:A1269334
8:97//Hs.109857:AA088385	F-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 mediating protein,
F-NT2RP2002706//CEREBELLIN 1 PRECURSOR//0.00042:367:61//Hs.662:M58	complete cds//2.0e-86:416:97//Hs.7943:AB006572
583	F-NT2RP2003297//EST//0.99:240:60//Hs.133228:A1052312
F-NT2RP2002710//Homo sapiens mRNA for KIAA0672 protein, complete c	F-NT2RP2003307//ESTs//5.6e-15:137:81//Hs.90020:AA442752
ds//8.0e-42:631:65//Hs.6336:AB014572	F-NT2RP2003308
F-NT2RP2002727	F-NT2RP2003329//ESTs. Highly similar to HYPOTHETICAL 54.9 KD PROT
F-NT2RP2002736//ESTs//3.2e-67:336:97//Hs.86583:AA761217	EIN CO2F5.7 IN CHROMOSOME III [Caenorhabditis elegans]//1.8e-102:5
F-NT2RP2002740//EST//1.0e-70:352:97//Hs.145168:A1150297	32:95//Hs.6092:T75227
F-NT2RP2002741//Human mRNA for Neuroblastoma, complete cds//2.4e-3	F-NT2RP2003339//ESTs//0.13:166:63//Hs.149649:A1346765

【0872】

【表571】

F-NT2RP2003347//ESTs//0.96:185:59//Hs.125003:H85963	F-NT2RP2003912//ESTs, Weakly similar to G2-SPECIFIC PROTEIN KINASE NIMA [Emmericella nidulans]//2.2e-113:632:92//Hs.50072:A1378221
F-NT2RP2003367//Human HsLIM15 mRNA for HsLIM15, complete cds//0.99:243:60//Hs.37181:D64108	F-NT2RP2003952//ESTs, Moderately similar to 60S RIBOSOMAL PROTEIN L32 [H.sapiens]//1.0:146:67//Hs.156920:AA489296
F-NT2RP2003391	F-NT2RP2003968//Homo sapiens hUBP mRNA for ubiquitin specific protease, complete cds//5.8e-30:165:96//Hs.35086:AB014458
F-NT2RP2003393	F-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete cds//7.9e-116:610:94//Hs.7302:AB007916
F-NT2RP2003394//Homo sapiens Ran-GTP binding protein mRNA, partial cds//0.86:416:57//Hs.4976:AF039023	F-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cds//3.2e-161:783:96//Hs.7316:AB018347
F-NT2RP2003401	F-NT2RP2003984
F-NT2RP2003433//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//3.7e-33:303:77//Hs.14038:R06800	F-NT2RP2003986//ESTs//1.3e-39:296:83//Hs.152482:A1050036
F-NT2RP2003445//EST//1.7e-06:154:65//Hs.142843:R36893	F-NT2RP2003988//Thiopurine S-methyltransferase//7.1e-44:532:70//Hs.51124:AF019369
F-NT2RP2003446//Prostaglandin receptor, epi subtype//0.81:273:61//Hs.159360:L22647	F-NT2RP2004013//ESTs, Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo sapiens]//7.0e-104:556:93//Hs.111081:A1380378
F-NT2RP2003456//EST//0.17:95:65//Hs.147190:A1193320	F-NT2RP2004014
F-NT2RP2003466//Homo sapiens chromosome 11, BAC CIT-HSP-311e8 (BC2 69730) containing the PFEN1 gene//4.3e-53:339:78//Hs.132874:AC004770	F-NT2RP2004041//Homo sapiens chromosome 19, cosmid F17127//6.0e-11:120:80//Hs.10116:AC004780
F-NT2RP2003480//Calpain, small polypeptide//1.1e-06:154:66//Hs.74451:X04106	F-NT2RP2004042
F-NT2RP2003499//Homo sapiens delta-catenin mRNA, complete cds//3.1e-10:481:60//Hs.80220:U96136	F-NT2RP2004066//Homo sapiens zinc finger protein (ZnF20) mRNA, complete cds//0.80:292:61//Hs.1147:AF011573
F-NT2RP2003506	F-NT2RP2004081//ESTs//5.7e-87:427:96//Hs.102296:A1217942
F-NT2RP2003511//Spectrin, beta, non-erythrocytic 1//0.76:189:62//Hs.107164:M96803	F-NT2RP2004098//Homo sapiens leucine-rich repeat protein SHOC-2 (SHOC-2) mRNA, complete cds//0.15:199:60//Hs.104315:AF054828
F-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//8.3e-78:403:94//Hs.78482:Y16270	F-NT2RP2004124//Homo sapiens mRNA for ephrin-A2//0.98:233:59//Hs.158306:AJ007292
F-NT2RP2003517//Platelet-derived growth factor beta polypeptide (s human sarcoma viral (v-sis) oncogene homolog)//1.3e-24:151:95//Hs.1976:M12783	F-NT2RP2004142
F-NT2RP2003522//Zinc finger protein 148 (pH2-52)//1.1e-17:512:60//Hs.112180:AF039019	F-NT2RP2004152//ESTs//5.7e-35:187:96//Hs.98977:AA625872
F-NT2RP2003533//ESTs//1.8e-76:373:98//Hs.140402:A1138765	F-NT2RP2004165//Homo sapiens serine kinase SRPK2 mRNA, complete cds//0.69:176:63//Hs.78353:U88666
F-NT2RP2003543//ESTs//9.3e-65:363:92//Hs.70643:AA030010	F-NT2RP2004170//ESTs//3.9e-05:380:61//Hs.143748:A1419966
F-NT2RP2003559//ESTs//0.00037:93:77//Hs.157564:A1356513	F-NT2RP2004172//ESTs//5.8e-18:104:99//Hs.157031:A1343501
F-NT2RP2003564//Sjogren syndrome antigen A1 (52kD, ribonucleoprotein autoantigen SS-A/Ro)//2.9e-28:664:63//Hs.1042:M62800	F-NT2RP2004187//ESTs, Moderately similar to zinc finger protein [H.sapiens]//1.7e-16:276:67//Hs.36778:AA626790
F-NT2RP2003567//Homo sapiens mRNA for KIAA0462 protein, partial cds//1.3e-114:541:98//Hs.129937:AB007931	F-NT2RP2004194//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//1.0:124:69//Hs.155302:U57317
F-NT2RP2003581//EST//1.0:59:76//Hs.158575:A1368947	F-NT2RP2004196
F-NT2RP2003596//ESTs, Weakly similar to No definition line found [C.elegans]//1.3e-63:224:95//Hs.34627:AA126463	F-NT2RP2004207//ESTs//3.8e-11:92:88//Hs.22678:AA604756
F-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP) mRNA, complete cds//1.7e-124:585:98//Hs.58488:U97067	F-NT2RP2004226//ESTs, Weakly similar to teg292 protein [M.musculus]//1.8e-80:386:98//Hs.68791:AA527270
F-NT2RP2003629//ESTs//2.0e-103:535:95//Hs.105633:AA479166	F-NT2RP2004232//Protein kinase C, mu//3.9e-36:448:67//Hs.2891:X75756
F-NT2RP2003643//Kallmann syndrome 1 sequence//0.85:216:61//Hs.89591:M97252	F-NT2RP2004239//ESTs//0.12:196:61//Hs.127209:AA976680
F-NT2RP2003668//Homo sapiens haemopoietic progenitor homeobox HPX4 2B (HPX42B) mRNA, complete cds//9.4e-47:371:80//Hs.125231:AF068006	F-NT2RP2004240//EST//1.0:134:63//Hs.104466:AA282536
F-NT2RP2003687//EST//2.9e-14:134:80//Hs.132635:A1032875	F-NT2RP2004242//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.27:313:59//Hs.129725:AF047487
F-NT2RP2003691//ESTs//8.2e-47:296:83//Hs.138852:AA284247	F-NT2RP2004245//ESTs, Weakly similar to No definition line found [C.elegans]//8.2e-51:474:74//Hs.108990:N25951
F-NT2RP2003702//DNA POLYMERASE EPSILON, CATALYTIC SUBUNIT A//0.85:190:61//Hs.18366:L09561	F-NT2RP2004270//MUELLERIAN INHIBITING FACTOR PRECURSOR//1.6e-06:49:0:60//Hs.112432:AC005263
F-NT2RP2003704//ESTs, Weakly similar to putative p150 [H.sapiens]//5.1e-44:269:91//Hs.139757:N95271	F-NT2RP2004300//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 3//0.35:157:67//Hs.37121:Z37544
F-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cds//8.3e-110:518:98//Hs.78494:AB011097	F-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, complete cds//1.5e-151:735:97//Hs.61152:AF000416
F-NT2RP2003713	F-NT2RP2004321//ESTs//2.6e-64:385:88//Hs.133128:W27735
F-NT2RP2003714//Homo sapiens hematopoietic cell derived zinc finger protein mRNA, complete cds//2.7e-56:252:83//Hs.86371:AF054180	F-NT2RP2004339//ESTs//3.3e-46:338:83//Hs.145091:AA814510
F-NT2RP2003727//EST//0.52:277:59//Hs.69507:AA111879	F-NT2RP2004347//ESTs//1.0:184:61//Hs.134469:AA731632
F-NT2RP2003737//Human E2 ubiquitin conjugating enzyme UbCH5C (UBCH5C) mRNA, complete cds//4.0e-55:584:71//Hs.118797:U39318	F-NT2RP2004364//ESTs//2.9e-70:366:95//Hs.14928:AA256202
F-NT2RP2003751	F-NT2RP2004365
F-NT2RP2003760	F-NT2RP2004366//Homo sapiens mRNA for DFFRY protein, abundant transcript//0.60:295:57//Hs.39163:AF000986
F-NT2RP2003764	F-NT2RP2004373
F-NT2RP2003769	F-NT2RP2004389//ESTs, Highly similar to HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III [Caenorhabditis elegans]//3.3e-97:477:98//Hs.30490:AA146916
F-NT2RP2003770//RETINOBLASTOMA BINDING PROTEIN 3//0.58:247:59//Hs.96055:U47677	F-NT2RP2004392//ESTs//2.6e-61:305:98//Hs.43100:AA186588
F-NT2RP2003777	F-NT2RP2004396//Homo sapiens BAC clone RGI35C18 from Tq21//1.4e-174:875:95//Hs.152759:AC005164
F-NT2RP2003781//ESTs, Weakly similar to C47D12.3 [C.elegans]//3.7e-63:356:92//Hs.16131:AA568689	F-NT2RP2004399//ESTs, Weakly similar to K01H12.1 [C.elegans]//1.2e-92:519:91//Hs.13275:A1341468
F-NT2RP2003793//ESTs//4.8e-68:392:92//Hs.93949:AA782955	F-NT2RP2004400//EST//0.018:150:65//Hs.158739:A1375367
F-NT2RP2003825//ESTs//7.6e-79:232:98//Hs.14347:AA287742	F-NT2RP2004412
F-NT2RP2003840//DNAJ PROTEIN HOMOLOG HsJ1//0.95:300:59//Hs.77768:X63368	F-NT2RP2004425//EST//0.049:145:64//Hs.160759:R36944
F-NT2RP2003857//EST//1.0:112:62//Hs.139216:AA244425	F-NT2RP2004463//ESTs//1.5e-40:207:98//Hs.98057:C15687
F-NT2RP2003859	F-NT2RP2004476//Homo sapiens TWIK-related acid-sensitive K ⁺ channel 1 (TASK) mRNA, complete cds//0.45:208:61//Hs.24040:AF006823
F-NT2RP2003871//ESTs//2.5e-44:222:99//Hs.146295:AA935780	F-NT2RP2004490
F-NT2RP2003885	F-NT2RP2004512//ESTs//0.0012:330:61//Hs.70258:A1091203
	F-NT2RP2004523//Human high-affinity copper uptake protein (hCTR1)

【0873】

【表572】

mRNA, complete cds//1.3e-29:270:79//Hs.73614:U83460	complete cds//0.22:498:59//Hs.137574:AF055917
F-NT2RP2004538//Homo sapiens mRNA for KIAA0591 protein, partial cd	F-NT2RP2005108//ESTs//0.74:145:63//Hs.116557:AA657838
s//4.6e-139:687:96//Hs.129908:AB011163	F-NT2RP2005116//Homo sapiens mRNA for KIAA0564 protein, partial cd
F-NT2RP2004551//ESTs//0.0075:285:62//Hs.149442:A1345891	s//6.4e-105:495:98//Hs.22616:AB014564
F-NT2RP2004568//Homo sapiens antigen NY-CO-16 mRNA, complete cds//	F-NT2RP2005126//H. sapiens mRNA for RNA helicase (Myc-regulated dea
8.8e-06:291:61//Hs.132206:AF039694	d box protein)//9.2e-29:157:98//Hs.100555:X98743
F-NT2RP2004580//Small inducible cytokine A5 (RANTES)//1.2e-45:334:	F-NT2RP2005139//ESTs//2.6e-91:479:95//Hs.125037:W42803
82//Hs.155464:AF088219	F-NT2RP2005140//ESTs//0.81:308:59//Hs.27308:AA534947
F-NT2RP2004587//Homo sapiens mRNA for KIAA0766 protein, complete c	F-NT2RP2005144//Homo sapiens tubby like protein 3 (TULP3) mRNA, co
ds//0.98:136:64//Hs.28020:AB018309	mplete cds//8.3e-91:447:96//Hs.132226:AF045583
F-NT2RP2004594//ESTs. Highly similar to MKR2 PROTEIN [Mus musculu	F-NT2RP2005147
s]//1.0:104:68//Hs.125729:N99898	F-NT2RP2005159//ESTs//1.5e-44:242:94//Hs.109819:A1357582
F-NT2RP2004600//Homo sapiens mRNA for Hrs. complete cds//0.20:260:	F-NT2RP2005162//ESTs. Weakly similar to Y53C12A.3 [C.elegans]//0.9
60//Hs.24756:U43895	7:80:73//Hs.107747:A1357868
F-NT2RP2004602//ESTs. Weakly similar to !!!! ALU SUBFAMILY J WARNI	F-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein
NG ENTRY !!!! [H. sapiens]//3.0e-59:273:93//Hs.12845:N28835	//4.4e-127:633:96//Hs.155218:AJ007509
F-NT2RP2004614//EST//0.99:103:68//Hs.148738:A1224908	F-NT2RP2005204//H. sapiens ST4 gene for ST4 Oncofetal antigen//0.00
F-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//8.4e-1	34:187:66//Hs.82128:AJ012159
04:496:98//Hs.5198:AJ006291	F-NT2RP2005227//Homo sapiens PAC clone DJ0905J08 from 7p12-pl4//1.
F-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cd	3e-66:340:95//Hs.8173:AC005189
s//5.2e-155:728:98//Hs.29956:AB007929	F-NT2RP2005239//EST//1.3e-05:215:66//Hs.129528:AA994783
F-NT2RP2004675//EST//0.65:151:62//Hs.130504:A1003839	F-NT2RP2005254//H. sapiens mRNA for PHAP12b protein//1.0:101:71//H
F-NT2RP2004681	s.84264:U70439
F-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cd	F-NT2RP2005270//Homo sapiens creatine transporter mRNA, complete c
s//4.1e-61:327:94//Hs.154919:AB014525	ds//0.56:114:68//Hs.154503:U36341
F-NT2RP2004709//ESTs//2.2e-05:98:77//Hs.161898:AA286942	F-NT2RP2005276//Homo sapiens acyl-CoA synthetase 4 (ACS4) mRNA, co
F-NT2RP2004710//ESTs//0.0035:76:82//Hs.108470:R93780	mplete cds//1.2e-40:594:65//Hs.81452:AF030555
F-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete c	F-NT2RP2005287//ESTs//8.2e-07:175:70//Hs.117134:A1383932
ds//2.1e-118:582:96//Hs.4236:AB007947	F-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRN
F-NT2RP2004743//EST//0.11:170:64//Hs.112670:AA609242	A. complete cds//2.3e-123:604:96//Hs.27007:AF060219
F-NT2RP2004767//EST//1.5e-09:303:65//Hs.148374:AA948183	F-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//1.3e-141:670:9
F-NT2RP2004768//ESTs. Highly similar to SERINE/THREONINE-PROTEIN	8//Hs.44766:AJ007590
KINASE PAK [Rattus norvegicus]//3.7e-110:548:96//Hs.85768:W16504	F-NT2RP2005293//EST//1.9e-50:254:98//Hs.162017:AA505833
F-NT2RP2004775//Homo sapiens transcriptional regulatory protein p5	F-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cd
4 mRNA, complete cds//0.025:547:57//Hs.107474:AF045451	s//3.6e-97:483:96//Hs.115763:AB014576
F-NT2RP2004791//Human endosome-associated protein (EEA1) mRNA, com	F-NT2RP2005325//Human LIM-homeobox domain protein (hLH-2) mRNA, co
plete cds//0.99:121:64//Hs.2864:L40157	mplete cds//2.6e-23:166:90//Hs.1569:U11701
F-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase	F-NT2RP2005336//Homo sapiens snRNA activating protein complex 190k
beta subunit (SCS) mRNA, partial cds//4.9e-118:594:95//Hs.40820:AF	D subunit (SNAP190) mRNA, complete cds//0.016:353:62//Hs.113265:AF
058953	032387
F-NT2RP2004802//ESTs//5.6e-16:116:91//Hs.153841:N36043	F-NT2RP2005344//Homo sapiens mRNA for KIAA0566 protein, partial cd
F-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds//	s//2.8e-30:456:66//Hs.44697:AB011138
6.8e-103:495:97//Hs.67052:AF054179	F-NT2RP2005354//ESTs//0.71:192:60//Hs.39063:AA708958
F-NT2RP2004841//Human transposon-like element mRNA//3.0e-70:519:83	F-NT2RP2005358//Homo sapiens methyl-CoG binding protein MBD3 (MBD
//Hs.84775:W23161	3) mRNA, complete cds//1.4e-100:489:96//Hs.107254:AC005943
F-NT2RP2004861//ESTs//6.7e-89:427:98//Hs.132980:A1290258	F-NT2RP2005360//ESTs//8.2e-35:190:95//Hs.163038:AA700122
F-NT2RP2004897//ESTs//6.4e-81:431:94//Hs.130961:N79111	F-NT2RP2005393//Homo sapiens CTG26 alternate open reading frame mR
F-NT2RP2004933//Homo sapiens mRNA for ZIP-kinase, complete cds//6.	NA, complete cds//0.87:244:59//Hs.113252:U80761
5e-84:418:95//Hs.25619:AB007144	F-NT2RP2005407
F-NT2RP2004936	F-NT2RP2005436//Homo sapiens mRNA for KIAA0561 protein, partial cd
F-NT2RP2004959	s//0.28:338:57//Hs.6189:AB011133
F-NT2RP2004961//Human mRNA for KIAA0665 gene, partial cds//7.2e-2	F-NT2RP2005441//ESTs//3.3e-45:238:96//Hs.5209:AA780068
6:456:66//Hs.70617:D31763	F-NT2RP2005453//ESTs//2.1e-20:115:99//Hs.133087:A1091164
F-NT2RP2004962//EST//2.8e-15:242:69//Hs.146794:A1149478	F-NT2RP2005457//ESTs. Highly similar to NADH-UBIQUINONE OXIDOREDU
F-NT2RP2004967//ESTs//0.0022:218:63//Hs.131987:A1239735	CTASE SUBUNIT B14.5B [Bos taurus]//8.5e-48:295:90//Hs.75017:AA1668
F-NT2RP2004978//Homo sapiens mRNA for KIAA0458 protein, complete c	53
ds//1.0:218:61//Hs.7414:AB007927	F-NT2RP2005464//ESTs//2.0e-99:495:96//Hs.3530:AA808243
F-NT2RP2004982//Human kinesin-like spindle protein HKSP (HKSP) mRN	F-NT2RP2005465//V-crk avian sarcoma virus CT10 oncogene homolog//
A. complete cds//0.13:260:60//Hs.41723:U37426	0.032:176:64//Hs.16:D10656
F-NT2RP2004985//Human mRNA for KIAA0144 gene, complete cds//4.8e-2	F-NT2RP2005472//ESTs//1.4e-34:180:98//Hs.158892:A1378412
2:431:65//Hs.8127:D63478	F-NT2RP2005476//Homo sapiens mRNA for KIAA0772 protein, complete c
F-NT2RP2004999	ds//9.9e-48:432:77//Hs.15519:AB018315
F-NT2RP2005000//Homo sapiens hyperpolarization-activated channel 1	F-NT2RP2005490//ESTs//4.5e-19:165:84//Hs.134382:AA083573
(IH1) mRNA, partial cds//0.99:269:58//Hs.124161:AF065164	F-NT2RP2005491
F-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete c	F-NT2RP2005495//ESTs//5.6e-96:452:99//Hs.145417:A1084164
ds//1.9e-160:782:97//Hs.155972:AB014515	F-NT2RP2005496//Human mRNA for KIAA0326 gene, partial cds//4.4e-4
F-NT2RP2005003//H. sapiens Stat5C mRNA//9.9e-44:430:75//Hs.68054:X8	8:621:68//Hs.6833:AB002324
2200	F-NT2RP2005498//Human protein phosphatase 2A beta subunit mRNA, co
F-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds//4.5	mplete cds//1.6e-63:503:78//Hs.7688:M64930
e-100:501:96//Hs.31575:AF100141	F-NT2RP2005501//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//
F-NT2RP2005018//Arachidonate 5-lipoxygenase//1.0:232:58//Hs.89499:	0.56:139:66//Hs.8546:U97669
J03600	F-NT2RP2005509//Glutamate-cysteine ligase (gamma-glutamylcysteine
F-NT2RP2005020//ESTs//1.2e-06:61:109//Hs.106160:AA527433	synthetase), regulatory (30.8kD)//1.0:291:59//Hs.89709:L35546
F-NT2RP2005022//Eukaryotic translation initiation factor 3 (eIF-3)	F-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCA
p36 subunit//0.095:271:60//Hs.139745:U39067	P-E) mRNA, complete cds//1.2e-82:444:92//Hs.119023:AF092563
F-NT2RP2005031//Homo sapiens mRNA for SCP-1, complete cds//0.99:33	F-NT2RP2005525//Homo sapiens mRNA for KIAA0764 protein, complete c
8:61//Hs.112743:D67035	ds//2.2e-19:112:99//Hs.6232:AB018307
F-NT2RP2005037//Homo sapiens mRNA for repressor protein, partial c	F-NT2RP2005531//ESTs. Weakly similar to erythrocyte membrane prote
ds//0.098:217:60//Hs.58167:D30612	in 4.1 [H. sapiens]//3.5e-50:366:83//Hs.61833:AA036735
F-NT2RP2005038//Homo sapiens protease-activated receptor 4 mRNA, c	F-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)

【0874】

【表573】

<p>//9.4e-155:747:97//Hs.159597:AJ012449 F-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.9e-131:618:98//Hs.62515:AB007963 F-NT2RP2005549//ESTs. Weakly similar to HYPOTHETICAL 32.0 KD PROTEIN C16C10.10 IN CHROMOSOME III [C.elegans]//2.5e-51:292:93//Hs.105684:H24407 F-NT2RP2005555//EST//0.046:308:57//Hs.145962:AI276822 F-NT2RP2005557//ESTs//4.6e-48:382:79//Hs.125014:AI422839 F-NT2RP2005581//ESTs//6.3e-28:166:93//Hs.87803:AA034436 F-NT2RP2005600//ESTs//1.6e-40:228:93//Hs.160085:AI218627 F-NT2RP2005605//ESTs//5.7e-13:115:86//Hs.37718:H60071 F-NT2RP2005620//Homo sapiens epsilon 2b mRNA, complete cds//3.1e-92:447:97//Hs.22398:AF062085 F-NT2RP2005622//ESTs//0.16:242:63//Hs.136395:AA523702 F-NT2RP2005635 F-NT2RP2005637//ESTs//0.055:96:69//Hs.105998:R90905 F-NT2RP2005640//ESTs//4.5e-16:107:92//Hs.150823:AI292145 F-NT2RP2005645//ESTs//2.7e-29:181:90//Hs.121653:AI375440 F-NT2RP2005651//Oxysterol binding protein//0.00011:122:69//Hs.143065:M86917 F-NT2RP2005654//Homo sapiens mRNA for KIAA0288 gene, complete cds//1.5e-08:351:62//Hs.91400:AB006626 F-NT2RP2005669//ESTs//0.016:185:64//Hs.97713:AA442239 F-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds//7.7e-96:462:98//Hs.25664:AF089814 F-NT2RP2005683//ESTs//0.83:242:62//Hs.136395:AA523702 F-NT2RP2005690//PYRROLINE-5-CARBOXYLATE REDUCTASE//2.5e-11:328:61//Hs.79217:MT7836 F-NT2RP2005694 F-NT2RP2005701//Homo sapiens protein phosphatase 2A B56-epsilon (P2A) mRNA, complete cds//0.15:496:55//Hs.79326:L76703 F-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//5.1e-126:599:97//Hs.61638:AB018342 F-NT2RP2005719//ESTs//0.58:326:60//Hs.157209:N57527 F-NT2RP2005722//Zinc finger protein 136 (clone pHZ-20)//8.2e-46:415:77//Hs.69740:U09367 F-NT2RP2005723//ESTs//1.0e-15:141:81//Hs.163747:AA174017 F-NT2RP2005726//EST//3.4e-15:96:95//Hs.156170:AI334191 F-NT2RP2005732//ESTs//0.99:162:62//Hs.154914:AA721086 F-NT2RP2005741//Homo sapiens chondroaderin gene, 5' flanking region and//0.80:362:58//Hs.97220:U96769 F-NT2RP2005748//H.sapiens ZNF33B gene//0.47:99:65//Hs.72991:X68688 F-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//2.5e-23:134:96//Hs.159651:AF068868 F-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//4.0e-102:486:98//Hs.26285:AF082516 F-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A-LIKE NUK-34//2.3e-05:425:56//Hs.79768:D21853 F-NT2RP2005767//Homolog 2 of Drosophila large discs//0.085:262:61//Hs.23205:X82895 F-NT2RP2005773//PYRROLINE-5-CARBOXYLATE REDUCTASE//2.0e-16:153:82//Hs.79217:MT7836 F-NT2RP2005775//Human thimet oligopeptidase (THOP1) mRNA, complete cds//1.7e-42:645:64//Hs.78769:Z50115 F-NT2RP2005781//ESTs//1.1e-19:132:90//Hs.13550:AI378556 F-NT2RP2005784//Inhibitor of DNA binding 4, dominant negative helix-loop-helix protein//2.9e-06:201:67//Hs.34853:U28368 F-NT2RP2005804//ESTs//1.2e-07:62:93//Hs.125509:AA883820 F-NT2RP2005812 F-NT2RP2005815//ESTs//1.9e-32:173:97//Hs.144587:AI193595 F-NT2RP2005835 F-NT2RP2005841//Homo sapiens retinal rod Na-Ca/K exchanger (NCKX1) mRNA, complete cds//0.94:148:65//Hs.59829:AB014602 F-NT2RP2005853 F-NT2RP2005857//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//5.4e-176:829:98//Hs.50758:AF092564 F-NT2RP2005859//ESTs//2.1e-97:537:92//Hs.131915:W22567 F-NT2RP2005868 F-NT2RP2005886//Human putative M phase phosphoprotein 1 (MPP1) mRNA, partial cds//0.26:728:57//Hs.240:L16782 F-NT2RP2005890//ESTs//2.0e-97:453:100//Hs.88671:AA279943 F-NT2RP2005901//ESTs//0.99:188:64//Hs.28639:R78360 F-NT2RP2005908//ESTs//2.5e-43:325:82//Hs.152340:AA521399 F-NT2RP2005933//ESTs. Highly similar to nucleoporin p54 [R.norvegicus]//7.9e-90:326:98//Hs.156882:AA292186 F-NT2RP2005942//H.sapiens PAP mRNA//5.1e-48:618:67//Hs.49007:X76770 F-NT2RP2005980//ESTs//2.8e-22:358:68//Hs.125446:AA883339 F-NT2RP2006023 F-NT2RP2006038//ESTs//8.0e-37:351:74//Hs.128787:AA418382</p>	<p>F-NT2RP2006043//Human novel homeobox mRNA for a DNA binding protein//0.51:271:59//Hs.37035:U07664 F-NT2RP2006052//ESTs//4.0e-05:233:63//Hs.124864:AA663093 F-NT2RP2006069//Human mRNA for KIAA0279 gene, partial cds//0.0082:770:58//Hs.57652:D87469 F-NT2RP2006071//ESTs//2.1e-24:396:65//Hs.104404:AI337416 F-NT2RP2006098//ESTs//0.97:125:67//Hs.97996:AA405970 F-NT2RP2006100 F-NT2RP2006103//ESTs//5.2e-11:102:83//Hs.125656:AA883135 F-NT2RP2006106//ESTs//1.6e-78:456:90//Hs.133496:AA315349 F-NT2RP2006141//ESTs//1.7e-20:262:72//Hs.128677:AA649240 F-NT2RP2006166 F-NT2RP2006184//H.sapiens p53 mRNA for transmembrane protein//1.0:94:73//Hs.74368:X69910 F-NT2RP2006186//Homo sapiens mRNA for KIAA0554 protein, partial cds//2.5e-114:567:96//Hs.109299:AB014554 F-NT2RP2006196//Homo sapiens mRNA for KIAA0772 protein, complete cds//2.0e-23:187:85//Hs.15519:AB018315 F-NT2RP2006200//ESTs//1.0:224:62//Hs.144100:AI205503 F-NT2RP2006219//H.sapiens mRNA for DGCR6 protein//4.4e-118:618:93//Hs.153910:X96484 F-NT2RP2006237 F-NT2RP2006238 F-NT2RP2006258//ESTs//0.0034:143:69//Hs.145798:AI269970 F-NT2RP2006261//H.sapiens mRNA for serine/threonine protein kinase ENK//0.019:111:71//Hs.157199:X97630 F-NT2RP2006275//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//2.4e-05:388:60//Hs.75111:D87258 F-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//2.1e-121:598:97//Hs.3404:AF035262 F-NT2RP2006320//ESTs. Moderately similar to maternal transcript Ma id [M.musculus]//1.9e-29:151:100//Hs.36794:AI038407 F-NT2RP2006321//ESTs//7.0e-15:141:82//Hs.71241:H09371 F-NT2RP2006323//Homo sapiens mRNA for NBPhox, complete cds//4.7e-06:170:70//Hs.87202:D82344 F-NT2RP2006333//Homo sapiens TRRAP protein (TRRAP) mRNA, complete cds//0.11:43:100//Hs.6892:AF076974 F-NT2RP2006334//Homo sapiens mRNA for KIAA0602 protein, partial cds//3.1e-05:233:65//Hs.37656:AB011174 F-NT2RP2006365//ESTs//8.9e-46:268:93//Hs.58403:AA058501 F-NT2RP2006393//ESTs//1.2e-20:159:86//Hs.146018:AA280341 F-NT2RP2006436//Human homeodomain-containing protein (HAWF) mRNA, complete cds//0.59:133:64//Hs.95838:AF059734 F-NT2RP2006441//ESTs//1.6e-82:400:98//Hs.143514:AI221934 F-NT2RP2006454//EST//5.2e-07:172:68//Hs.157742:AI360509 F-NT2RP2006456 F-NT2RP2006464//Homo sapiens mRNA for AND-1 protein//1.1e-149:545:98//Hs.72160:AJ006266 F-NT2RP2006467 F-NT2RP2006472 F-NT2RP2006514//ESTs//5.6e-05:192:66//Hs.135750:AA160048 F-NT2RP2006554//EST//0.60:116:65//Hs.160110:AA922134 F-NT2RP2006565//Homo sapiens secretory carrier-associated membrane protein (SCAMP) mRNA, complete cds//2.1e-115:669:90//Hs.31218:AF038966 F-NT2RP2006571//Cytochrome P450, subfamily IIA (phenobarbital-inducible), polypeptide 6//2.1e-24:476:64//Hs.73864:U20209 F-NT2RP2006573 F-NT2RP2006598//ESTs//1.3e-16:137:85//Hs.131350:AA805223 F-NT2RP3000002//ESTs//3.6e-32:215:86//Hs.155446:AA188180 F-NT2RP3000031//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//1.9e-137:637:98//Hs.6764:AJ011972 F-NT2RP3000046//Homo sapiens TTF-1 interacting peptide 20 mRNA, partial cds//9.1e-07:568:61//Hs.79531:AF000560 F-NT2RP3000047 F-NT2RP3000050//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//1.2e-58:633:69//Hs.37138:U35376 F-NT2RP3000055//ESTs//1.2e-07:200:66//Hs.127362:AA954961 F-NT2RP3000068 F-NT2RP3000072//EST//0.99:199:63//Hs.8469:T40769 F-NT2RP3000080//Landsteiner-Wiener blood group glycoprotein//4.8e-41:353:78//Hs.108287:L27670 F-NT2RP3000085//Propionyl-coA carboxylase alpha chain//7.9e-30:56:56//Hs.80741:X14608 F-NT2RP3000092//EST//2.0e-15:94:97//Hs.145389:AI253140 F-NT2RP3000109//ESTs//6.8e-11:77:96//Hs.153931:AI243595 F-NT2RP3000134//Homo sapiens PAC clone DJ0905J08 from Tpl2-pl4//5.0e-94:438:100//Hs.8173:AC005189 F-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds//2.9e-182:849:98//Hs.13273:AB011164</p>
---	---

【0875】

【表574】

F-NT2RP3000149//Human Line-1 repeat mRNA with 2 open reading frame s//4.1e-20:133:94//Hs.23094:M19503
 F-NT2RP3000186//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//6.6e-08:152:71//Hs.127338:AB007961
 F-NT2RP3000197//ESTs//1.1e-58:301:96//Hs.87461:AA292779
 F-NT2RP3000207
 F-NT2RP3000220
 F-NT2RP3000233//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//6.6e-20:509:58//Hs.122967:AF059569
 F-NT2RP3000235//ESTs//1.7e-06:220:62//Hs.42771:N26740
 F-NT2RP3000247//Human mRNA for KIAA0218 gene, complete cds//6.7e-11:691:86//Hs.75863:D86972
 F-NT2RP3000251//ESTs//6.7e-48:245:97//Hs.28249:AA203733
 F-NT2RP3000252
 F-NT2RP3000255
 F-NT2RP3000267//ESTs//0.14:53:92//Hs.151586:W45568
 F-NT2RP3000299//Homo sapiens enhancer of filamentation (HEF1) mRNA, complete cds//1.7e-13:214:67//Hs.80261:L43821
 F-NT2RP3000312//ESTs//2.6e-50:255:97//Hs.146263:AA255863
 F-NT2RP3000320//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.0088:236:63//Hs.102732:U88153
 F-NT2RP3000324//ESTs//3.8e-10:102:83//Hs.55495:A1091242
 F-NT2RP3000333//ESTs, Weakly similar to mitogen-activated kinase kinase 5 [H.sapiens]//0.57:189:65//Hs.46146:AA418097
 F-NT2RP3000341//Human mRNA for KIAA0392 gene, partial cds//1.1e-49:442:78//Hs.40100:AB002390
 F-NT2RP3000348
 F-NT2RP3000350//H.sapiens mRNA for GTP-binding protein//0.93:164:59//Hs.78582:X80754
 F-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//1.8e-43:649:66//Hs.101642:X60673
 F-NT2RP3000361//ESTs//2.6e-112:531:98//Hs.17672:AA305921
 F-NT2RP3000366//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-18A [Lymnaea stagnalis]//4.0e-116:596:95//Hs.21094:A1337016
 F-NT2RP3000393//ESTs//2.6e-18:137:89//Hs.115600:AA351639
 F-NT2RP3000397//ESTs//8.7e-44:355:73//Hs.121961:AA777873
 F-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds//1.6e-175:841:97//Hs.28307:AF071185
 F-NT2RP3000418//Human Line-1 repeat mRNA with 2 open reading frame s//2.7e-33:610:65//Hs.23094:M19503
 F-NT2RP3000433//ESTs//1.5e-32:246:69//Hs.120892:AA724948
 F-NT2RP3000439//Adenosine A2b receptor//0.44:210:62//Hs.45743:X68487
 F-NT2RP3000441
 F-NT2RP3000449//ESTs//0.60:177:64//Hs.132605:A1051562
 F-NT2RP3000451//Receptor protein-tyrosine kinase EDDR1//0.95:315:58//Hs.75562:U48705
 F-NT2RP3000456//ESTs//7.5e-23:140:92//Hs.5209:AA780068
 F-NT2RP3000484//EST//2.5e-06:166:67//Hs.149950:A1289822
 F-NT2RP3000487//ESTs//1.2e-63:311:98//Hs.143304:A1084058
 F-NT2RP3000512//Homo sapiens box 83//3.1e-18:109:97//Hs.49931:X16667
 F-NT2RP3000526//ESTs//3.7e-74:424:93//Hs.42991:N21379
 F-NT2RP3000527//Human mRNA for KIAA0211 gene, complete cds//8.0e-36:706:63//Hs.79347:D86966
 F-NT2RP3000531//ESTs//9.6e-75:392:95//Hs.144148:H08308
 F-NT2RP3000542//ESTs//3.2e-88:448:96//Hs.30622:AA486412
 F-NT2RP3000561//EST//0.88:92:64//Hs.148290:AA908404
 F-NT2RP3000562//ESTs//1.1e-112:522:99//Hs.125153:AA453723
 F-NT2RP3000578
 F-NT2RP3000582//ESTs//2.1e-82:413:97//Hs.118544:R17277
 F-NT2RP3000584
 F-NT2RP3000590//ESTs//1.0:134:64//Hs.12969:N56904
 F-NT2RP3000592//Paired basic amino acid cleaving system 4//3.4e-05:502:57//Hs.77234:AB001914
 F-NT2RP3000596//ESTs//6.8e-71:361:95//Hs.118741:AA179811
 F-NT2RP3000599//ESTs, Weakly similar to T19810.6 [C.elegans]//9.3e-61:355:92//Hs.114622:AA693492
 F-NT2RP3000603//Human mRNA for KIAA0227 gene, partial cds//6.3e-10:553:58//Hs.79170:D86980
 F-NT2RP3000605//ESTs//5.8e-51:283:94//Hs.127152:A1421203
 F-NT2RP3000622//ESTs//1.7e-10:72:98//Hs.155360:AA984683
 F-NT2RP3000624//64 KD AUTOANTIGEN D1//0.99:194:61//Hs.79386:X54162
 F-NT2RP3000628//ESTs//0.96:221:61//Hs.131161:A1017333
 F-NT2RP3000632//ESTs//4.4e-53:244:77//Hs.143010:AA767904
 F-NT2RP3000644//Small inducible cytokine A5 (RANTES)//3.0e-49:343:84//Hs.155464:AF088219
 F-NT2RP3000661
 F-NT2RP3000665//Homo sapiens putative transcription factor CA150 mRNA, complete cds//0.62:305:59//Hs.13063:AF017789
 F-NT2RP3000685
 F-NT2RP3000690//EST//1.0:149:64//Hs.140263:AA709001
 F-NT2RP3000736//ESTs//5.3e-26:146:97//Hs.98613:D83884
 F-NT2RP3000739//ESTs//0.0046:66:87//Hs.6880:W26854
 F-NT2RP3000742//ESTs//5.5e-08:311:61//Hs.152224:A1369426
 F-NT2RP3000753//ESTs//2.6e-63:318:97//Hs.153000:AA777765
 F-NT2RP3000759//Homo sapiens mRNA for follistatin-related protein (FRP), complete cds//1.6e-38:245:91//Hs.2427:D89937
 F-NT2RP3000815
 F-NT2RP3000825//EST//1.0:220:61//Hs.135944:M45132
 F-NT2RP3000826//Homo sapiens deltex (Dx) mRNA, complete cds//0.00040:263:65//Hs.124024:AF053700
 F-NT2RP3000836//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 HOMOLOG 2 [H.sapiens]//1.1e-71:363:96//Hs.23803:AA126476
 F-NT2RP3000841//EST//0.36:224:60//Hs.162094:AA524012
 F-NT2RP3000845//H.sapiens mRNA for serine/threonine protein kinase EMK//6.5e-48:593:68//Hs.157199:X97630
 F-NT2RP3000847//ESTs//0.0028:56:92//Hs.116406:AA209520
 F-NT2RP3000850//Small inducible cytokine A5 (RANTES)//2.0e-49:323:86//Hs.155464:AF088219
 F-NT2RP3000852
 F-NT2RP3000859//ESTs//0.39:169:62//Hs.148948:AA699918
 F-NT2RP3000865//EST//0.15:236:62//Hs.123366:AA811476
 F-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds//6.4e-31:766:60//Hs.15432:U53445
 F-NT2RP3000869//Human plectin (PLEC1) mRNA, complete cds//1.1e-13:701:60//Hs.79706:U53204
 F-NT2RP3000875
 F-NT2RP3000901//ESTs//8.2e-26:191:87//Hs.18793:R99101
 F-NT2RP3000904//EST//2.4e-49:240:100//Hs.160842:A1348374
 F-NT2RP3000917
 F-NT2RP3000919//MAP KINASE PHOSPHATASE-1//0.19:340:60//Hs.109895:X68277
 F-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//7.7e-44:351:83//Hs.2953:X84407
 F-NT2RP3000980//ESTs//6.5e-10:102:81//Hs.86950:A1204212
 F-NT2RP3000994//ESTs//4.1e-120:571:98//Hs.127295:AA918411
 F-NT2RP3001004//ESTs//1.1e-76:438:88//Hs.144554:N92198
 F-NT2RP3001007
 F-NT2RP3001055//ESTs, Weakly similar to weak similarity to procollagen alpha chain (I) chain [C.elegans]//2.9e-121:588:98//Hs.128781:AA160707
 F-NT2RP3001057//ESTs, Highly similar to ZINC FINGER PROTEIN 45 [Homo sapiens]//9.8e-54:282:97//Hs.30303:A1244662
 F-NT2RP3001081//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.7e-51:534:74//Hs.27007:AF060219
 F-NT2RP3001084//Homo sapiens mRNA for KIAA0782 protein, partial cds//3.7e-16:474:60//Hs.21264:AB018325
 F-NT2RP3001096//Homo sapiens mRNA for cartilage-associated protein (CASP)//4.4e-16:428:60//Hs.155481:AJ006470
 F-NT2RP3001107//Human mRNA for KIAA0215 gene, complete cds//2.8e-34:712:64//Hs.82292:D86969
 F-NT2RP3001109//ESTs//1.2e-67:323:99//Hs.134734:A1337050
 F-NT2RP3001111
 F-NT2RP3001113//EST//1.1e-33:173:99//Hs.112640:AA609088
 F-NT2RP3001115//EST//1.3e-22:122:100//Hs.162990:AA688023
 F-NT2RP3001116//ESTs//1.1e-15:93:98//Hs.58412:W74779
 F-NT2RP3001119//Homo sapiens BC-2 protein mRNA, complete cds//0.96:258:61//Hs.12107:AF042384
 F-NT2RP3001120//Zinc finger protein 136 (clone pH2-20)//2.4e-77:687:75//Hs.69740:U09367
 F-NT2RP3001126//Homo sapiens mRNA for KIAA0775 protein, complete cds//0.00018:341:60//Hs.94790:AB018318
 F-NT2RP3001133//Homo sapiens box AA//0.00011:484:59//Hs.77637:M74297
 F-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//1.1e-180:851:98//Hs.5378:AB018305
 F-NT2RP3001147
 F-NT2RP3001150//PUTATIVE TACHYKININ RECEPTOR//0.97:257:59//Hs.957:M84605
 F-NT2RP3001155//Homo sapiens mRNA for AMD-1 protein//1.7e-191:891:98//Hs.72160:AJ006256
 F-NT2RP3001176
 F-NT2RP3001214//EST//0.88:218:60//Hs.161147:A1417859
 F-NT2RP3001216//ESTs//1.5e-66:340:96//Hs.105994:W19981
 F-NT2RP3001221//ESTs, Weakly similar to W05D6.7 [C.elegans]//1.7e-97:512:95//Hs.103816:AA130866
 F-NT2RP3001232//EST//0.0016:116:71//Hs.136498:AA594010
 F-NT2RP3001236//ESTs//3.7e-97:455:99//Hs.157488:A1362756
 F-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B//1.7e-20:501:62/

【0876】

【表575】

/Hs.103042:L06237	F-NT2RP3001245//ESTs//1.1e-80:434:93//Hs.22587:AA743132	F-NT2RP3001646	F-NT2RP3001671//Homo sapiens mRNA for NSI-binding protein (NSI-BP)
F-NT2RP3001253//Human prepromultimerin mRNA, complete cds//0.99:29	F-NT2RP3001253//Human prepromultimerin mRNA, complete cds//0.99:29	//1.1e-172:816:98//Hs.159597:AJ012449	//1.1e-172:816:98//Hs.159597:AJ012449
3:60//Hs.32934:U27109	F-NT2RP3001253//Human prepromultimerin mRNA, complete cds//0.99:29	F-NT2RP3001672//ESTs//5.0e-16:138:82//Hs.151864:T69027	F-NT2RP3001672//ESTs//5.0e-16:138:82//Hs.151864:T69027
F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete c	F-NT2RP3001260//Homo sapiens mRNA for KIAA0726 protein, complete c	F-NT2RP3001676//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA	F-NT2RP3001676//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA
ds//1.2e-48:761:64//Hs.107809:AB018269	ds//1.2e-48:761:64//Hs.107809:AB018269	[Pseudomonas fluorescens]//9.0e-53:375:85//Hs.41127:AA555184	[Pseudomonas fluorescens]//9.0e-53:375:85//Hs.41127:AA555184
F-NT2RP3001268//Zinc finger protein 45 (a Kruppel-associated box	F-NT2RP3001268//Zinc finger protein 45 (a Kruppel-associated box	F-NT2RP3001678//Human mRNA for KIAA0233 gene, complete cds//0.21:3	F-NT2RP3001678//Human mRNA for KIAA0233 gene, complete cds//0.21:3
(KRAB) domain polypeptide//1.2e-42:454:72//Hs.41728:L75847	(KRAB) domain polypeptide//1.2e-42:454:72//Hs.41728:L75847	21:65//Hs.79077:D87071	21:65//Hs.79077:D87071
F-NT2RP3001272//ESTs//5.0e-21:162:87//Hs.69149:AA102566	F-NT2RP3001272//ESTs//5.0e-21:162:87//Hs.69149:AA102566	F-NT2RP3001679//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROT	F-NT2RP3001679//ESTs, Highly similar to HYPOTHETICAL 68.7 KD PROT
F-NT2RP3001274	F-NT2RP3001274	EIN ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]//4.0e-111:5	EIN ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]//4.0e-111:5
F-NT2RP3001281//ESTs//2.1e-39:186:73//Hs.161662:AA836811	F-NT2RP3001281//ESTs//2.1e-39:186:73//Hs.161662:AA836811	18:99//Hs.20364:AI420022	18:99//Hs.20364:AI420022
F-NT2RP3001291//Human mRNA for KIAA0281 gene, complete cds//2.4e-4	F-NT2RP3001291//Human mRNA for KIAA0281 gene, complete cds//2.4e-4	F-NT2RP3001688//Homo sapiens mRNA expressed in thyroid gland//1.0:	F-NT2RP3001688//Homo sapiens mRNA expressed in thyroid gland//1.0:
8:544:69//Hs.31463:D87457	8:544:69//Hs.31463:D87457	230:63//Hs.7486:D83198	230:63//Hs.7486:D83198
F-NT2RP3001307//Human homeodomain protein (Prox 1) mRNA, complete	F-NT2RP3001307//Human homeodomain protein (Prox 1) mRNA, complete	F-NT2RP3001690//EST//0.15:291:59//Hs.162336:AA564329	F-NT2RP3001690//EST//0.15:291:59//Hs.162336:AA564329
cds//0.72:151:68//Hs.159437:U44060	cds//0.72:151:68//Hs.159437:U44060	F-NT2RP3001698//ESTs//0.24:134:69//Hs.129551:AA885219	F-NT2RP3001698//ESTs//0.24:134:69//Hs.129551:AA885219
F-NT2RP3001318//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase	F-NT2RP3001318//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase	F-NT2RP3001708//ESTs, Weakly similar to TWISTED GASTRULATION PROTE	F-NT2RP3001708//ESTs, Weakly similar to TWISTED GASTRULATION PROTE
(glycogen debranching enzyme, glycogen storage disease type III)//	(glycogen debranching enzyme, glycogen storage disease type III)//	IN PRECURSOR [D.melanogaster]//1.4e-31:191:94//Hs.131279:AA486291	IN PRECURSOR [D.melanogaster]//1.4e-31:191:94//Hs.131279:AA486291
0.012:522:56//Hs.904:U84010	0.012:522:56//Hs.904:U84010	F-NT2RP3001712//Human SLP-76 associated protein mRNA, complete cds	F-NT2RP3001712//Human SLP-76 associated protein mRNA, complete cds
F-NT2RP3001325//ESTs//2.9e-80:396:97//Hs.99838:AA204731	F-NT2RP3001325//ESTs//2.9e-80:396:97//Hs.99838:AA204731	//0.41:259:59//Hs.58435:AF001862	//0.41:259:59//Hs.58435:AF001862
F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds//1.6e-3	F-NT2RP3001338//Human mRNA for KIAA0211 gene, complete cds//1.6e-3	F-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEI	F-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEI
0:345:73//Hs.79347:D86966	0:345:73//Hs.79347:D86966	N 1 PRECURSOR [Mus musculus]//7.6e-159:747:98//Hs.6823:W18181	N 1 PRECURSOR [Mus musculus]//7.6e-159:747:98//Hs.6823:W18181
F-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete c	F-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete c	F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding pro	F-NT2RP3001724//Homo sapiens chromodomain-helicase-DNA-binding pro
ds//6.3e-67:559:80//Hs.18586:AB007920	ds//6.3e-67:559:80//Hs.18586:AB007920	tein mRNA, complete cds//4.4e-161:565:97//Hs.159273:AF054177	tein mRNA, complete cds//4.4e-161:565:97//Hs.159273:AF054177
F-NT2RP3001340//Homo sapiens hyperpolarization-activated channel 1	F-NT2RP3001340//Homo sapiens hyperpolarization-activated channel 1	F-NT2RP3001727//ESTs, Highly similar to HYPOTHETICAL 37.7 KD PROT	F-NT2RP3001727//ESTs, Highly similar to HYPOTHETICAL 37.7 KD PROT
(IH1) mRNA, partial cds//0.00019:473:61//Hs.124161:AF065164	(IH1) mRNA, partial cds//0.00019:473:61//Hs.124161:AF065164	EIN ZK686.3 IN CHROMOSOME III [Caenorhabditis elegans]//3.5e-116:5	EIN ZK686.3 IN CHROMOSOME III [Caenorhabditis elegans]//3.5e-116:5
F-NT2RP3001355//ESTs, Weakly similar to ADP-ATP CARRIER PROTEIN, L	F-NT2RP3001355//ESTs, Weakly similar to ADP-ATP CARRIER PROTEIN, L	54:98//Hs.144332:AA046836	54:98//Hs.144332:AA046836
LIVER ISOFORM T2 [H.sapiens]//1.1e-81:421:96//Hs.32508:H29831	LIVER ISOFORM T2 [H.sapiens]//1.1e-81:421:96//Hs.32508:H29831	F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds//1.3e-10	F-NT2RP3001730//Human mRNA for KIAA0128 gene, partial cds//1.3e-10
F-NT2RP3001356//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.1	F-NT2RP3001356//Homo sapiens Nck-2 (NCK2) mRNA, complete cds//0.1	5:811:78//Hs.90998:D50918	5:811:78//Hs.90998:D50918
5:313:60//Hs.129725:AF047487	5:313:60//Hs.129725:AF047487	F-NT2RP3001739	F-NT2RP3001739
F-NT2RP3001374//ESTs//0.98:269:59//Hs.125303:AA873022	F-NT2RP3001374//ESTs//0.98:269:59//Hs.125303:AA873022	F-NT2RP3001752//ELK1, member of ETS oncogene family//7.2e-35:299:8	F-NT2RP3001752//ELK1, member of ETS oncogene family//7.2e-35:299:8
F-NT2RP3001383//Homo sapiens mRNA for Sck, partial cds//0.73:173:6	F-NT2RP3001383//Homo sapiens mRNA for Sck, partial cds//0.73:173:6	0//Hs.116549:AL009172	0//Hs.116549:AL009172
5//Hs.30965:AB001451	5//Hs.30965:AB001451	F-NT2RP3001753//Human putative cerebral cortex transcriptional reg	F-NT2RP3001753//Human putative cerebral cortex transcriptional reg
F-NT2RP3001384//Homo sapiens mRNA for HRHFB2018, partial cds//2.1	F-NT2RP3001384//Homo sapiens mRNA for HRHFB2018, partial cds//2.1	ulator T-Brain-1 (Tbr-1) mRNA, complete cds//0.10:528:56//Hs.2213	ulator T-Brain-1 (Tbr-1) mRNA, complete cds//0.10:528:56//Hs.2213
e-158:743:98//Hs.146214:AB015332	e-158:743:98//Hs.146214:AB015332	8:U49250	8:U49250
F-NT2RP3001392//ESTs//0.013:246:63//Hs.95111:AA514595	F-NT2RP3001392//ESTs//0.013:246:63//Hs.95111:AA514595	F-NT2RP3001764//Human protein-tyrosine phosphatase mRNA, complete	F-NT2RP3001764//Human protein-tyrosine phosphatase mRNA, complete
F-NT2RP3001396//ESTs//5.6e-16:141:85//Hs.97664:H10783	F-NT2RP3001396//ESTs//5.6e-16:141:85//Hs.97664:H10783	cds//2.4e-47:725:64//Hs.41688:U27193	cds//2.4e-47:725:64//Hs.41688:U27193
F-NT2RP3001398//Zinc finger protein 45 (a Kruppel-associated box	F-NT2RP3001398//Zinc finger protein 45 (a Kruppel-associated box	F-NT2RP3001777//Human eukaryotic translation initiation factor (el	F-NT2RP3001777//Human eukaryotic translation initiation factor (el
(KRAB) domain polypeptide//1.0e-05:189:66//Hs.41728:L75847	(KRAB) domain polypeptide//1.0e-05:189:66//Hs.41728:L75847	F3) mRNA, complete cds//0.42:198:61//Hs.57783:U78525	F3) mRNA, complete cds//0.42:198:61//Hs.57783:U78525
F-NT2RP3001399//Homo sapiens mitochondrial citrate transport prote	F-NT2RP3001399//Homo sapiens mitochondrial citrate transport prote	F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cd	F-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cd
in (CTP) mRNA, 3' end//0.77:132:66//Hs.111024:L77567	in (CTP) mRNA, 3' end//0.77:132:66//Hs.111024:L77567	s//9.1e-153:710:98//Hs.28169:AB007928	s//9.1e-153:710:98//Hs.28169:AB007928
F-NT2RP3001407//EST//0.015:167:65//Hs.42217:H96658	F-NT2RP3001407//EST//0.015:167:65//Hs.42217:H96658	F-NT2RP3001792//Human M4 protein mRNA, complete cds//5.6e-27:358:6	F-NT2RP3001792//Human M4 protein mRNA, complete cds//5.6e-27:358:6
F-NT2RP3001420//ESTs//1.0:214:60//Hs.91226:AA649047	F-NT2RP3001420//ESTs//1.0:214:60//Hs.91226:AA649047	9//Hs.79024:L03532	9//Hs.79024:L03532
F-NT2RP3001426	F-NT2RP3001426	F-NT2RP3001799//ESTs//0.0088:178:64//Hs.134938:AI091361	F-NT2RP3001799//ESTs//0.0088:178:64//Hs.134938:AI091361
F-NT2RP3001427	F-NT2RP3001427	F-NT2RP3001819//Collagen, type IX, alpha 3//0.026:530:58//Hs.5356	F-NT2RP3001819//Collagen, type IX, alpha 3//0.026:530:58//Hs.5356
F-NT2RP3001428//Neurotrophic tyrosine kinase, receptor, type 1//1.	F-NT2RP3001428//Neurotrophic tyrosine kinase, receptor, type 1//1.	3:L41162	3:L41162
8e-73:431:91//Hs.85844:X66397	8e-73:431:91//Hs.85844:X66397	F-NT2RP3001844//Homo sapiens mRNA for hair keratin acidic 3-11//0.	F-NT2RP3001844//Homo sapiens mRNA for hair keratin acidic 3-11//0.
F-NT2RP3001432//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX	F-NT2RP3001432//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX	90:379:58//Hs.32950:X82634	90:379:58//Hs.32950:X82634
WARNING ENTRY !!!! [H.sapiens]//6.9e-05:195:65//Hs.115868:AA568393	WARNING ENTRY !!!! [H.sapiens]//6.9e-05:195:65//Hs.115868:AA568393	F-NT2RP3001854//ESTs//1.5e-100:501:96//Hs.72217:AA166729	F-NT2RP3001854//ESTs//1.5e-100:501:96//Hs.72217:AA166729
F-NT2RP3001447	F-NT2RP3001447	F-NT2RP3001855//Human homeobox-containing protein mRNA, complete c	F-NT2RP3001855//Human homeobox-containing protein mRNA, complete c
F-NT2RP3001449//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.00033:187:6	F-NT2RP3001449//RYANODINE RECEPTOR, SKELETAL MUSCLE//0.00033:187:6	ds//7.8e-35:481:67//Hs.158225:U68727	ds//7.8e-35:481:67//Hs.158225:U68727
8//Hs.89631:U48508	8//Hs.89631:U48508	F-NT2RP3001857//ESTs//2.7e-85:414:98//Hs.151001:AA564706	F-NT2RP3001857//ESTs//2.7e-85:414:98//Hs.151001:AA564706
F-NT2RP3001453//ESTs//0.020:260:60//Hs.97882:AA203212	F-NT2RP3001453//ESTs//0.020:260:60//Hs.97882:AA203212	F-NT2RP3001896//ESTs, Weakly similar to F20D12.3 gene product [C.e	F-NT2RP3001896//ESTs, Weakly similar to F20D12.3 gene product [C.e
F-NT2RP3001457//ESTs//9.4e-29:165:94//Hs.71749:AA988323	F-NT2RP3001457//ESTs//9.4e-29:165:94//Hs.71749:AA988323	legans]//2.9e-94:452:98//Hs.54952:AA872675	legans]//2.9e-94:452:98//Hs.54952:AA872675
F-NT2RP3001459	F-NT2RP3001459	F-NT2RP3001898//Homo sapiens mRNA for synaptogyrin Ia//0.65:245:61	F-NT2RP3001898//Homo sapiens mRNA for synaptogyrin Ia//0.65:245:61
F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA,	F-NT2RP3001472//Homo sapiens Sox-like transcriptional factor mRNA,	//Hs.6139:AL022326	//Hs.6139:AL022326
complete cds//4.2e-10:168:70//Hs.32317:AF072836	complete cds//4.2e-10:168:70//Hs.32317:AF072836	F-NT2RP3001915//ESTs//1.1e-83:397:99//Hs.157125:AA273896	F-NT2RP3001915//ESTs//1.1e-83:397:99//Hs.157125:AA273896
F-NT2RP3001490//ESTs//3.1e-35:198:94//Hs.163665:AA250877	F-NT2RP3001490//ESTs//3.1e-35:198:94//Hs.163665:AA250877	F-NT2RP3001926//EST//0.53:362:57//Hs.127917:AA969185	F-NT2RP3001926//EST//0.53:362:57//Hs.127917:AA969185
F-NT2RP3001495//ESTs//2.5e-47:239:98//Hs.128045:AA970231	F-NT2RP3001495//ESTs//2.5e-47:239:98//Hs.128045:AA970231	F-NT2RP3001929//ESTs//7.4e-16:141:82//Hs.138852:AA284247	F-NT2RP3001929//ESTs//7.4e-16:141:82//Hs.138852:AA284247
F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor T	F-NT2RP3001497//Homo sapiens multiple membrane spanning receptor T	F-NT2RP3001931	F-NT2RP3001931
RCB (TRCB) mRNA, complete cds//2.8e-172:804:98//Hs.28285:AF064801	RCB (TRCB) mRNA, complete cds//2.8e-172:804:98//Hs.28285:AF064801	F-NT2RP3001938//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//	F-NT2RP3001938//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//
F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-B)	F-NT2RP3001527//Human lymphoid-specific SP100 homolog (LYSP100-B)	0.0022:268:61//Hs.106070:U22398	0.0022:268:61//Hs.106070:U22398
mRNA, complete cds//9.4e-139:743:91//Hs.85283:U36500	mRNA, complete cds//9.4e-139:743:91//Hs.85283:U36500	F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete c	F-NT2RP3001943//Homo sapiens mRNA for KIAA0675 protein, complete c
F-NT2RP3001529//ESTs, Moderately similar to topoisomerase I C-term	F-NT2RP3001529//ESTs, Moderately similar to topoisomerase I C-term	ds//5.8e-167:815:96//Hs.15869:AB014575	ds//5.8e-167:815:96//Hs.15869:AB014575
inal fragment [H.sapiens]//0.28:224:65//Hs.105912:AI431328	inal fragment [H.sapiens]//0.28:224:65//Hs.105912:AI431328	F-NT2RP3001944//ESTs//0.00052:60:91//Hs.131731:AI339335	F-NT2RP3001944//ESTs//0.00052:60:91//Hs.131731:AI339335
F-NT2RP3001538//ESTs//4.1e-05:139:71//Hs.148425:AI198074	F-NT2RP3001538//ESTs//4.1e-05:139:71//Hs.148425:AI198074	F-NT2RP3001969	F-NT2RP3001969
F-NT2RP3001554//Microtubule-associated protein 1A//9.8e-16:327:64//	F-NT2RP3001554//Microtubule-associated protein 1A//9.8e-16:327:64//	F-NT2RP3001989//EST//0.00016:263:63//Hs.144096:AI032180	F-NT2RP3001989//EST//0.00016:263:63//Hs.144096:AI032180
Hs.147918:U38291	Hs.147918:U38291	F-NT2RP3002002//Small inducible cytokine A5 (RANTES)//4.0e-61:293:	F-NT2RP3002002//Small inducible cytokine A5 (RANTES)//4.0e-61:293:
F-NT2RP3001580//Insulin-like growth factor binding protein 2//1.9	F-NT2RP3001580//Insulin-like growth factor binding protein 2//1.9	83//Hs.155464:AF088219	83//Hs.155464:AF088219
e-06:426:59//Hs.162:X16302	e-06:426:59//Hs.162:X16302	F-NT2RP3002004//H.sapiens mRNA for FAST kinase//5.2e-28:104:100//H	F-NT2RP3002004//H.sapiens mRNA for FAST kinase//5.2e-28:104:100//H
F-NT2RP3001587//Guanine nucleotide binding protein (G protein), al	F-NT2RP3001587//Guanine nucleotide binding protein (G protein), al	s.75087:X86779	s.75087:X86779
pha 11 (Gq class)//0.049:185:65//Hs.1686:M69013	pha 11 (Gq class)//0.049:185:65//Hs.1686:M69013	F-NT2RP3002007//ESTs//0.025:88:69//Hs.163310:AA856946	F-NT2RP3002007//ESTs//0.025:88:69//Hs.163310:AA856946
F-NT2RP3001589//Human mRNA for tryptophan hydroxylase (EC 1.14.16.	F-NT2RP3001589//Human mRNA for tryptophan hydroxylase (EC 1.14.16.	F-NT2RP3002014//ESTs//4.8e-70:291:98//Hs.123693:AA283821	F-NT2RP3002014//ESTs//4.8e-70:291:98//Hs.123693:AA283821
4)//9.6e-51:345:82//Hs.144563:AF057280	4)//9.6e-51:345:82//Hs.144563:AF057280	F-NT2RP3002033//Homo sapiens mRNA for HYA22, complete cds//0.021:1	F-NT2RP3002033//Homo sapiens mRNA for HYA22, complete cds//0.021:1
F-NT2RP3001607//ESTs//1.3e-07:299:63//Hs.43231:N22688	F-NT2RP3001607//ESTs//1.3e-07:299:63//Hs.43231:N22688	75:67//Hs.147189:D88153	75:67//Hs.147189:D88153
F-NT2RP3001608//ESTs//5.7e-14:85:98//Hs.161133:AI091349	F-NT2RP3001608//ESTs//5.7e-14:85:98//Hs.161133:AI091349	F-NT2RP3002045//ESTs, Highly similar to ALPHA-ADAPTIN [M.musculus]	F-NT2RP3002045//ESTs, Highly similar to ALPHA-ADAPTIN [M.musculus]
F-NT2RP3001621//ESTs//1.6e-106:310:96//Hs.128505:AA306435	F-NT2RP3001621//ESTs//1.6e-106:310:96//Hs.128505:AA306435	//3.8e-48:353:81//Hs.127507:AA993745	//3.8e-48:353:81//Hs.127507:AA993745
F-NT2RP3001629	F-NT2RP3001629	F-NT2RP3002054//ESTs, Weakly similar to KIAA0319 [H.sapiens]//3.0	F-NT2RP3002054//ESTs, Weakly similar to KIAA0319 [H.sapiens]//3.0
F-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//1.4	F-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//1.4	e-25:212:83//Hs.71622:AA195155	e-25:212:83//Hs.71622:AA195155
e-62:276:97//Hs.9899:AF099149	e-62:276:97//Hs.9899:AF099149	F-NT2RP3002056//ESTs, Highly similar to RETINOBLASTOMA BINDING PR	F-NT2RP3002056//ESTs, Highly similar to RETINOBLASTOMA BINDING PR
F-NT2RP3001642//ESTs//1.0:148:63//Hs.159495:T70173	F-NT2RP3001642//ESTs//1.0:148:63//Hs.159495:T70173	OTEIN I [Homo sapiens]//4.2e-82:407:97//Hs.131888:AI091806	OTEIN I [Homo sapiens]//4.2e-82:407:97//Hs.131888:AI091806

【0877】

【表576】

F-NT2RP3002057//Human Line-1 repeat mRNA with 2 open reading frame s//3.7e-21:168:85//Hs.23094:M19503	F-NT2RP3002663//ESTs, Highly similar to OXYSTEROL-BINDING PROTEIN [Homo sapiens]//4.1e-38:493:70//Hs.41086:A1337400
F-NT2RP3002062//EST//0.46:198:62//Hs.157711:A1359710	F-NT2RP3002671//ESTs//3.7e-05:288:59//Hs.161359:A1421991
F-NT2RP3002063//Membrane metallo-endopeptidase (neutral endopeptidase, enkephalinase, CALLA, CD10)//0.91:194:65//Hs.1298:J03779	F-NT2RP3002682//ESTs, Weakly similar to F17C11.8 [C.elegans]//1.6e-61:294:100//Hs.128750:A1367584
F-NT2RP3002081	F-NT2RP3002687
F-NT2RP3002097//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//0.073:297:61//Hs.102732:U88153	F-NT2RP3002688//EST//1.0:312:58//Hs.156800:A1352200
F-NT2RP3002102//EST//2.8e-16:237:67//Hs.136255:T70256	F-NT2RP3002701//EST//0.00083:55:87//Hs.159750:A1393657
F-NT2RP3002108	F-NT2RP3002713//ESTs//0.93:229:61//Hs.150459:A1279514
F-NT2RP3002142//ESTs//4.3e-138:654:98//Hs.5729:AA306018	F-NT2RP3002763//ESTs//1.7e-97:419:96//Hs.121593:W86291
F-NT2RP3002146//H.sapiens mRNA for RanGTPase activating protein 1//0.27:276:62//Hs.5923:X82260	F-NT2RP3002770//Homo sapiens G protein-coupled receptor kinase 6 (GRK6) gene, partial cds//0.91:161:62//Hs.129736:AF040753
F-NT2RP3002147//Human DNA sequence from clone 431H6 on chromosome 16. Contains a novel gene with some homology to mouse Hm1 (Hematological and Neurological expressed sequence 1) downstream of a putative CpG island. Contains ESTs and GSSs//6.0e-51:204:99//Hs.107256:AL031009	F-NT2RP3002785
F-NT2RP3002151//G1 to S phase transition 1//2.6e-37:292:81//Hs.2707:X17644	F-NT2RP3002799//EST//1.7e-17:199:73//Hs.118694:AA148713
F-NT2RP3002163//Human DNA fragmentation factor-45 mRNA, complete cds//0.46:224:60//Hs.155344:U91985	F-NT2RP3002810//ESTs, Weakly similar to KIAA0062 [H.sapiens]//1.4e-76:423:93//Hs.41058:AA844350
F-NT2RP3002165//ESTs, Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNCP [Mus musculus]//3.0e-61:340:93//Hs.11379:AA594140	F-NT2RP3002818//Homo sapiens jerky gene product homolog mRNA, complete cds//2.2e-55:615:70//Hs.105940:AF004715
F-NT2RP3002166//EST//0.039:114:69//Hs.140335:AA737046	F-NT2RP3002861//ESTs//1.1e-88:468:94//Hs.159821:AA524070
F-NT2RP3002173//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//4.0e-39:255:72//Hs.141429:AA631915	F-NT2RP3002869//ESTs//3.4e-23:132:97//Hs.148873:T33582
F-NT2RP3002181//ESTs//3.6e-111:518:99//Hs.128505:AA306435	F-NT2RP3002876//Homo sapiens mRNA for B120, complete cds//2.7e-90:557:88//Hs.123090:AB001895
F-NT2RP3002244//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)//0.98:242:57//Hs.114001:Z20656	F-NT2RP3002877//ESTs//1.1e-19:160:84//Hs.118273:AA626040
F-NT2RP3002248	F-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.8e-181:853:98//Hs.6162:AB018314
F-NT2RP3002255//ESTs//8.4e-19:227:75//Hs.122817:AA772261	F-NT2RP3002911//ESTs//2.8e-07:160:70//Hs.140402:A1138765
F-NT2RP3002273//Homo sapiens homeobox protein A10 (HOXA10) gene, complete cds//0.42:189:62//Hs.110637:AC004080	F-NT2RP3002948//ESTs, Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//1.4e-133:645:97//Hs.3826:U69560
F-NT2RP3002276//ESTs//8.2e-97:463:98//Hs.45120:AA225139	F-NT2RP3002953//Homo sapiens mRNA for KIAA0588 protein, complete cds//5.2e-13:594:57//Hs.74599:AB011160
F-NT2RP3002303//ESTs//7.1e-10:96:87//Hs.135700:AA89386	F-NT2RP3002955//Homo sapiens mRNA for KIAA0719 protein, complete cds//0.76:412:57//Hs.21198:AB018262
F-NT2RP3002304//Protein phosphatase 1, catalytic subunit, beta isoform//1.3e-05:496:60//Hs.21537:X80910	F-NT2RP3002969//EST//3.7e-50:272:94//Hs.162331:AA563870
F-NT2RP3002330//ESTs//1.3e-81:482:90//Hs.121460:AA744871	F-NT2RP3002972//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter//5.1e-35:361:75//Hs.8003:AC004997
F-NT2RP3002343//Homo sapiens potassium channel mRNA, complete cds//0.30:462:56//Hs.143624:AF033383	F-NT2RP3002978//ESTs//2.8e-46:253:95//Hs.151924:A1287703
F-NT2RP3002351//NAD-DEPENDENT METHYLENETETRAHYDROFOLATE DEHYDROGENASE//1.6e-65:588:75//Hs.154672:X16396	F-NT2RP3002985//Human TF1B related factor hBRF (hBRF) mRNA, complete cds//0.071:550:58//Hs.32935:U28838
F-NT2RP3002352//Homo sapiens mRNA for protein encoded by cxcorf5 (7-17A) gene//4.2e-166:770:98//Hs.6483:Y16355	F-NT2RP3002988//EST//0.0016:180:63//Hs.147632:A1218308
F-NT2RP3002377//Homo sapiens mRNA for KIAA0788 protein, partial cds//7.5e-161:911:89//Hs.2397:Z70200	F-NT2RP3003008//Human DNA-binding protein (HRC1) mRNA, complete cds//0.59:201:63//Hs.72925:W91083
F-NT2RP3002399	F-NT2RP3003032//ESTs//9.1e-40:241:92//Hs.113363:C06446
F-NT2RP3002402//ESTs, Weakly similar to F02E9.6 [C.elegans]//4.3e-41:233:94//Hs.22880:AA056274	F-NT2RP3003059//ESTs//0.0015:399:58//Hs.136895:AA897749
F-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//3.9e-140:649:99//Hs.12707:AB014578	F-NT2RP3003061//Ankyrin 1, erythrocytic//4.5e-14:633:59//Hs.1242:X16609
F-NT2RP3002484//ESTs//0.95:166:63//Hs.149993:A1291310	F-NT2RP3003068//EST//0.00014:80:83//Hs.121993:AA777928
F-NT2RP3002501//ESTs//0.92:43:90//Hs.119314:AA432108	F-NT2RP3003071//ESTs//1.1e-62:315:98//Hs.16141:W56079
F-NT2RP3002512//Homo sapiens mRNA for KIAA0466 protein, partial cds//1.0:173:61//Hs.81234:AB007935	F-NT2RP3003078
F-NT2RP3002529//Human vacuolar protein sorting homolog h-vps45 mRNA, complete cds//4.4e-146:763:93//Hs.57738:U35246	F-NT2RP3003101
F-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//5.9e-180:833:98//Hs.19542:AB018272	F-NT2RP3003121//EST, Moderately similar to !!!! ALU SUBFAMILY SC W ARNING ENTRY !!!! [H.sapiens]//0.98:88:68//Hs.99715:AA292700
F-NT2RP3002549//ESTs, Weakly similar to POLYPOIS LOCUS PROTEIN 1 [H.sapiens]//1.3e-42:510:70//Hs.96759:AA469984	F-NT2RP3003133//EST//8.0e-17:218:68//Hs.134815:A1090740
F-NT2RP3002566//Carnitine acetyltransferase//0.032:226:62//Hs.12068:X78706	F-NT2RP3003138//Homo sapiens vasopressin-activated calcium mobilizing putative receptor protein (VACM-1) mRNA, complete cds//0.013:438:57//Hs.101299:AF017061
F-NT2RP3002587//EST//4.8e-31:330:74//Hs.139415:AA426054	F-NT2RP3003139//ESTs//0.020:260:61//Hs.59142:W88975
F-NT2RP3002590//EST//1.3e-40:202:100//Hs.144716:A1187919	F-NT2RP3003145//Homo sapiens aortic carboxypeptidase-like protein ACLP mRNA, complete cds//2.2e-20:430:63//Hs.118397:AF053944
F-NT2RP3002602//RYANODINE RECEPTOR, SKELETAL MUSCLE//1.3e-06:280:63//Hs.89631:U48508	F-NT2RP3003150
F-NT2RP3002603	F-NT2RP3003157//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//2.0e-72:894:68//Hs.37138:U35376
F-NT2RP3002628//Homo sapiens mRNA for MSJ-1, complete cds//1.5e-05:264:61//Hs.3845:AB014888	F-NT2RP3003185//Homo sapiens mRNA for KIAA0521 protein, partial cds//0.045:410:59//Hs.6150:AB011093
F-NT2RP3002631//Homo sapiens ADAM 21 mRNA, partial cds//0.97:320:58//Hs.121287:AF029900	F-NT2RP3003193//Zinc finger protein 10 (KOX 1)//2.4e-74:737:71//Hs.2479:X78933
F-NT2RP3002650//Homo sapiens mRNA for cartilage-associated protein (CASP)//2.6e-13:441:63//Hs.155481:AJ006470	F-NT2RP3003197//ESTs//1.8e-24:130:100//Hs.162504:AA668211
F-NT2RP3002659//Human TAR RNA loop binding protein (TRP-185) mRNA, complete cds//1.7e-05:615:58//Hs.151518:U38847	F-NT2RP3003203//ESTs//3.5e-30:232:82//Hs.6880:W26854
F-NT2RP3002660//ESTs//2.9e-32:164:100//Hs.152982:AA584308	F-NT2RP3003204//ESTs//3.1e-109:524:98//Hs.152982:AA584308
	F-NT2RP3003210//ESTs//3.6e-16:113:91//Hs.121030:AA625325
	F-NT2RP3003212//EST//1.0e-52:500:74//Hs.161635:W22525
	F-NT2RP3003230//Human mRNA for actin binding protein p57, complete cds//6.0e-55:587:70//Hs.109606:D44497
	F-NT2RP3003242//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//1.2e-129:617:98//Hs.155223:AF055460
	F-NT2RP3003251//H.sapiens Staf50 mRNA//1.1e-68:651:76//Hs.68054:X82200
	F-NT2RP3003264//Human bullous 230 kDa pemphigoid antigen (BPAG1) mRNA, complete cds//0.069:382:59//Hs.620:M69225
	F-NT2RP3003278//Homo sapiens hook2 protein (HOOK2) mRNA, complete cds//0.98:261:59//Hs.30792:AF044924

【0878】

【表577】

F-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//4.2 e-133:694:93//Hs.11702:L36983	F-NT2RP3003846//Homo sapiens mRNA for KIAA0725 protein, partial cd s//1.3e-37:335:68//Hs.26450:AB018268
F-NT2RP3003290//Human mRNA for RTP, complete cds//6.3e-66:662:71//Hs.75789:D87953	F-NT2RP3003870//Homo sapiens mRNA for KIAA0800 protein, complete c ds//1.3e-175:805:99//Hs.118738:AB018343
F-NT2RP3003301//EST//1.0:58:74//Hs.158575:A1368947	F-NT2RP3003876//ESTs, Highly similar to Rabin3 [R.norvegicus]//6.8 e-39:243:90//Hs.124832:AA846576
F-NT2RP3003302//Human Line-1 repeat mRNA with 2 open reading frame s//3.1e-91:681:80//Hs.23094:M19503	F-NT2RP3003914//ESTs, Weakly similar to UDP-GLUCOSE:GLYCOPROTEIN G LUCOSYLTRANSFERASE PRECURSOR [D.melanogaster]//1.1e-107:499:99//H s.105794:AA701659
F-NT2RP3003311//ESTs//0.95:308:59//Hs.27308:AA534947	F-NT2RP3003918//Homo sapiens VAMP-associated protein of 33 kDa (VA P-33) mRNA, complete cds//8.3e-49:404:77//Hs.9006:AF057358
F-NT2RP3003313//ESTs//0.0016:345:61//Hs.143304:A1084058	F-NT2RP3003932//ESTs//0.94:278:58//Hs.15661:W02396
F-NT2RP3003327//H.sapiens Stat50 mRNA//8.0e-31:253:67//Hs.68054:X8 2200	F-NT2RP3003989//ESTs//1.0:174:64//Hs.8095:A1359006
F-NT2RP3003330	F-NT2RP3003992//Cyclic nucleotide gated channel (photoreceptor), c GMP gated 2 (beta)//0.00070:433:58//Hs.93909:AF042498
F-NT2RP3003344	F-NT2RP3004013//ESTs, Moderately similar to M-phase phosphoprotein 4 [H.sapiens]//2.8e-127:617:97//Hs.142151:AA984061
F-NT2RP3003346//H.sapiens mRNA for delta 4-3-oxosteroid 5 beta-red uctase//1.2e-42:644:66//Hs.2638:Z28339	F-NT2RP3004016//Human p300/CBP-associated factor (P/CAF) mRNA, com plete cds//0.0086:283:62//Hs.155302:U57317
F-NT2RP3003353//Breast cancer 1, early onset//0.30:145:67//Hs.6674 6:L78833	F-NT2RP3004041//EST//0.98:264:58//Hs.127552:AA953234
F-NT2RP3003377//Human mRNA for cadherin-15, complete cds//0.019:41 6:60//Hs.148090:D83542	F-NT2RP3004051//Human mRNA for KIAA0319 gene, complete cds//7.0e-6 3:774:67//Hs.26441:AB002317
F-NT2RP3003384//ESTs//1.1e-65:346:96//Hs.35012:R92791	F-NT2RP3004070//EST//6.8e-22:163:85//Hs.132635:A1032875
F-NT2RP3003385//ESTs, Highly similar to SKD3 [M.musculus]//7.0e-7 4:384:96//Hs.21263:H16363	F-NT2RP3004078//Regulatory factor (trans-acting) 2 (influences HLA class II expression)//5.3e-90:520:90//Hs.100007:X76091
F-NT2RP3003403//ESTs//4.9e-12:335:63//Hs.87258:AA463850	F-NT2RP3004093
F-NT2RP3003409//Human DHHC-domain-containing cysteine-rich protein mRNA, complete cds//3.2e-22:430:63//Hs.113272:U90653	F-NT2RP3004095//Human clone 23732 mRNA, partial cds//3.3e-27:372:6 9//Hs.81281:U79258
F-NT2RP3003411//Human metallothionein-1e gene (hMT-1e)//0.99:116:6 2//Hs.74170:M10942	F-NT2RP3004110//Human mRNA for KIAA0392 gene, partial cds//1.2e-2 0:211:77//Hs.40100:AB002390
F-NT2RP3003427//ESTs//0.24:447:61//Hs.160907:A1422830	F-NT2RP3004125//ESTs, Highly similar to OOCYTE ZINC FINGER PROTEI N XLCOF.1 [Xenopus laevis]//1.0e-126:590:99//Hs.129888:A1096509
F-NT2RP3003433//Protein tyrosine phosphatase, non-receptor type 12 //1.0:243:61//Hs.62:M93425	F-NT2RP3004145
F-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, comp lete cds//1.7e-182:853:98//Hs.14934:AF004828	F-NT2RP3004148
F-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cd s//5.2e-175:826:98//Hs.26450:AB018268	F-NT2RP3004155//Homo sapiens timing protein CLK-1 mRNA, complete c ds//2.1e-121:578:98//Hs.157113:AF032900
F-NT2RP3003491//Ryanodine receptor 2 (cardiac)//1.0:148:66//Hs.908 21:X98330	F-NT2RP3004189//ESTs//1.3e-80:409:97//Hs.151001:AA564706
F-NT2RP3003500//ESTs//0.86:211:62//Hs.136037:AA013302	F-NT2RP3004206//Human mRNA for stac, complete cds//1.0:245:60//Hs. 56045:D86640
F-NT2RP3003543//Homo sapiens clone 23790 unknown protein mRNA, com plete cds//0.64:626:58//Hs.150828:AF038169	F-NT2RP3004207//Transcription factor 3 (E2A immunoglobulin enhance r binding factors E12/E47)//0.095:281:62//Hs.101047:M31523
F-NT2RP3003552	F-NT2RP3004209//ESTs//5.8e-87:458:94//Hs.155303:A1221835
F-NT2RP3003555//ESTs//1.4e-12:81:98//Hs.144487:A1418322	F-NT2RP3004215//ESTs//0.074:56:80//Hs.163590:H43361
F-NT2RP3003564//EST//4.5e-08:186:69//Hs.116769:AA630365	F-NT2RP3004242
F-NT2RP3003572//EST//0.27:105:69//Hs.162134:AA526311	F-NT2RP3004246//EST//0.20:219:63//Hs.161920:AA483240
F-NT2RP3003576//ESTs//1.2e-57:277:84//Hs.138852:AA284247	F-NT2RP3004253//ESTs//1.2e-35:204:96//Hs.143588:A1149140
F-NT2RP3003589//RAS-RELATED PROTEIN RAB-8//6.3e-38:373:73//Hs.1231 09:X56741	F-NT2RP3004258//Human gene for neurofilament subunit M (NF-M)//7.2 e-07:369:59//Hs.71346:Y00067
F-NT2RP3003621//HEPATOCYTE GROWTH FACTOR ACTIVATOR PRECURSOR//8.0 e-09:564:61//Hs.104:D14012	F-NT2RP3004262//Homo sapiens heat shock protein hsp40-3 mRNA, comp lete cds//1.0e-154:733:98//Hs.158471:AF088982
F-NT2RP3003625	F-NT2RP3004282//Homo sapiens torsinA (DYT1) mRNA, complete cds//4. 2e-26:597:61//Hs.19261:AF007871
F-NT2RP3003656	F-NT2RP3004332
F-NT2RP3003659	F-NT2RP3004334//ESTs//8.8e-27:142:99//Hs.28068:H06285
F-NT2RP3003665//ESTs//0.015:221:62//Hs.153705:AA527586	F-NT2RP3004341//EST//0.0068:213:64//Hs.153208:X98426
F-NT2RP3003672//ESTs//0.70:351:57//Hs.27633:N76184	F-NT2RP3004348//ESTs//1.2e-18:126:93//Hs.58595:AA830999
F-NT2RP3003680//Human Bcl2, p53 binding protein Bbp/53BP2 (BBP/53B P2) mRNA, complete cds//0.013:190:63//Hs.44585:U58334	F-NT2RP3004349//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTE IN XK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//3.9e-45:33 7:83//Hs.141429:AA631915
F-NT2RP3003686//Homo sapiens clone 24519 unknown mRNA, partial cds //0.69:246:62//Hs.118463:AF055000	F-NT2RP3004378//ESTs, Weakly similar to weak similarity to procoll agen alpha chain I(V) chain [C.elegans]//4.3e-125:608:98//Hs.12878 1:AA160707
F-NT2RP3003701//EST//0.93:79:69//Hs.145285:A1249848	F-NT2RP3004399//H.sapiens mRNA for leucine-rich primary response p rotein 1//2.3e-141:804:90//Hs.123122:X97249
F-NT2RP3003716//Homo sapiens KIAA0405 mRNA, complete cds//8.3e-24: 478:61//Hs.48998:AB007865	F-NT2RP3004424//ESTs, Weakly similar to JTV-1 [H.sapiens]//3.2e-12 2:609:96//Hs.20132:AA203113
F-NT2RP3003726//Homo sapiens mRNA for KIAA0757 protein, complete c ds//7.4e-150:700:98//Hs.48513:AB018300	F-NT2RP3004428//Homo sapiens ALR mRNA, complete cds//0.00044:458:6 0//Hs.153638:AF010403
F-NT2RP3003746	F-NT2RP3004451//Bone morphogenetic protein 8 (osteogenic protein 2)//0.00023:357:59//Hs.99948:M97016
F-NT2RP3003795//ESTs//7.1e-20:228:74//Hs.159571:AA454230	F-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete c ds//2.0e-124:583:99//Hs.27349:AB007917
F-NT2RP3003799	F-NT2RP3004466//Homo sapiens mRNA for KIAA0654 protein, partial cd s//0.48:399:58//Hs.22616:AB014564
F-NT2RP3003800//Gardner-Rasheed feline sarcoma viral (v-fgr) oncog ene homolog//4.7e-41:432:73//Hs.1422:M19722	F-NT2RP3004470//EST//1.3e-56:331:91//Hs.136830:AA769219
F-NT2RP3003805//Myosin, heavy polypeptide 6, cardiac muscle, alpha (cardiomyopathy, hypertrophic 1)//0.98:242:57//Hs.114001:Z20656	F-NT2RP3004472
F-NT2RP3003809//Human transcription factor, forkhead related activ ator 4 (FHEAC-4) mRNA, complete cds//5.1e-07:624:59//Hs.96028:AF04 2832	F-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cd s//9.8e-152:715:98//Hs.5003:AB007925
F-NT2RP3003819//Human ring zinc-finger protein (ZNF127-Xp) gene an d 5' flanking sequence//0.84:171:63//Hs.102877:U41315	F-NT2RP3004480//ESTs, Highly similar to VACUOLAR SORTING PROTEIN 35 [Saccharomyces cerevisiae]//4.6e-118:547:99//Hs.124768:AA307735
F-NT2RP3003825	
F-NT2RP3003828//ESTs//2.1e-12:434:61//Hs.156864:A1346481	
F-NT2RP3003831	
F-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence// 2.6e-48:242:98//Hs.25300:AF070611	
F-NT2RP3003842//Integrin, beta 8//1.0:345:60//Hs.832:M73780	

【0879】

【表578】

F-NT2RP3004490//Homo sapiens mRNA for Musashi, complete cds//2.3e-156:752:97//Hs.158311:AB012851
 F-NT2RP3004498//ESTs. Moderately similar to ROSA26AS [M.musculus]/3.5e-89:425:99//Hs.126082:AI077718
 F-NT2RP3004503//EST//5.3e-49:399:81//Hs.162335:AA564256
 F-NT2RP3004504//Homo sapiens mRNA for KIAA0479 protein, partial cds//1.0:370:59//Hs.158244:AB007948
 F-NT2RP3004507//Human zinc finger protein (MAZ) mRNA//0.86:129:66//Hs.7647:M94046
 F-NT2RP3004527//EST//0.053:260:62//Hs.123314:AA810110
 F-NT2RP3004534//ESTs//3.5e-78:370:99//Hs.132808:AI031571
 F-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds//2.7e-146:679:98//Hs.75970:AB014532
 F-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds//9.1e-171:793:98//Hs.74750:AB011126
 F-NT2RP3004566//ESTs. Highly similar to ZINC FINGER PROTEIN MLZ-4 [Mus musculus]//2.2e-66:362:94//Hs.125870:AI364967
 F-NT2RP3004569
 F-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF15) mRNA, complete cds//3.3e-181:860:97//Hs.122752:AF026445
 F-NT2RP3004574//Homo sapiens mRNA for KIAA0454 protein, partial cds//4.0e-85:422:97//Hs.129928:AB007923
 F-NT2RP3004594//Homo sapiens mRNA for AND-1 protein//3.7e-160:796:95//Hs.72160:AJ006266
 F-NT2RP3004617//ESTs. Weakly similar to estrogen-responsive finger protein, etp [H.sapiens]//6.4e-13:356:64//Hs.124138:AI266336
 F-NT2RP3004618//ESTs//1.5e-42:481:70//Hs.130768:AA909232
 F-NT2RP3004669//Human plectin (PLEC1) mRNA, complete cds//0.0099:538:56//Hs.79706:U53204
 F-NT2RP3004670//Homo sapiens sox1 gene//0.11:311:58//Hs.144029:Y13435
 F-NT2RP4000008//ESTs. Highly similar to CHLORINE CHANNEL PROTEIN P64 [Bos taurus]//8.0e-177:827:98//Hs.118991:AA675919
 F-NT2RP4000023//ESTs//1.4e-33:182:96//Hs.122722:AA455668
 F-NT2RP4000035//ESTs//1.1e-23:283:72//Hs.142147:AA706495
 F-NT2RP4000049//Homo sapiens decoy receptor 2 mRNA, complete cds//6.8e-83:556:85//Hs.129844:AF029761
 F-NT2RP4000051//Homo sapiens mRNA for cartilage-associated protein (CASP)//4.9e-13:441:62//Hs.155481:AJ006470
 F-NT2RP4000078//Homo sapiens mRNA for NS1-binding protein (NS1-BP) //8.0e-151:720:97//Hs.159597:AJ012449
 F-NT2RP4000102//ESTs//8.8e-33:184:82//Hs.93054:H47743
 F-NT2RP4000109//Homo sapiens mRNA for MECF5, partial cds//1.4e-167:774:99//Hs.57929:AB011538
 F-NT2RP4000111
 F-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//1.1e-115:548:98//Hs.64691:AB007952
 F-NT2RP4000147//Human mRNA for KIAA0041 gene, partial cds//0.00045:212:63//Hs.75520:026069
 F-NT2RP4000150
 F-NT2RP4000151//Homo sapiens chromosome 7q22 sequence//0.98:431:59//Hs.3386:AF053356
 F-NT2RP4000159
 F-NT2RP4000167
 F-NT2RP4000185//ESTs//1.1e-51:240:68//Hs.33020:N31946
 F-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.6e-175:825:98//Hs.13999:AB014600
 F-NT2RP4000212//ESTs//1.6e-10:74:95//Hs.111885:AA422006
 F-NT2RP4000214//ESTs//3.9e-11:225:68//Hs.59793:AA451731
 F-NT2RP4000218//Human G protein-coupled receptor (STRL22) mRNA, complete cds//6.2e-34:425:71//Hs.46468:U45984
 F-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP)//8.6e-158:771:97//Hs.155481:AJ006470
 F-NT2RP4000246//ESTs. Highly similar to NPC DERIVED PROLINE RICH PROTEIN 1 [M.musculus]//1.9e-62:384:89//Hs.115498:AA436298
 F-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//9.4e-130:604:99//Hs.43728:AF091092
 F-NT2RP4000263
 F-NT2RP4000290//EST//1.0:149:63//Hs.136928:AA812580
 F-NT2RP4000312//Human mRNA for KIAA0147 gene, partial cds//1.5e-42:685:63//Hs.158132:D63481
 F-NT2RP4000321//Homo sapiens gene for insulin receptor substrate-2, complete cds//8.6e-05:547:57//Hs.143648:AB000732
 F-NT2RP4000323//Human HCF1 gene related mRNA sequence//0.48:589:58//Hs.83634:U52112
 F-NT2RP4000355
 F-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds//6.4e-142:654:99//Hs.107478:AB018281
 F-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds//8.5e-137:649:97//Hs.31323:AF044195
 F-NT2RP4000370//ESTs. Weakly similar to MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR [S.cerevisiae]//1.2e-09:157:76//Hs.97950:AI382073
 F-NT2RP4000376//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//0.098:291:59//Hs.994:M95678
 F-NT2RP4000381//Myosin, heavy polypeptide 7, cardiac muscle, beta//0.00025:509:59//Hs.929:M57965
 F-NT2RP4000398//Zinc finger protein 140 (clone pHZ-39)//4.9e-60:469:68//Hs.154205:U09368
 F-NT2RP4000415//ESTs//0.85:89:67//Hs.152312:AA485688
 F-NT2RP4000417//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//0.014:178:66//Hs.125315:AF027156
 F-NT2RP4000424//Human G protein-coupled receptor (STRL22) mRNA, complete cds//2.0e-34:431:73//Hs.46468:U45984
 F-NT2RP4000448//Human mRNA for KIAA0118 gene, partial cds//1.9e-37:360:75//Hs.154326:D42087
 F-NT2RP4000449//EST//0.84:113:65//Hs.145274:AI249468
 F-NT2RP4000455//ALPHA-2C-1 ADRENERGIC RECEPTOR//0.063:221:61//Hs.123022:J03853
 F-NT2RP4000457//H.sapiens mRNA for herpesvirus associated ubiquitin-specific protease (HAUSP)//1.1e-05:532:57//Hs.78683:ZT2499
 F-NT2RP4000480//Homo sapiens mRNA, complete cds//0.056:655:60//Hs.133151:AB001535
 F-NT2RP4000481//Human mRNA for KIAA0268 gene, partial cds//0.46:272:58//Hs.78862:D87742
 F-NT2RP4000498//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds//0.94:133:69//Hs.159234:U89995
 F-NT2RP4000500//V-myb avian myeloblastosis viral oncogene homolog-like 2//0.60:335:61//Hs.74605:X13293
 F-NT2RP4000515//ESTs//2.9e-45:253:95//Hs.104898:AA429594
 F-NT2RP4000517//EST//0.043:131:64//Hs.99030:AA443904
 F-NT2RP4000518//Homo sapiens mRNA for ATP-dependent RNA helicase, partial//2.0e-34:203:93//Hs.99423:AJ010840
 F-NT2RP4000519//Human mRNA for KIAA0374 gene, complete cds//0.33:154:66//Hs.100837:AB002372
 F-NT2RP4000524
 F-NT2RP4000528
 F-NT2RP4000541//ESTs//2.1e-51:251:99//Hs.157240:AI348154
 F-NT2RP4000556//ESTs. Highly similar to 60S RIBOSOMAL PROTEIN L11 [R.norvegicus]//1.1e-27:162:93//Hs.25597:H93026
 F-NT2RP4000560//ESTs//2.5e-09:181:66//Hs.122609:AA778351
 F-NT2RP4000588//ESTs//1.4e-46:533:70//Hs.8836:AA181053
 F-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds//1.0e-139:666:98//Hs.4214:AF067730
 F-NT2RP4000638//Fibroblast growth factor 2 (basic)//1.0:226:61//Hs.56066:J04513
 F-NT2RP4000648//ESTs//2.5e-11:116:80//Hs.115449:AA418396
 F-NT2RP4000657//Homo sapiens bone morphogenetic protein 11 (BMP11) mRNA, complete cds//0.00056:367:60//Hs.144626:AF100907
 F-NT2RP4000704//Homo sapiens mRNA expressed in 19week fetal lung, clone IMAGE:300856//8.0e-167:676:98//Hs.50748:AB004848
 F-NT2RP4000713//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//6.9e-07:494:61//Hs.113286:U77783
 F-NT2RP4000724//ESTs. Weakly similar to pol/env ORF [H.sapiens]//2.8e-46:411:78//Hs.111817:T80622
 F-NT2RP4000728//Homo sapiens mRNA for KIAA0606 protein, partial cds//9.9e-43:350:71//Hs.38176:AB011178
 F-NT2RP4000737//Human mRNA for KIAA0252 gene, partial cds//0.97:409:60//Hs.83419:D87440
 F-NT2RP4000739//DESMOPLAKIN 1 AND 11//0.99:192:63//Hs.74316:AL031058
 F-NT2RP4000781//Homo sapiens mRNA for APC 2 protein, complete cds//0.023:351:60//Hs.20912:AB012162
 F-NT2RP4000787//Human mRNA for ESPI/CRP2, complete cds//0.0051:276:58//Hs.70327:D42123
 F-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds//4.8e-176:816:98//Hs.25132:AB007939
 F-NT2RP4000833//Homo sapiens PAC clone DJ0905J08 from 7p12-p14//1.3e-93:438:99//Hs.8173:AC005189
 F-NT2RP4000837//Homo sapiens SALL1 gene, partial//5.9e-05:470:59//Hs.123094:X98833
 F-NT2RP4000839//ESTs//5.7e-11:133:82//Hs.103852:M27603
 F-NT2RP4000855//Homo sapiens DNA-binding protein (CROC-1B) mRNA, complete cds//1.4e-37:680:63//Hs.75875:U49278
 F-NT2RP4000865//Zinc finger protein 136 (clone pHZ-20)//2.0e-96:415:78//Hs.69740:U09367
 F-NT2RP4000878//ESTs//2.7e-16:390:63//Hs.163451:AI206803
 F-NT2RP4000879//ESTs//0.89:184:64//Hs.122333:AA782843
 F-NT2RP4000907//Homo sapiens BAC clone RG118D07 from 7q31//4.5e-5

【0880】

【表579】

2:933:61//Hs.3781:AC004142	F-NT2RP4001336//ESTs//1.0:128:67//Hs.99598:AA603110
F-NT2RP4000915//Homo sapiens mRNA for ZNF198 protein//3.0e-80:584:78//Hs.109526:AJ224901	F-NT2RP4001339
F-NT2RP4000918	F-NT2RP4001343
F-NT2RP4000925//Homo sapiens KIAA0405 mRNA, complete cds//1.9e-47:861:61//Hs.48998:AB007865	F-NT2RP4001345//Lecithin-cholesterol acyltransferase//8.0e-39:686:64//Hs.112125:M12625
F-NT2RP4000927//ESTs//0.37:159:63//Hs.147949:A1341503	F-NT2RP4001351//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds//2.0e-31:784:62//Hs.15432:U53445
F-NT2RP4000928//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2) mRNA, partial cds//1.1e-164:781:97//Hs.24812:AF069532	F-NT2RP4001353//Homo sapiens chromosome 7q22 sequence//0.0034:497:57//Hs.125742:AF053356
F-NT2RP4000929//ESTs//0.88:284:60//Hs.141317:A1281371	F-NT2RP4001372
F-NT2RP4000955//Human mRNA for cadherin-15, complete cds//0.0019:495:58//Hs.148090:D83542	F-NT2RP4001373//Homo sapiens clone DtlP1b11 mRNA, CAG repeat region//0.43:290:58//Hs.82101:Z50194
F-NT2RP4000973//Homo sapiens mRNA for MSJ-1, complete cds//1.2e-05:318:60//Hs.3845:AB014888	F-NT2RP4001375
F-NT2RP4000975//ESTs//0.0051:345:61//Hs.143304:A1084058	F-NT2RP4001379//TRICHOHYALIN//8.2e-05:591:58//Hs.82276:L09190
F-NT2RP4000979	F-NT2RP4001389//EST//5.3e-27:212:84//Hs.160402:A1393918
F-NT2RP4000984	F-NT2RP4001407//Homo sapiens mRNA for RGS5, complete cds//0.93:218:58//Hs.24950:AB008109
F-NT2RP4000989//Homo sapiens Tax interaction protein 1 mRNA, partial cds//0.85:257:63//Hs.12956:U90913	F-NT2RP4001414//Human mRNA for KIAA0202 gene, partial cds//6.3e-78:818:71//Hs.80712:D86957
F-NT2RP4000996//ESTs//4.3e-10:329:62//Hs.33085:AA258068	F-NT2RP4001433//Zinc finger protein 10 (KIX 1)//1.1e-88:839:73//Hs.2479:X78933
F-NT2RP4000997//Human plectin (PLEC1) mRNA, complete cds//1.0:218:58//Hs.79706:U53204	F-NT2RP4001442
F-NT2RP4001004	F-NT2RP4001447//Homo sapiens mRNA for KIAA0783 protein, complete cds//0.0075:218:63//Hs.41153:AB018326
F-NT2RP4001006//ESTs, Moderately similar to ROSA26AS [M.musculus]/7.4e-90:425:99//Hs.126082:A1077718	F-NT2RP4001474//ESTs, Weakly similar to probable CBP3 protein homolog [C.elegans]/2.1e-90:460:96//Hs.26676:AA033997
F-NT2RP4001010//Homo sapiens PSD-95/SAP90-associated protein-2 mRNA, partial cds//2.8e-19:689:61//Hs.113287:AF009204	F-NT2RP4001483//Oxoglutarate dehydrogenase (lipoamide)//8.1e-61:480:75//Hs.75533:D10523
F-NT2RP4001029//Human transcription factor LSF mRNA, complete cds//9.6e-84:778:74//Hs.154970:U03494	F-NT2RP4001498//ESTs, Weakly similar to GA BINDING PROTEIN BETA-2 CHAIN [H.sapiens]/0.25:216:60//Hs.63220:AA522707
F-NT2RP4001041//Human endosome-associated protein (EEA1) mRNA, complete cds//0.95:170:64//Hs.2864:L40157	F-NT2RP4001502//ESTs//2.6e-41:206:99//Hs.159257:M40395
F-NT2RP4001057//EST//9.6e-05:122:72//Hs.132518:AA928157	F-NT2RP4001507//H.sapiens mRNA for RanGTPase activating protein 1//0.51:281:61//Hs.5923:X82260
F-NT2RP4001064//Homo sapiens mRNA for cartilage-associated protein (CASP)//7.2e-13:441:63//Hs.155481:AJ006470	F-NT2RP4001524//ESTs, Weakly similar to F13B12.1 [C.elegans]/9.4e-30:173:94//Hs.5570:A1377863
F-NT2RP4001078//ESTs//1.3e-29:165:95//Hs.113817:AA702497	F-NT2RP4001529//Human transcription factor LSF mRNA, complete cds//1.3e-35:329:76//Hs.154970:U03494
F-NT2RP4001079//Homo sapiens mRNA for putative Ca2+-transporting ATPase, partial//1.4e-131:634:98//Hs.106778:AJ010953	F-NT2RP4001547//Homo sapiens forkhead protein FREAC-2 mRNA, complete cds//0.0015:221:65//Hs.44481:U13220
F-NT2RP4001080//Polypyrimidine tract binding protein (hnRNP 1) [alternative products]/0.025:166:66//Hs.146459:X66975	F-NT2RP4001551//Human BRCA2 region, mRNA sequence CG003//0.56:428:59//Hs.30649:U50534
F-NT2RP4001086//Homo sapiens mRNA for KIAA0592 protein, partial cds//1.5e-85:604:86//Hs.13273:AB011164	F-NT2RP4001555//EST//0.99:225:64//Hs.96863:AA347174
F-NT2RP4001095	F-NT2RP4001567
F-NT2RP4001100//ESTs, Weakly similar to C17G10.1 [C.elegans]/1.4e-93:448:98//Hs.105837:AA536054	F-NT2RP4001568//ESTs, Weakly similar to HYPOTHETICAL 32.6 KD PROTEIN IN MET30-CBR5 INTERGENIC REGION [Saccharomyces cerevisiae]/1.1e-54:252:83//Hs.158208:AA167836
F-NT2RP4001117//ESTs, Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]/2.2e-26:171:92//Hs.14038:R06800	F-NT2RP4001571//ESTs//3.0e-94:475:96//Hs.65322:AA019410
F-NT2RP4001122//Human mRNA for histone H1x, complete cds//0.99:185:66//Hs.109804:D64142	F-NT2RP4001574
F-NT2RP4001126//ESTs, Moderately similar to The KIAA0138 gene product is novel. [H.sapiens]/5.8e-37:185:100//Hs.126925:AA931237	F-NT2RP4001575//Homo sapiens mRNA for ARE1-like protein//1.8e-169:796:98//Hs.108826:AL031228
F-NT2RP4001136//ESTs//3.4e-09:125:77//Hs.143382:AA476266	F-NT2RP4001592
F-NT2RP4001143//ESTs//1.0:282:57//Hs.157423:A1358261	F-NT2RP4001610//Human involucrin mRNA//0.94:462:59//Hs.157091:M13903
F-NT2RP4001148//ESTs//0.82:206:62//Hs.129259:AA992207	F-NT2RP4001614//ESTs//0.71:331:58//Hs.116533:A1343952
F-NT2RP4001149//EST//1.3e-17:140:88//Hs.101727:H16171	F-NT2RP4001634
F-NT2RP4001150//AXONIN-1 PRECURSOR//1.7e-07:562:59//Hs.2998:X67734	F-NT2RP4001638//ESTs, Weakly similar to HYPOTHETICAL 117.9 KD PROTEIN IN FKHI-STH1 INTERGENIC REGION [S.cerevisiae]/8.6e-57:287:97//Hs.117439:C18436
F-NT2RP4001159//EST//0.26:125:66//Hs.152092:AA377324	F-NT2RP4001644//Human mRNA for MNK1, complete cds//1.7e-53:415:80//Hs.5591:AB000409
F-NT2RP4001174//ESTs//2.9e-103:502:98//Hs.125886:AA884264	F-NT2RP4001656//ESTs, Highly similar to PHENYLALANYL-TRNA SYNTHETASE MITOCHONDRIAL PRECURSOR [Saccharomyces cerevisiae]/1.0:311:59//Hs.57969:AA203629
F-NT2RP4001206//EST//0.33:125:66//Hs.152092:AA377324	F-NT2RP4001677//Homo sapiens short form transcription factor C-MAF (c-maf) mRNA, complete cds//0.19:162:67//Hs.30250:AF055376
F-NT2RP4001207	F-NT2RP4001679//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.2e-50:332:86//Hs.113283:AF018080
F-NT2RP4001210//ESTs//3.1e-95:460:97//Hs.46913:A1017636	F-NT2RP4001696
F-NT2RP4001213//KRAB zinc finger protein (alternative products)//1.1e-45:187:74//Hs.22556:U37251	F-NT2RP4001725//Galactokinase 1//1.0:202:63//Hs.92357:L76927
F-NT2RP4001219//ESTs//1.4e-69:352:96//Hs.116392:AA936262	F-NT2RP4001730//Human growth/differentiation factor 1 (GDF-1) mRNA, complete cds//0.0035:247:62//Hs.92614:M62302
F-NT2RP4001228//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//7.2e-28:855:60//Hs.122967:AF059569	F-NT2RP4001739//Complement component 8, gamma polypeptide//0.74:654:56//Hs.1285:U08198
F-NT2RP4001235//Homo sapiens Jagged 2 mRNA, complete cds//1.0:257:59//Hs.106387:AF029778	F-NT2RP4001753//Zinc finger protein 84 (HPF2)//4.5e-29:476:67//Hs.9450:M27878
F-NT2RP4001256//Human mRNA for KIAA0273 gene, complete cds//0.96:247:62//Hs.75899:D87463	F-NT2RP4001760//ESTs//1.0:411:60//Hs.108548:AA081656
F-NT2RP4001260//Syntrophin, alpha (dystrophin-associated protein A 1, 59kD, acidic component)//0.015:246:62//Hs.31121:U40571	F-NT2RP4001790//Homo sapiens PAC clone DJ0604G05 from 7q22-q31.1//9.1e-34:400:68//Hs.154212:AC004522
F-NT2RP4001274//Homo sapiens clone 24674 mRNA sequence//1.2e-06:259:64//Hs.71168:AF070578	F-NT2RP4001803//Human high conductance inward rectifier potassium
F-NT2RP4001276//Homo sapiens CACF9 mRNA, partial cds//7.6e-06:266:62//Hs.110826:U80736	
F-NT2RP4001313//Homo sapiens mitochondrial outer membrane protein (OM40) mRNA, nuclear gene encoding mitochondrial protein, complete cds//2.3e-31:535:65//Hs.30928:AF043250	
F-NT2RP4001315//EST//9.5e-20:146:88//Hs.158755:A1375917	

【0881】

【表580】

channel alpha subunit mRNA, complete cds//0.028:580:58//Hs.2363:L3
6069
F-NTZRP4001822//ESTs//3.4e-50:307:90//Hs.113509:AA132131
F-NTZRP4001823//Human facio-genital dysplasia (FGD1) mRNA, complete
cds//3.1e-07:509:59//Hs.1572:U11690
F-NTZRP4001828
F-NTZRP4001838//Human mRNA for KIAA0071 gene, partial cds//6.9e-5
5:555:73//Hs.78398:D31888
F-NTZRP4001841//ESTs//0.99:215:60//Hs.136895:AA897749
F-NTZRP4001849//Homo sapiens mRNA for KIAA0672 protein, complete c
ds//5.6e-57:813:65//Hs.6336:AB014572
F-NTZRP4001861//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNI
NG ENTRY !!!! [H.sapiens]//4.8e-12:84:94//Hs.140232:AA705170
F-NTZRP4001889
F-NTZRP4001893//Homo sapiens BAC clone GS166A23 from 7p21//4.4e-10
8:535:97//Hs.15144:AC005014
F-NTZRP4001896
F-NTZRP4001901//ESTs//1.4e-50:291:93//Hs.67991:AA147848
F-NTZRP4001927
F-NTZRP4001938//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.
sapiens]//2.8e-54:375:84//Hs.119294:A1379442
F-NTZRP4001946//EST//0.050:268:60//Hs.148341:AA921894
F-NTZRP4001950//EST//7.9e-14:336:63//Hs.112810:AA610063
F-NTZRP4001953//ESTs//0.018:206:65//Hs.130105:AA904868
F-NTZRP4001966//Human DNA sequence from clone 1052M9 on chromosome
Xq25. Contains the SH2D1A gene for SH2 domain protein 1A, Duncan
s disease (lymphoproliferative syndrome) (DSHP), part of a 60S Aci
dic Ribosomal protein 1 (RPLP1) LIKE gene and part of a mouse DOC4
LIKE gene. Contains ESTs and GSSs//1.7e-54:788:65//Hs.23796:AL022
718
F-NTZRP4001975//Homo sapiens homeobox protein Six3 (SIX3) gene, co
mplete cds//0.0019:279:65//Hs.159439:AF092047
F-NTZRP4002018//ESTs, Highly similar to RING CANAL PROTEIN [Droso
phila melanogaster]//0.58:463:55//Hs.3826:U69560
F-NTZRP4002047//EST//2.5e-13:102:90//Hs.148997:A1243139
F-NTZRP4002052
F-NTZRP4002058//ESTs//5.2e-41:347:72//Hs.121961:AA777873
F-NTZRP4002071//Homo sapiens TTACGG repeat binding factor 2 (hTRF
2) mRNA, complete cds//0.97:227:60//Hs.100030:AF002999
F-NTZRP4002075
F-NTZRP4002078//ESTs, Moderately similar to zinc finger protein [H.
sapiens]//1.0e-38:243:90//Hs.139115:AA325104
F-NTZRP4002081//TATA box binding protein//0.0059:310:60//Hs.1100:M
55654
F-NTZRP4002083//H.sapiens Pur (pur-alpha) mRNA, complete cds//0.00
15:152:70//Hs.25180:M96684
F-NTZRP4002408//Human protein kinase C-L (PRKCL) mRNA, complete cd
s//8.0e-10:401:59//Hs.89616:M55284
F-NTZRP4002791//Ataxin 1//1.0:215:61//Hs.74520:X79204
F-NTZRP4002888
F-NTZRP4002905//ESTs//3.4e-50:280:94//Hs.131697:H14960
F-NTZRP5003459//Glyceraldehyde-3-phosphate dehydrogenase//1.3e-35:
193:96//Hs.74456:U34995
F-NTZRP5003461//ESTs//3.6e-104:513:98//Hs.88088:AA521071
F-NTZRP5003477//Eukaryotic translation initiation factor 3 (eIF-3)
p36 subunit//0.18:271:60//Hs.139745:U39067
F-NTZRP5003492
F-NTZRP5003500//Homo sapiens mRNA for heparan-sulfate 6-sulfotrans
ferase, complete cds//6.1e-56:750:69//Hs.132884:AB006179
F-NTZRP5003506//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69
G12//5.1e-14:348:62//Hs.154050:AC004131
F-NTZRP5003512//Homo sapiens mRNA for KIAA0642 protein, partial cd
s//0.94:202:63//Hs.8152:AB014542
F-NTZRP5003522
F-NTZRP5003524//ESTs//8.7e-08:340:62//Hs.152730:A1308943
F-NTZRP5003534
F-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cd
s//4.0e-69:373:94//Hs.108258:AB007934
F-OVARC1000004//ESTs//6.0e-38:216:93//Hs.163801:A1391729
F-OVARC1000006//ESTs, Highly similar to HISTONE H2A [Cairina mosc
hata]//4.4e-75:355:99//Hs.36727:A1051983
F-OVARC1000013//ESTs//0.65:331:58//Hs.146326:AA534304
F-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds//1.8e-
171:815:98//Hs.81449:AF058922
F-OVARC1000017//Homo sapiens mRNA for NTAk, complete cds//0.50:48
2:58//Hs.113264:AB005060
F-OVARC1000035//Homo sapiens CA17 protein mRNA, complete cds//2.2
e-37:238:89//Hs.69469:AF064603
F-OVARC1000058//ESTs//1.1e-23:132:97//Hs.61809:AA503549
F-OVARC1000060//ESTs, Highly similar to ribonuclease 6 precursor
[H.sapiens]//6.7e-60:305:97//Hs.31696:H50008
F-OVARC1000068//ESTs//3.8e-10:69:100//Hs.89048:AA282798
F-OVARC1000071//ESTs//1.9e-36:202:95//Hs.125013:AA400543
F-OVARC1000085
F-OVARC1000087//EST//1.0:199:58//Hs.122919:AA768442
F-OVARC1000091//Homo sapiens Jagged 2 mRNA, complete cds//0.00017:
414:59//Hs.106387:AF029778
F-OVARC1000092//ESTs//4.6e-06:410:60//Hs.152250:AA203600
F-OVARC1000106//ESTs, Weakly similar to C25A1.1 [C.elegans]//2.9e-
73:406:92//Hs.109463:A1205174
F-OVARC1000109
F-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein
(OA4B-18) mRNA, complete cds//5.3e-135:663:96//Hs.3688:AF069250
F-OVARC1000114//Homo sapiens mRNA for KIAA0562 protein, complete c
ds//3.4e-43:532:72//Hs.118401:AB011134
F-OVARC1000133//ESTs//9.4e-50:249:98//Hs.159146:A1384010
F-OVARC1000139
F-OVARC1000145//ESTs//1.6e-09:87:90//Hs.25219:AA291293
F-OVARC1000148//ESTs//4.4e-28:146:100//Hs.133223:AA677414
F-OVARC1000151
F-OVARC1000168//ESTs//2.3e-48:264:95//Hs.14539:H67305
F-OVARC1000191//Thrombopoietin (myeloproliferative leukemia virus
oncogene ligand, megakaryocyte growth and development factor)//0.1
0:504:59//Hs.154083:U7D136
F-OVARC1000198//ESTs//1.3e-103:505:97//Hs.149341:A1249131
F-OVARC1000209//EST//1.0:73:72//Hs.162600:AA594840
F-OVARC1000212//ESTs//1.7e-17:121:91//Hs.50473:W68834
F-OVARC1000240//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE,
CYTOPLASMIC [Homo sapiens]//2.7e-31:264:79//Hs.151895:AA196379
F-OVARC1000241//Homo sapiens clone 23698 mRNA sequence//3.4e-35:46
6:68//Hs.8136:U81984
F-OVARC1000288//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//0.0
0084:170:65//Hs.107747:A1357868
F-OVARC1000302//EST//4.1e-05:249:60//Hs.136432:AA555306
F-OVARC1000304//ESTs//1.0:252:64//Hs.12126:AA203287
F-OVARC1000309//ESTs, Highly similar to BRAIN ENRICHED HYALURONAN
BINDING PROTEIN PRECURSOR [Felis catus]//0.51:193:66//Hs.6194:A13
78579
F-OVARC1000321
F-OVARC1000326//Homo sapiens T-type calcium channel alpha-1 subuni
t mRNA, complete cds//0.0018:507:60//Hs.122359:AF051946
F-OVARC1000335//ESTs//9.3e-39:202:98//Hs.132849:AA779444
F-OVARC1000347
F-OVARC1000384//Homo sapiens (clone PEBP2aA1) core-binding factor,
runt domain, alpha subunit 1 (CBFA1) mRNA, 3' end of cds//3.4e-0
6:353:62//Hs.121895:AF001450
F-OVARC1000408//Human mRNA for KIAA0140 gene, complete cds//0.94:2
31:64//Hs.156016:D50930
F-OVARC1000411//EST//0.43:234:59//Hs.124673:AA858162
F-OVARC1000414//EST//5.2e-05:105:72//Hs.98827:AA435682
F-OVARC1000420//Human mRNA for KIAA0140 gene, complete cds//0.86:2
31:58//Hs.156016:D50930
F-OVARC1000427//ESTs, Moderately similar to ORF1 [H.sapiens]//1.7
e-25:190:84//Hs.139513:AA259082
F-OVARC1000431//ESTs//0.041:356:57//Hs.139907:AA621615
F-OVARC1000437//Filamin 1 (actin-binding protein-280)//0.93:281:60
//Hs.76279:X53416
F-OVARC1000440//Human PINCH protein mRNA, complete cds//8.8e-21:11
6:99//Hs.83987:U09284
F-OVARC1000442//ESTs//2.0e-19:207:78//Hs.134071:A1377423
F-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete c
ds//3.2e-140:566:99//Hs.12334:AB014583
F-OVARC1000461//ESTs//1.0e-39:215:95//Hs.131532:A1024524
F-OVARC1000465//Homo sapiens clone 24781 mRNA sequence//1.0:252:58
//Hs.108112:AF070640
F-OVARC1000466//ESTs//3.6e-14:189:71//Hs.164041:R51854
F-OVARC1000473//ESTs//0.00012:77:85//Hs.29173:AA134926
F-OVARC1000479
F-OVARC1000486//ESTs//4.2e-07:409:60//Hs.99280:AA453036
F-OVARC1000496//ESTs//6.0e-14:240:69//Hs.131900:A1023327
F-OVARC1000520//Homo sapiens supervillin mRNA, complete cds//6.9e-
115:539:99//Hs.111285:AF051850
F-OVARC1000526//ESTs//2.9e-08:368:61//Hs.42771:M26740
F-OVARC1000533//EST//3.4e-14:137:82//Hs.123405:AA813492
F-OVARC1000543//ESTs//0.13:278:61//Hs.54894:N98475
F-OVARC1000556//ESTs//1.4e-31:217:90//Hs.106385:W26667
F-OVARC1000557//ESTs//3.8e-20:208:76//Hs.138919:AA827410
F-OVARC1000564//Human dsRNA adenosine deaminase DRADA2b (DRADA2b)
mRNA, complete cds//0.87:135:66//Hs.85302:U76421
F-OVARC1000573//ESTs//2.1e-22:268:76//Hs.121852:AA776358

【0882】

【表581】

F-OVARC1000576//ESTs//9.4e-22:124:98//Hs.24220:W22200	F-OVARC1001040//ESTs//2.2e-38:204:96//Hs.128927:A1168074
F-OVARC1000578//EST//4.7e-31:335:74//Hs.162881:AA652729	F-OVARC1001044//EST//0.036:304:61//Hs.137342:AA017385
F-OVARC1000588//Human BMK1 alpha kinase mRNA, complete cds//0.67:263:63//Hs.3080:U29725	F-OVARC1001051
F-OVARC1000605//EST//1.0:148:62//Hs.163346:AA883722	F-OVARC1001055//Human pre-B cell enhancing factor (PBEF) mRNA, complete cds//1.1e-46:381:81//Hs.154968:U02020
F-OVARC1000622//EST//4.3e-50:313:88//Hs.149580:A1281881	F-OVARC1001062//ESTs//0.020:265:60//Hs.146226:A1312873
F-OVARC1000640//ESTs//2.6e-55:441:80//Hs.105319:AA470097	F-OVARC1001065//ESTs, Weakly similar to C50F4.12 [C.elegans]//1.4e-21:183:84//Hs.46680:AA809451
F-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, complete cds//1.6e-78:424:93//Hs.86859:D43772	F-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds//6.6e-132:620:98//Hs.3426:AF082657
F-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete cds//1.6e-100:536:94//Hs.111862:AB011162	F-OVARC1001072//ESTs//1.1e-24:289:74//Hs.139614:AA709013
F-OVARC1000678//EST//1.3e-08:131:77//Hs.145970:A1277106	F-OVARC1001074//ESTs//0.059:198:63//Hs.59974:AA001937
F-OVARC1000679//ESTs//0.66:223:61//Hs.134782:H74279	F-OVARC1001085//H. sapiens mRNA for sortilin//0.99:142:67//Hs.104247:X98248
F-OVARC1000681//EST//0.017:315:61//Hs.147799:A1221639	F-OVARC1001092//Homo sapiens mRNA for JMS protein, complete CDS (clone IMAGE 53337, LNLc110F1857Q7 (RZPD Berlin) and LNLc110G0913Q7 (RZPD Berlin))//1.3e-75:289:95//Hs.21753:AJ005897
F-OVARC1000682//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds//4.8e-153:549:99//Hs.125315:AF027156	F-OVARC1001107//Homo sapiens SKB1Hs mRNA, complete cds//1.2e-73:351:86//Hs.12912:AF015913
F-OVARC1000689//Homo sapiens clone 24640 mRNA sequence//0.030:479:57//Hs.4764:AB018306	F-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds//2.1e-151:710:98//Hs.26584:AF051782
F-OVARC1000700	F-OVARC1001117//ESTs//3.8e-73:347:99//Hs.116029:AA813102
F-OVARC1000703//ESTs//0.41:100:68//Hs.160699:A1284320	F-OVARC1001118
F-OVARC1000722//Homo sapiens chromosome 1q21-lq23 beta-1,4-galactosyltransferase mRNA, complete cds//1.2e-110:451:91//Hs.13476:AF038661	F-OVARC1001129
F-OVARC1000730//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//2.9e-53:318:91//Hs.7049:A1141736	F-OVARC1001154//Granulin//2.4e-94:686:83//Hs.75451:AF055008
F-OVARC1000746//ESTs//3.2e-123:570:99//Hs.127295:AA918411	F-OVARC1001161//ESTs//2.2e-40:208:97//Hs.113006:AA621725
F-OVARC1000769//ESTs//0.072:177:67//Hs.142573:AA601196	F-OVARC1001162
F-OVARC1000771//ESTs, Moderately similar to RAS-RELATED PROTEIN RA8-2 [H.sapiens]//1.2e-38:194:99//Hs.157059:W28130	F-OVARC1001167
F-OVARC1000781//ESTs//4.0e-14:113:89//Hs.41972:AA626793	F-OVARC1001169//ESTs//0.81:158:63//Hs.48527:A1078279
F-OVARC1000787//EST//0.92:91:64//Hs.163258:AA828835	F-OVARC1001170//ESTs//9.0e-87:412:99//Hs.116550:AA813287
F-OVARC1000800//ESTs//1.6e-44:193:81//Hs.163971:N27584	F-OVARC1001171//ESTs//4.9e-26:167:79//Hs.139158:AA226159
F-OVARC1000802//ESTs//4.6e-43:395:80//Hs.115401:AA400032	F-OVARC1001173//ESTs, Moderately similar to GLUTAMATE DEHYDROGENASE 1 PRECURSOR [Homo sapiens]//1.8e-11:192:69//Hs.130020:AA887581
F-OVARC1000834//ESTs//1.9e-91:431:99//Hs.154450:AA069390	F-OVARC1001176//Homo sapiens chromosome 19, cosmid R26529//0.61:387:58//Hs.91103:AC005551
F-OVARC1000846//Homo sapiens mRNA for KIAA0643 protein, partial cds//1.9e-151:432:100//Hs.155995:AB014543	F-OVARC1001180//ESTs, Weakly similar to ubiquitin S6(1) [D.melanogaster]//1.5e-13:199:71//Hs.109966:C06057
F-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//3.3e-137:632:99//Hs.18910:AF045584	F-OVARC1001188//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTEIN IN VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.4e-52:324:90//Hs.114673:W72675
F-OVARC1000862//ESTs, Highly similar to gene Fif protein [M.musculus]//6.1e-31:183:93//Hs.108620:AA418155	F-OVARC1001200//ESTs//3.9e-16:104:94//Hs.125520:AA883889
F-OVARC1000876//Human DNA binding protein FKHL15 (FKHL15) mRNA, complete cds//0.54:133:69//Hs.159234:U89995	F-OVARC1001232//Cyclin A//0.95:124:67//Hs.85137:X51688
F-OVARC1000883//ESTs//0.44:54:63//Hs.98183:AA471143	F-OVARC1001240//EST//0.017:351:60//Hs.120655:AA745676
F-OVARC1000885//EST//0.91:152:63//Hs.160765:A1313233	F-OVARC1001243//ESTs//0.78:291:59//Hs.132458:A1424825
F-OVARC1000886//ESTs//4.6e-08:375:61//Hs.131653:A1025777	F-OVARC1001244//RING3 PROTEIN//2.8e-19:118:95//Hs.75243:D42040
F-OVARC1000890	F-OVARC1001261//EST//1.9e-42:225:96//Hs.158854:A1377837
F-OVARC1000891	F-OVARC1001268//ESTs//0.66:239:61//Hs.132525:AA576821
F-OVARC1000897//ESTs//1.1e-07:145:69//Hs.119878:AA706818	F-OVARC1001270//ESTs//0.99:204:60//Hs.144647:AA625224
F-OVARC1000912//EST//3.6e-08:376:61//Hs.158782:A1376601	F-OVARC1001271//Homo sapiens mRNA for KIAA0643 protein, partial cds//6.8e-144:644:96//Hs.155995:AB014543
F-OVARC1000915//Homo sapiens mRNA for KIAA0600 protein, partial cds//2.3e-85:419:97//Hs.9028:AF039691	F-OVARC1001282//ESTs, Weakly similar to Ydr438wp [S.cerevisiae]//0.11:355:60//Hs.108812:AA044835
F-OVARC1000924//ESTs//3.6e-113:540:98//Hs.66058:AA424456	F-OVARC1001296//ESTs//1.1e-46:237:98//Hs.33746:N78172
F-OVARC1000936//Human endogenous retrovirus envelope region mRNA (PL1)//4.3e-64:623:72//Hs.114440:M11119	F-OVARC1001306//Homo sapiens nuclear receptor co-repressor N-CoR mRNA, complete cds//0.20:188:64//Hs.152455:AF044209
F-OVARC1000937//EST//2.4e-39:170:96//Hs.129138:AA988078	F-OVARC1001329//ESTs//1.4e-97:486:97//Hs.125886:AA884264
F-OVARC1000945//ESTs, Weakly similar to protein tyrosine phosphatase [H.sapiens]//2.4e-29:157:97//Hs.136243:AA307843	F-OVARC1001330
F-OVARC1000948	F-OVARC1001339//Solute carrier family 4, anion exchanger, member 2 (erythrocyte membrane protein band 3-like 1)//0.021:232:62//Hs.79410:U62531
F-OVARC1000959//EST//0.65:293:55//Hs.134725:A1088986	F-OVARC1001341//ESTs, Weakly similar to C17G10.1 [C.elegans]//2.5e-76:363:99//Hs.105837:AA536054
F-OVARC1000960//Ley L-L//1.4e-41:425:72//Hs.37062:AC005952	F-OVARC1001342//EST//0.98:97:65//Hs.148210:AA897493
F-OVARC1000964//ESTs//1.4e-95:486:96//Hs.57079:D45288	F-OVARC1001344//EST//5.3e-10:241:64//Hs.138777:N67251
F-OVARC1000971//ESTs//0.19:198:62//Hs.153429:A1283069	F-OVARC1001357//Homo sapiens jerky gene product homolog mRNA, complete cds//0.64:198:61//Hs.105940:AF004715
F-OVARC1000984//Breakpoint cluster region protein BCR//0.26:365:56//Hs.2557:Y00661	F-OVARC1001360//ESTs//4.9e-87:429:97//Hs.130145:A1264633
F-OVARC1000996//Human p300/CBP-associated factor (P/CAF) mRNA, complete cds//6.8e-10:312:65//Hs.155302:U57317	F-OVARC1001369//ESTs//6.3e-07:371:62//Hs.131653:A1025777
F-OVARC1000999//Homo sapiens mRNA for chemokine LEC precursor, complete cds//0.0056:209:62//Hs.10458:AF088219	F-OVARC1001372//Homo sapiens mRNA for KIAA0654 protein, partial cds//1.4e-69:533:74//Hs.109299:AB014554
F-OVARC1001000//EST//4.2e-24:242:77//Hs.128952:AA984114	F-OVARC1001376//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//2.5e-49:365:73//Hs.129735:AF010144
F-OVARC1001004	F-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL//4.1e-149:683:99//Hs.151428:AJ224819
F-OVARC1001010	F-OVARC1001391//Homo sapiens methyl-CpG binding protein MB02 (MBD2) mRNA, complete cds//0.097:235:65//Hs.25674:AF072242
F-OVARC1001011//ESTs, Moderately similar to Tera [M.musculus]//3.8e-47:234:99//Hs.110327:AA205866	F-OVARC1001399//ESTs//1.1e-35:264:83//Hs.59379:W28225
F-OVARC1001032//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 ENHANCER-BINDING PROTEIN 2//0.0076:624:57//Hs.75063:AL023584	F-OVARC1001417//Homo sapiens EXLMI mRNA, complete cds//1.3e-150:707:98//Hs.21586:AB006651
F-OVARC1001034//ESTs, Highly similar to mitogen-induced [M.musculus]//3.9e-97:578:89//Hs.111974:A1050735	F-OVARC1001419//Homo sapiens GOK (STIM1) mRNA, complete cds//1.6e-

【0883】

【表582】

49:586:69//Hs.74597:U52426
 F-OVARC1001425//ESTs//2.4e-11:258:67//Hs.119197:T83651
 F-OVARC1001436
 F-OVARC1001442
 F-OVARC1001453
 F-OVARC1001476//ESTs. Weakly similar to HYPOTHETICAL 38.6 KD PROTEIN IN TIF4631-KRE11 INTERGENIC REGION [S.cerevisiae]//1.9e-125:581:99//Hs.110950:A1041823
 F-OVARC1001480//ESTs//0.95:125:72//Hs.152584:AA584568
 F-OVARC1001489//EST//4.9e-72:341:100//Hs.148191:AA897343
 F-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds//2.6e-86:479:92//Hs.6534:AF016507
 F-OVARC1001506//Polycystic kidney disease 1 (autosomal dominant)//1.1e-97:538:92//Hs.75813:L33243
 F-OVARC1001525
 F-OVARC1001542//Envoplakin//0.34:258:60//Hs.25482:U53786
 F-OVARC1001547//EST//0.0046:237:62//Hs.54638:N90595
 F-OVARC1001555
 F-OVARC1001577//Homo sapiens SRp45 splicing factor retropseudogene mRNA//6.8e-57:275:98//Hs.155160:AF031166
 F-OVARC1001600//ESTs. Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.0035:271:60//Hs.108465:A1144299
 F-OVARC1001610//ESTs. Weakly similar to F2E10.5 [C.elegans]//1.4e-43:216:99//Hs.120002:A1038398
 F-OVARC1001611
 F-OVARC1001615//EST//0.99:135:68//Hs.129410:AA993500
 F-OVARC1001668//Homo sapiens mRNA for KIAA572 protein, partial cds//3.3e-37:217:94//Hs.14409:AB011144
 F-OVARC1001702//Homo sapiens mRNA for hSOX20 protein, complete cds//5.9e-49:393:81//Hs.95582:AB006867
 F-OVARC1001703//EST//1.7e-24:172:88//Hs.121198:AA757229
 F-OVARC1001711//Fms-related tyrosine kinase 3 ligand//0.049:353:61//Hs.428:U03858
 F-OVARC1001713//ESTs//8.9e-37:263:86//Hs.110298:AA621807
 F-OVARC1001726//ESTs//2.0e-12:121:82//Hs.153332:AA236863
 F-OVARC1001731//Tropomyosin beta chain (skeletal muscle)//1.7e-83:617:80//Hs.155652:X06825
 F-OVARC1001745//EST//0.75:174:64//Hs.146778:A1148588
 F-OVARC1001762
 F-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//1.4e-150:706:98//Hs.155377:U97670
 F-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds//9.8e-117:580:96//Hs.15869:AB014575
 F-OVARC1001768//ESTs//0.035:179:64//Hs.87279:A1218697
 F-OVARC1001791
 F-OVARC1001795//ESTs//0.19:68:76//Hs.37699:AA062830
 F-OVARC1001802//EST//3.7e-45:254:92//Hs.130620:A1005102
 F-OVARC1001805//Homo sapiens mRNA for KIAA0744 protein, complete cds//0.77:362:58//Hs.116753:AB018287
 F-OVARC1001809//Human N-type calcium channel alpha-1 subunit mRNA, complete cds//2.2e-07:435:62//Hs.69949:M94172
 F-OVARC1001812//ESTs//3.0e-47:360:83//Hs.141756:AA700825
 F-OVARC1001813//EST//1.8e-57:277:100//Hs.162414:AA573453
 F-OVARC1001820//ESTs//1.4e-64:310:99//Hs.137398:AA164567
 F-OVARC1001828//EST//1.0e-09:184:66//Hs.130435:AA923537
 F-OVARC1001846//ESTs//1.8e-80:410:97//Hs.114539:N54973
 F-OVARC1001861
 F-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence//3.9e-20:122:95//Hs.25300:AF070611
 F-OVARC1001879//Homo sapiens putative tumor suppressor gene 26 protein alpha 2 delta calcium channel subunit mRNA, complete cds//0.042:199:67//Hs.127436:AF040709
 F-OVARC1001880//Interferon regulatory factor 5//1.1e-06:489:60//Hs.54434:U51127
 F-OVARC1001883//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//9.5e-33:509:68//Hs.158095:AB007953
 F-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//2.6e-57:300:96//Hs.6216:AF061749
 F-OVARC1001901//ESTs//2.3e-07:185:69//Hs.145630:A1263834
 F-OVARC1001911//EST//0.88:101:66//Hs.162622:AA601261
 F-OVARC1001916//H.sapiens mRNA for prepronociceptin//1.0:540:58//Hs.89040:U48263
 F-OVARC1001928
 F-OVARC1001942//Human plectin (PLEC1) mRNA, complete cds//0.038:290:62//Hs.79706:U53204
 F-OVARC1001943//ESTs. Weakly similar to HYPOTHETICAL 62.2 KD PROTEIN IN ZK652.6 IN CHROMOSOME III [C.elegans]//2.3e-119:565:98//Hs.5392:AA313794

F-OVARC1001949//KRAB zinc finger protein (alternative products)//1.8e-17:294:67//Hs.22556:U37251
 F-OVARC1001950//ESTs//1.5e-15:300:65//Hs.138501:A1051228
 F-OVARC1001987//ESTs//6.7e-34:202:92//Hs.115600:AA351639
 F-OVARC1001989//ESTs. Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-23:213:78//Hs.105292:AA504776
 F-OVARC1002044//EST//0.26:164:66//Hs.161094:N30417
 F-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//6.6e-160:739:98//Hs.108258:AB007934
 F-OVARC1002066//ESTs//1.8e-103:482:99//Hs.124923:A1375865
 F-OVARC1002082//EST//2.5e-09:213:67//Hs.112810:AA610063
 F-OVARC1002107
 F-OVARC1002112//Homo sapiens histone macroH2A1.2 mRNA, complete cds//2.7e-101:498:96//Hs.75258:AF054174
 F-OVARC1002127//ESTs//1.6e-76:397:96//Hs.33432:R83913
 F-OVARC1002138//Homo sapiens p60 katanin mRNA, complete cds//3.5e-20:399:62//Hs.112725:AF056022
 F-OVARC1002143//EST//4.2e-09:240:65//Hs.140547:AA812795
 F-OVARC1002156//EST//0.35:112:66//Hs.136761:AA738097
 F-OVARC1002158//ESTs. Weakly similar to Y53C12A.3 [C.elegans]//7.4e-07:329:58//Hs.107747:A1357868
 F-OVARC1002165//H.sapiens BDP1 mRNA for protein-tyrosine-phosphatase//0.00010:300:64//Hs.118929:X79568
 F-OVARC1002182//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//0.19:178:64//Hs.108447:AJ000517
 F-PLACE1000004//ESTs//0.79:332:59//Hs.120221:AA731230
 F-PLACE1000005//ESTs//1.8e-10:89:87//Hs.158913:A1378928
 F-PLACE1000007//Homo sapiens ubiquitin hydrolyzing enzyme 1 (UBH1) mRNA, partial cds//1.2e-52:550:72//Hs.42400:AF022789
 F-PLACE1000014
 F-PLACE1000031
 F-PLACE1000040//ESTs//3.1e-18:123:91//Hs.138387:AA873088
 F-PLACE1000048//ESTs//1.2e-43:387:78//Hs.61199:AA024494
 F-PLACE1000050//ESTs//1.8e-84:421:96//Hs.128632:A1076755
 F-PLACE1000061//Ribosomal protein L37a//5.5e-29:177:93//Hs.1946:L06499
 F-PLACE1000066//ESTs. Weakly similar to coded for by C. elegans CDNA yk10c10.3 [C.elegans]//1.4e-47:266:93//Hs.30026:A1356771
 F-PLACE1000078//ESTs. Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.sapiens]//6.4e-15:203:70//Hs.157422:R05366
 F-PLACE1000081//Human transporter protein (glr) mRNA, complete cds//0.30:324:60//Hs.76460:U49082
 F-PLACE1000094
 F-PLACE1000133//ESTs. Highly similar to TRANSCRIPTION FACTOR BTF3 [Homo sapiens]//6.2e-82:476:92//Hs.111081:A1380378
 F-PLACE1000142//ESTs. Weakly similar to enoyl-CoA hydratase [H.sapiens]//7.7e-27:205:85//Hs.9670:AA632135
 F-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds//2.5e-151:737:97//Hs.151017:AF058291
 F-PLACE1000185
 F-PLACE1000213
 F-PLACE1000214//ESTs//0.00059:335:59//Hs.143849:A1167255
 F-PLACE1000236//Fanconi anemia, complementation group A//0.44:306:61//Hs.86297:X99226
 F-PLACE1000246//ESTs//7.3e-80:457:89//Hs.57209:M22022
 F-PLACE1000292//ESTs//1.8e-05:323:60//Hs.59962:A1278202
 F-PLACE1000308//EST//0.0024:253:62//Hs.144238:M52294
 F-PLACE1000332//EST//5.6e-18:223:74//Hs.99532:AA461047
 F-PLACE1000347//ESTs//6.4e-33:169:99//Hs.122975:AA428675
 F-PLACE1000374//Human CCAAT-box-binding factor (CBF) mRNA, complete cds//0.26:45:95//Hs.147991:M37197
 F-PLACE1000380//Homo sapiens proline and glutamic acid rich nuclear protein isoform mRNA, partial cds//1.0:262:58//Hs.102732:U88153
 F-PLACE1000383//Myotubular myopathy 1//1.1e-50:669:67//Hs.75302:U46024
 F-PLACE1000401//Homo sapiens mRNA for KIAA0616 protein, partial cds//0.036:471:58//Hs.6051:AB014516
 F-PLACE1000406//ESTs. Highly similar to PTB-ASSOCIATED SPLICING FACTOR [Homo sapiens]//8.7e-63:346:93//Hs.19501:AA742260
 F-PLACE1000420//Homo sapiens mRNA for KIAA0602 protein, partial cds//0.0023:216:65//Hs.37656:AB011174
 F-PLACE1000421//Human lipid-activated protein kinase PRK1 mRNA, complete cds//0.55:212:63//Hs.2499:U33053
 F-PLACE1000424
 F-PLACE1000435//Homo sapiens mRNA for XPR2 protein//0.58:674:55//Hs.44766:AJ007590
 F-PLACE1000444//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//2.7e-52:421:80//Hs.69747:M35531
 F-PLACE1000453//Human mRNA for MTC8a protein, complete cds//0.026:

【0884】

【表583】

240:60//Hs.31551:D43638	28:421:66//Hs.8763:W30741
F-PLACE1000481//Oxytocin receptor//1.6e-25:347:71//Hs.2820:X64878	F-PLACE1001238
F-PLACE1000492//Human mRNA for KIAA0355 gene, complete cds//0.58:3	F-PLACE1001241//ESTs//1.1e-22:225:79//Hs.159786:R49494
02:60//Hs.153014:AB002353	F-PLACE1001257//ESTs//1.9e-23:165:89//Hs.126518:AA913929
F-PLACE1000540//EST//0.32:229:59//Hs.163011:AA700573	F-PLACE1001272//COATOMER BETA' SUBUNIT//0.012:50:96//Hs.75724:X704
F-PLACE1000547//Human heparan sulfate proteoglycan (HSPG2) mRNA, c	76
omplete cds//0.0046:223:65//Hs.75578:M85289	F-PLACE1001279//ESTs//0.97:377:59//Hs.152628:W51283
F-PLACE1000562	F-PLACE1001280//Homo sapiens hyperpolarization-activated channel 1
F-PLACE1000564//ESTs//8.0e-35:247:89//Hs.12999:AA278538	(IH1) mRNA, partial cds//1.2e-08:586:58//Hs.124161:AF065164
F-PLACE1000583//Homo sapiens clone 23939 mRNA sequence//6.6e-47:52	F-PLACE1001294//Homo sapiens mRNA for myosin phosphatase target su
5:72//Hs.21838:AF038179	bunit 1 (MYPT1)//0.91:221:61//Hs.16533:D87930
F-PLACE1000588//Guanylate binding protein 1, interferon-inducible,	F-PLACE1001304//Human zinc finger protein mRNA, complete cds//8.6
67kd//2.3e-85:503:88//Hs.62661:M55542	e-08:370:60//Hs.42672:AF016052
F-PLACE1000596//Homo sapiens mRNA for NS1-binding protein (NS1-BP)	F-PLACE1001311//ESTs//1.7e-44:480:73//Hs.155384:Z78385
//1.2e-165:798:97//Hs.159597:AJ012449	F-PLACE1001323//ESTs//1.1e-25:151:95//Hs.134120:AA699591
F-PLACE1000599//ESTs//0.65:201:58//Hs.98216:AA758751	F-PLACE1001351
F-PLACE1000610//Homo sapiens mRNA for KIAA0642 protein, partial cd	F-PLACE1001366//Homo sapiens mRNA for KIAA0799 protein, partial cd
s//0.98:215:60//Hs.8152:AB014542	s//2.8e-26:155:95//Hs.61338:AB018342
F-PLACE1000611//ESTs//7.2e-20:406:64//Hs.128966:AA620986	F-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//
F-PLACE1000636	3.4e-44:393:79//Hs.152005:AF009615
F-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase	F-PLACE1001383//ESTs//1.0:159:65//Hs.128501:AA973748
mRNA, complete cds//5.0e-154:747:96//Hs.5819:AF102265	F-PLACE1001384//Homo sapiens multi POZ domain protein MUPP1 (MUPP
F-PLACE1000656//Homo sapiens mRNA for JM4 protein, complete CDS (c	1) mRNA, complete cds//2.6e-09:117:84//Hs.21301:AF093419
lone IMAGE 546750 and LNLCL110F1857Q7 (RZPD Berlin))//7.5e-158:77	F-PLACE1001387//ESTs, Weakly similar to EPIDERMAL GROWTH FACTOR RE
5:97//Hs.29595:AJ005896	CEPTOR KINASE SUBSTRATE EPS8 (H.sapiens)//0.0083:187:64//Hs.5399:
F-PLACE1000706//Homo sapiens transcription intermediary factor 1	N30646
(TIF1) mRNA, complete cds//1.0e-57:675:69//Hs.128763:AF009353	F-PLACE1001395//Homo sapiens mRNA for putative DNA methyltransfera
F-PLACE1000712//EST//0.56:171:61//Hs.112790:AA609949	se, complete CDS//0.0038:496:57//Hs.97681:AJ223333
F-PLACE1000716//Human mRNA for KIAA0258 gene, complete cds//6.1e-3	F-PLACE1001399//Human melanoma antigen recognized by T-cells (MAR
8:426:70//Hs.47313:D87447	T-1) mRNA//7.0e-45:456:75//Hs.154069:U06452
F-PLACE1000748//ESTs//2.6e-43:233:95//Hs.110754:AA112288	F-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequ
F-PLACE1000749//Human MAGE-9 antigen (MAGE9) gene, complete cds//	ence//6.5e-71:365:96//Hs.110404:AF091087
0.72:331:57//Hs.37110:U10694	F-PLACE1001414//EST//1.2e-75:364:98//Hs.136622:AA633232
F-PLACE1000755//NUCLEOLIN//0.0038:186:66//Hs.79110:M60858	F-PLACE1001440//ESTs//2.8e-05:163:66//Hs.141082:H18987
F-PLACE1000769	F-PLACE1001456//EST//0.95:132:61//Hs.20373:R09510
F-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cd	F-PLACE1001468//ESTs//0.00019:184:66//Hs.126536:A1379455
s//1.1e-139:663:98//Hs.31921:AB014548	F-PLACE1001484//EST//8.6e-18:190:76//Hs.160992:HS2716
F-PLACE1000786//Myosin, heavy polypeptide 9, non-muscle//8.5e-06:3	F-PLACE1001502//Apolipoprotein E//2.5e-05:306:60//Hs.76260:M12529
62:59//Hs.44782:Z82215	F-PLACE1001503
F-PLACE1000793//ESTs//2.7e-62:315:97//Hs.16141:W56079	F-PLACE1001517//ESTs//1.9e-12:138:78//Hs.120352:AA718914
F-PLACE1000798//ESTs//1.4e-55:316:93//Hs.139119:N32189	F-PLACE1001534//EST//0.015:121:65//Hs.144156:R85753
F-PLACE1000841//EST//0.47:143:61//Hs.144096:A1032180	F-PLACE1001545
F-PLACE1000849//Homo sapiens CAGF9 mRNA, partial cds//1.6e-06:266:	F-PLACE1001551
63//Hs.110826:U80736	F-PLACE1001570//EST//0.58:286:59//Hs.120202:AA728835
F-PLACE1000856//ESTs//2.6e-60:319:96//Hs.25994:AA470000	F-PLACE1001602//Human POU domain protein (Brn-3b) mRNA, complete c
F-PLACE1000863//EST//9.4e-29:249:78//Hs.121919:AA777428	ds//0.013:159:66//Hs.266:U06233
F-PLACE1000909//ESTs//0.97:214:60//Hs.128601:AA906455	F-PLACE1001603//Homo sapiens nitric oxide synthase (NOS1) mRNA, complete cds
F-PLACE1000931//ESTs//2.1e-46:592:70//Hs.154244:AA195201	//1.1e-10:133:77//Hs.146406:AF069987
F-PLACE1000948	F-PLACE1001608//ESTs//0.022:187:60//Hs.145915:A1342230
F-PLACE1000972//Homo sapiens enhancer of filamentation (HEF1) mRN	F-PLACE1001610//ESTs//1.4e-77:377:97//Hs.115700:AA808005
A, complete cds//7.9e-10:294:66//Hs.80261:L43821	F-PLACE1001611//Human facio-genital dysplasia (FGD1) mRNA, complete
F-PLACE1000977//ESTs, Weakly similar to coded for by C. elegans cD	cds//0.96:141:66//Hs.1572:U11690
NA yk28h2.5 [C. elegans]//9.3e-45:309:88//Hs.13531:R61789	F-PLACE1001632//Homo sapiens mRNA for KIAA0798 protein, complete c
F-PLACE1000979//Zinc finger protein 91 (HPF7, HTF10)//0.0034:229:6	ds//3.4e-76:702:75//Hs.159277:AB018341
2//Hs.8597:L11672	F-PLACE1001634//ESTs//1.2e-43:260:92//Hs.134064:A1276198
F-PLACE1000987//Homo sapiens mRNA for KIAA0724 protein, complete c	F-PLACE1001640
ds//2.6e-141:694:96//Hs.158497:AB018267	F-PLACE1001672//EST//2.8e-21:201:82//Hs.123341:AA810927
F-PLACE1001000//ESTs//0.0035:116:73//Hs.144532:H39913	F-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein
F-PLACE1001007//Guanylate cyclase 2D, membrane (retina-specific)//	(OA48-18) mRNA, complete cds//2.8e-148:726:96//Hs.3688:AF069250
0.050:338:61//Hs.1974:M92432	F-PLACE1001692//ESTs, Highly similar to S-ACYL FATTY ACID SYNTHAS
F-PLACE1001010//H.sapiens mRNA for retrotransposon//1.6e-45:371:80	E THIOESTERASE, MEDIUM CHAIN [Rattus norvegicus]//1.1e-95:481:92//
//Hs.6940:Z48633	Hs.24309:A125696
F-PLACE1001015//ESTs//8.6e-27:211:71//Hs.88040:AA256876	F-PLACE1001705//Human RNA polymerase III subunit (RPC39) mRNA, com
F-PLACE1001024	plete cds//6.0e-30:347:76//Hs.101555:U93869
F-PLACE1001036//EST//1.0:133:65//Hs.161424:A1424741	F-PLACE1001716//Human mRNA for KIAA0191 gene, partial cds//2.1e-6
F-PLACE1001054//Human plectin (PLEC1) mRNA, complete cds//0.98:28	9:369:73//Hs.12413:D83776
4:59//Hs.79706:U53204	F-PLACE1001720//ESTs//1.2e-27:146:99//Hs.106432:A1391686
F-PLACE1001062	F-PLACE1001729//Homo sapiens mRNA for KIAA0522 protein, partial cd
F-PLACE1001076//EST//0.84:223:59//Hs.161147:A1417859	s//0.0084:484:60//Hs.129892:AB011094
F-PLACE1001088	F-PLACE1001739//Histidine-rich calcium binding protein//0.14:240:6
F-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds//	4//Hs.1480:M60052
1.0e-96:489:96//Hs.95448:AF065485	F-PLACE1001740//ESTs//4.9e-32:343:74//Hs.139158:AA226159
F-PLACE1001104//ESTs//0.19:249:64//Hs.152627:AA595817	F-PLACE1001745
F-PLACE1001118//Homo sapiens KRAB domain zinc finger protein (ZFP3	F-PLACE1001746//ESTs//7.0e-15:168:80//Hs.46601:N78361
7) mRNA, complete cds//8.2e-66:676:71//Hs.150406:AF022158	F-PLACE1001748//Homo sapiens metalloprotease 1 (MP1) mRNA, complet
F-PLACE1001136//Amphiregulin (schwannoma-derived growth factor)//	e cds//2.8e-160:773:97//Hs.4812:AF061243
1.5e-16:122:91//Hs.1257:M30704	F-PLACE1001756//Homo sapiens tapasin (NCS-17) mRNA, complete cds//
F-PLACE1001168	2.7e-35:269:83//Hs.5247:AF029750
F-PLACE1001171//ESTs//4.3e-12:214:72//Hs.141392:R95135	F-PLACE1001761//ESTs//6.9e-27:159:93//Hs.78277:AA131283
F-PLACE1001185//ESTs, Weakly similar to ZK792.1 [C.elegans]//1.6e-	F-PLACE1001771//Human putative calcium influx channel (htrp3) mRN

【0885】

【表584】

A, complete cds//3.4e-52:548:72//Hs.150981:U47050	F-PLACE1002625
F-PLACE1001781	F-PLACE1002655//GELSOLIN PRECURSOR, PLASMA//1.7e-36:693:62//Hs.80562:X04412
F-PLACE1001799//EST//5.4e-07:145:70//Hs.121840:AA776115	F-PLACE1002665//EST//0.15:156:65//Hs.161793:AA380706
F-PLACE1001810//ESTs//0.024:134:67//Hs.43134:AA766138	F-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds//1.1e-187:804:97//Hs.124903:AF068180
F-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//3.6e-110:546:96//Hs.40820:AF058953	F-PLACE1002714//Human involucrin mRNA//3.6e-08:509:60//Hs.157091:M13903
F-PLACE1001821	F-PLACE1002722//Human protease-activated receptor 3 (PAR3) mRNA, complete cds//0.34:230:58//Hs.159196:U92971
F-PLACE1001844//ESTs//5.4e-45:387:79//Hs.61199:AA024494	F-PLACE1002768//EST//0.37:126:69//Hs.125353:AA877080
F-PLACE1001845//ESTs//2.5e-47:232:100//Hs.120809:AA150214	F-PLACE1002772//ESTs//0.0017:147:69//Hs.132439:AA923728
F-PLACE1001869//EST//1.0:139:59//Hs.122285:AA781906	F-PLACE1002775//EST//5.5e-09:129:75//Hs.135336:A1049827
F-PLACE1001897//ESTs//0.29:348:57//Hs.139993:A1343257	F-PLACE1002782//Homo sapiens l-l receptor candidate protein mRNA, complete cds//0.0031:298:62//Hs.26285:AF082516
F-PLACE1001912//ESTs//4.0e-10:95:89//Hs.13475:R18220	F-PLACE1002794//ESTs//0.71:125:66//Hs.97441:A1368926
F-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//4.0e-153:685:95//Hs.17839:AF099936	F-PLACE1002811//Human mRNA for KIAA0172 gene, partial cds//5.8e-46:567:70//Hs.77546:D79994
F-PLACE1001928//H. sapiens HUM9 mRNA//0.063:196:66//Hs.2750:X74837	F-PLACE1002815
F-PLACE1001983//Homo sapiens Jagged 2 mRNA, complete cds//9.8e-06:431:58//Hs.105387:AF029778	F-PLACE1002816//Homo sapiens mRNA for KIAA0600 protein, partial cds//4.3e-70:687:73//Hs.9028:AF039691
F-PLACE1001989	F-PLACE1002834//ESTs//2.6e-41:393:74//Hs.120206:A1089163
F-PLACE1002004	F-PLACE1002839//ESTs//0.26:177:63//Hs.149013:A1334167
F-PLACE1002046	F-PLACE1002851//EST//0.0034:102:72//Hs.129630:A1000405
F-PLACE1002052//Human mRNA for phospholipase C, complete cds//0.0092:465:58//Hs.153322:D42108	F-PLACE1002853//ESTs//1.1e-20:136:90//Hs.125895:AA889024
F-PLACE1002066//EST//0.49:307:61//Hs.150652:AA908555	F-PLACE1002881//Interleukin 10//1.1e-41:454:72//Hs.2180:M57627
F-PLACE1002072//EST//1.0:103:65//Hs.116488:F13707	F-PLACE1002908//ESTs//3.8e-48:325:88//Hs.54702:A1040029
F-PLACE1002073//Homo sapiens mRNA for KIAA0606 protein, partial cds//4.2e-39:635:64//Hs.38176:AB011178	F-PLACE1002941//ESTs//5.0e-18:128:88//Hs.17376:AA855056
F-PLACE1002090//Homo sapiens signal recognition particle 72 (SRP72) mRNA, complete cds//4.3e-83:388:99//Hs.5171:AF069765	F-PLACE1002962
F-PLACE1002115//EST//0.18:215:62//Hs.135747:A1002637	F-PLACE1002968//ESTs, Highly similar to trg gene product [R.norvegicus]//0.031:372:59//Hs.8021:A1041815
F-PLACE1002119//Human transcription factor ETR101 mRNA, complete cds//6.2e-13:384:61//Hs.737:M62831	F-PLACE1002991
F-PLACE1002140//EST, Moderately similar to ALPHA-1-ANTITRYPSIN PRECURSOR [Homo sapiens]//0.89:60:75//Hs.144290:T61747	F-PLACE1002993
F-PLACE1002150//ESTs//0.56:245:64//Hs.24119:AA115631	F-PLACE1002996//ESTs, Weakly similar to T2003.3 [C.elegans]//1.3e-12:104:86//Hs.124808:T86959
F-PLACE1002157//Human mRNA for KIAA0392 gene, partial cds//2.8e-51:440:79//Hs.40100:AB002390	F-PLACE1003025//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0510//0.99:192:64//Hs.92660:AB007979
F-PLACE1002163//ESTs//0.76:212:61//Hs.112494:A1366891	F-PLACE1003027//Homo sapiens mRNA for KIAA0516 protein, partial cds//2.0e-131:632:97//Hs.129872:AB011088
F-PLACE1002170//ESTs//6.5e-09:108:76//Hs.41418:H90627	F-PLACE1003044//Homo sapiens mRNA for KIAA0667 protein, partial cds//2.7e-14:555:58//Hs.154740:AB014567
F-PLACE1002171//ESTs//3.5e-81:493:89//Hs.122553:H66674	F-PLACE1003045
F-PLACE1002205//Human clone 23695 mRNA sequence//0.00080:472:60//Hs.90798:U79289	F-PLACE1003092//ESTs//1.1e-108:506:99//Hs.22119:AA885491
F-PLACE1002213//ESTs//0.041:146:67//Hs.119162:AA399989	F-PLACE1003100//Human Hep27 protein mRNA, complete cds//2.9e-66:650:73//Hs.102137:U31875
F-PLACE1002227//ESTs//9.4e-06:173:66//Hs.127882:A1024442	F-PLACE1003108//EST//0.016:181:65//Hs.119762:AA703419
F-PLACE1002256//ESTs//1.8e-93:440:99//Hs.128700:AA970935	F-PLACE1003136
F-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frames//2.3e-75:434:83//Hs.23094:M19503	F-PLACE1003145
F-PLACE1002319//ESTs//0.82:188:62//Hs.50918:AA036675	F-PLACE1003153//ESTs//3.1e-09:209:65//Hs.111583:AA463590
F-PLACE1002342//EST//0.61:148:66//Hs.144319:AA280279	F-PLACE1003174//ESTs//0.073:97:69//Hs.12992:W01997
F-PLACE1002395//ESTs//1.2e-18:168:83//Hs.3853:AA034291	F-PLACE1003176//ESTs//3.3e-60:296:90//Hs.58239:AA215797
F-PLACE1002399//EST//0.0011:166:65//Hs.137500:AA436710	F-PLACE1003190//Homo sapiens C19steroid specific UDP-glucuronosyltransferase mRNA, complete cds//0.98:221:60//Hs.139756:U59209
F-PLACE1002433//ESTs//1.2e-14:151:80//Hs.161837:AA421067	F-PLACE1003200//EST//0.0021:309:60//Hs.140561:AA765532
F-PLACE1002437//Human ATP binding cassette transporter (ABCR) mRNA, complete cds//2.6e-23:458:66//Hs.40993:AF000148	F-PLACE1003205//EST//1.2e-07:204:65//Hs.147372:A1208770
F-PLACE1002438//EST//0.81:48:77//Hs.158575:A1368947	F-PLACE1003238//ESTs//7.4e-62:343:94//Hs.121302:AA758208
F-PLACE1002450//Homo sapiens KRAB domain zinc finger protein (ZFP37) mRNA, complete cds//7.1e-07:270:66//Hs.150406:AF022158	F-PLACE1003249//Insulin-like growth factor 1 (somatomedin C)//0.99:175:62//Hs.85112:X57025
F-PLACE1002465	F-PLACE1003256
F-PLACE1002474//Homo sapiens mRNA for matrilin-4, partial//1.3e-14:369:63//Hs.129361:AJ007581	F-PLACE1003258//H. sapiens mRNA for ZYG homologue//0.00020:217:64//Hs.29285:X99802
F-PLACE1002477//ESTs//3.5e-13:125:71//Hs.145032:AA343523	F-PLACE1003296//ESTs//2.6e-14:80:86//Hs.155441:AA533106
F-PLACE1002493	F-PLACE1003302//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//4.3e-51:700:67//Hs.37138:U35376
F-PLACE1002499	F-PLACE1003334
F-PLACE1002500//Human putative zinc transporter ZnT-3 (ZnT-3) mRNA, complete cds//4.3e-19:708:59//Hs.111967:U76010	F-PLACE1003342//ESTs//0.94:310:57//Hs.131502:A1023308
F-PLACE1002514//ESTs//3.1e-07:178:66//Hs.70932:AA126482	F-PLACE1003343//EST//1.2e-09:114:77//Hs.103418:AA035568
F-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//2.9e-144:583:95//Hs.88756:AB018256	F-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds//2.6e-144:773:92//Hs.6564:U92715
F-PLACE1002532//Homo sapiens BAC clone RG300E22 from Tq21-q31.1//3.1e-115:566:96//Hs.99348:AC004774	F-PLACE1003361//ESTs, Weakly similar to ATP SYNTHASE A CHAIN [Trypanosoma brucei brucei]//8.9e-35:332:78//Hs.163820:H71277
F-PLACE1002537//Thiopurine S-methyltransferase//1.9e-28:198:86//Hs.51124:AF019369	F-PLACE1003366//Homo sapiens dysferlin mRNA, complete cds//7.9e-06:502:57//Hs.143897:AF075575
F-PLACE1002571//Homo sapiens mRNA for TP55, complete cds//0.99:274:59//Hs.138202:AF027866	F-PLACE1003369//NUCLEOLIN//0.00037:282:60//Hs.79110:M60858
F-PLACE1002578//ESTs//7.3e-10:185:73//Hs.41418:H90627	F-PLACE1003373//EST//1.1e-11:420:63//Hs.156592:A1343009
F-PLACE1002583//EST//0.0028:348:61//Hs.160396:A1393725	F-PLACE1003375//EST//0.75:119:68//Hs.160270:A1149069
F-PLACE1002591//Human mRNA for actin binding protein p57, complete cds//2.8e-27:279:74//Hs.109606:D44497	F-PLACE1003383
F-PLACE1002598//EST//0.011:209:62//Hs.131470:A1024187	F-PLACE1003394//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-1
F-PLACE1002604//EST//0.47:220:61//Hs.145434:A1198915	

【0886】

【表585】

4 [Rattus norvegicus]//8.9e-113:590.94//Hs.125175:AI142546
 F-PLACE1003401//ESTs//0.55:176:66//Hs.154292:AA886178
 F-PLACE1003420//Macrophage stimulating 1 (hepatocyte growth factor-like)//0.40:206:62//Hs.30223:X90846
 F-PLACE1003454//ESTs//0.98:74:72//Hs.127131:AA150912
 F-PLACE1003478//EST//5.0e-06:183:69//Hs.127524:AA952874
 F-PLACE1003493//Protein-tyrosine kinase 7//0.98:232:63//Hs.90572:U33635
 F-PLACE1003516//Human knpi repeat mRNA (cdna clone pcd-kpni-8), 3' end//3.4e-85:357:86//Hs.103948:K00627
 F-PLACE1003519//ESTs//1.6e-33:288:72//Hs.159510:AA297145
 F-PLACE1003521//H.sapiens mRNA for retrotransposon//1.4e-45:269:76//Hs.6940:248633
 F-PLACE1003528//ESTs//0.65:120:68//Hs.162376:AA570248
 F-PLACE1003537//ESTs, Weakly similar to ZK858.6 [C.elegans]//3.6e-110:543:97//Hs.120416:AA057428
 F-PLACE1003553
 F-PLACE1003566//ESTs//0.0015:508:59//Hs.5724:AA156780
 F-PLACE1003575//Homo sapiens cdc14 homolog mRNA, complete cds//4.4e-05:499:58//Hs.65993:AF000367
 F-PLACE1003583//ESTs//5.5e-19:448:63//Hs.161701:AA225932
 F-PLACE1003584//EST//1.6e-46:263:94//Hs.147412:AI209194
 F-PLACE1003592//ESTs, Moderately similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//1.4e-50:287:93//Hs.154799:AA130620
 F-PLACE1003593//ESTs//0.0025:318:61//Hs.106771:AA806965
 F-PLACE1003596//Integral transmembrane protein 1//1.9e-54:685:68//Hs.89650:L38961
 F-PLACE1003602//Homo sapiens mRNA expressed in placenta//3.4e-140:679:97//Hs.56851:083200
 F-PLACE1003605//Homo sapiens Cdc14B2 phosphatase mRNA, partial cds//0.00065:236:64//Hs.22116:AF064104
 F-PLACE1003611//EST//0.00015:318:59//Hs.28788:R66896
 F-PLACE1003618//Human Line-1 repeat mRNA with 2 open reading frames//1.3e-122:737:87//Hs.23094:M19503
 F-PLACE1003625//ESTs//1.6e-16:103:96//Hs.111223:N51105
 F-PLACE1003638//ESTs//0.60:305:57//Hs.19104:W07762
 F-PLACE1003669//ESTs, Weakly similar to 3-7 gene product [H.sapiens]//0.021:445:58//Hs.158275:AI365413
 F-PLACE1003704//Human mRNA for KIAA0301 gene, partial cds//0.014:622:56//Hs.76730:AB002299
 F-PLACE1003709//Homo sapiens protein kinase (BUB1) mRNA, complete cds//1.4e-133:689:95//Hs.98658:AF053305
 F-PLACE1003711//ESTs//2.2e-14:178:77//Hs.114831:T57101
 F-PLACE1003723//Homo sapiens mRNA for T lymphocyte specific adaptor protein//8.5e-09:393:60//Hs.103527:AJ000553
 F-PLACE1003738//ESTs, Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//1.8e-53:260:99//Hs.102928:AI346344
 F-PLACE1003760//ESTs//5.1e-08:334:63//Hs.43675:AA805648
 F-PLACE1003762//ESTs//1.0:59:83//Hs.29863:W28983
 F-PLACE1003768//Human knpi repeat mRNA (cdna clone pcd-kpni-4), 3' end//2.7e-40:608:68//Hs.139107:K00629
 F-PLACE1003771//ESTs//6.6e-10:226:65//Hs.15776:T91944
 F-PLACE1003783
 F-PLACE1003784//Homo sapiens mRNA for KIAA0765 protein, partial cds//1.0:457:57//Hs.62318:AB018308
 F-PLACE1003795//Human homologue of yeast sec7 mRNA, complete cds//0.85:314:60//Hs.1050:M85169
 F-PLACE1003833//ESTs, Weakly similar to C27H6.5 [C.elegans]//0.00059:201:68//Hs.40806:AA018786
 F-PLACE1003850//ESTs//0.0088:220:61//Hs.145504:AI254165
 F-PLACE1003858//EST//0.77:137:61//Hs.146935:AI168124
 F-PLACE1003864//ESTs//0.11:225:59//Hs.160910:AI370359
 F-PLACE1003870//EST//7.2e-18:283:69//Hs.135497:AI091257
 F-PLACE1003885//H.sapiens PAP mRNA//2.4e-75:759:72//Hs.49007:X76770
 F-PLACE1003886
 F-PLACE1003888//Human mRNA for phospholipase C, complete cds//8.4e-55:702:67//Hs.153322:D42108
 F-PLACE1003892//ESTs//2.4e-13:258:67//Hs.28039:H24050
 F-PLACE1003900//ESTs//3.5e-14:271:66//Hs.28589:AI004944
 F-PLACE1003903//CTP synthetase//1.6e-49:528:71//Hs.84112:X52142
 F-PLACE1003915//ESTs, Highly similar to ARGINYL-TRNA SYNTHETASE, MITOCHONDRIAL PRECURSOR [Saccharomyces cerevisiae]//1.2e-49:251:98//Hs.65831:F03069
 F-PLACE1003923//Interferon, alpha 16//0.48:278:60//Hs.56303:M28585
 F-PLACE1003932//EST//0.00060:221:63//Hs.163044:AA707537
 F-PLACE1003936//ESTs//0.86:211:62//Hs.150751:AI123536
 F-PLACE1003968//Human 5'-AMP-activated protein kinase, gamma-1 subunit mRNA, complete cds//2.0e-47:522:71//Hs.3136:U42412
 F-PLACE1004103//ESTs//8.6e-35:226:89//Hs.78973:AI026812
 F-PLACE1004104//ESTs//1.0:179:61//Hs.163935:AA506940
 F-PLACE1004114//ESTs//1.3e-52:323:89//Hs.35156:AA148516
 F-PLACE1004118//Spleen focus forming virus (SFFV) proviral integration oncogene sp1//0.85:164:64//Hs.153045:X52056
 F-PLACE1004128//Guanine nucleotide binding protein (G protein), beta polypeptide 1//3.1e-41:422:74//Hs.3620:X04526
 F-PLACE1004149//ESTs, Weakly similar to F48F7.1 [C.elegans]//8.2e-82:418:96//Hs.156161:AI333779
 F-PLACE1004156//ESTs//0.10:166:63//Hs.133279:AI053552
 F-PLACE1004161//Human mRNA for KIAA0200 gene, complete cds//0.85:269:64//Hs.76986:D83785
 F-PLACE1004183//EST//1.3e-40:224:94//Hs.156603:AI343666
 F-PLACE1004197//ESTs//2.8e-91:441:98//Hs.97269:AA292201
 F-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds//1.3e-145:695:98//Hs.24640:AF069493
 F-PLACE1004242//ESTs//0.99:213:60//Hs.117311:AA699722
 F-PLACE1004256//EST//0.019:364:58//Hs.122395:AA789273
 F-PLACE1004257//ESTs//0.77:154:64//Hs.112582:AA608689
 F-PLACE1004258//ESTs, Weakly similar to vanilloid receptor subtype 1 [R.norvegicus]//1.1e-98:479:97//Hs.31718:M29128
 F-PLACE1004270//Homo sapiens CACF9 mRNA, partial cds//0.00010:369:63//Hs.110826:U80736
 F-PLACE1004274//Homo sapiens mRNA for KIAA0445 protein, complete cds//0.085:573:56//Hs.154139:AB007914
 F-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, complete cds//2.0e-157:756:97//Hs.127007:AF084830
 F-PLACE1004284//ESTs//3.6e-71:344:99//Hs.145870:AI271884
 F-PLACE1004289//ESTs//2.6e-57:370:85//Hs.16740:AA586576
 F-PLACE1004302//FACTOR VIII INTRON 22 PROTEIN//0.032:513:59//Hs.83363:M34677
 F-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//9.3e-152:797:94//Hs.11171:Y11588
 F-PLACE1004336
 F-PLACE1004358//Homo sapiens connector enhancer of XSR-like protein CNK1 mRNA, complete cds//1.9e-140:688:97//Hs.16232:AF100153
 F-PLACE1004376//ESTs, Weakly similar to F27D4.4 [C.elegans]//3.9e-109:521:98//Hs.14079:AA306552
 F-PLACE1004384//Human HsLIM15 mRNA for HsLIM15, complete cds//2.0e-49:466:76//Hs.37181:D64108
 F-PLACE1004388
 F-PLACE1004405//EST//0.010:191:64//Hs.147600:AI217871
 F-PLACE1004425//ESTs//2.1e-20:124:80//Hs.94195:W03579
 F-PLACE1004428//H.sapiens mRNA for Branched chain Acyl-CoA Oxidase//1.0:552:58//Hs.9795:X95190
 F-PLACE1004437//Human NAD+-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds//9.9e-131:536:99//Hs.155410:U49283
 F-PLACE1004451//ESTs//5.9e-18:203:73//Hs.156097:AI348867
 F-PLACE1004460
 F-PLACE1004467//ESTs//8.0e-17:345:66//Hs.112993:AA824363
 F-PLACE1004471//EST//9.3e-69:463:84//Hs.116391:AA644085
 F-PLACE1004473//ESTs//0.93:358:58//Hs.33263:AA724416
 F-PLACE1004491//EST//2.5e-58:285:99//Hs.97603:AA398163
 F-PLACE1004506//CD81 ANTIGEN//7.2e-06:228:63//Hs.54457:M33680
 F-PLACE1004510//Homo sapiens cofactor of initiator function (CIF15D) mRNA, complete cds//2.5e-147:699:97//Hs.122752:AF026445
 F-PLACE1004516//EST//1.0e-26:343:71//Hs.142595:M24150
 F-PLACE1004518
 F-PLACE1004548//EST//0.84:193:62//Hs.99583:AA461314
 F-PLACE1004550//ESTs, Weakly similar to No definition line found [C.elegans]//4.0e-120:627:94//Hs.107387:AA058854
 F-PLACE1004564//EST//1.0:240:62//Hs.16824:T91371
 F-PLACE1004629//Centromere protein B (80kd)//0.0015:242:64//Hs.85004:X05299
 F-PLACE1004645
 F-PLACE1004646//Retinal pigment epithelium-specific protein (65kd)//1.4e-12:386:63//Hs.2133:U18991
 F-PLACE1004658//ESTs//0.52:273:61//Hs.97252:AA291590
 F-PLACE1004664
 F-PLACE1004672//Human ABL gene, exon 1b and intron 1b, and putative M8604 Met protein (M8604 Met) gene//1.5e-66:357:95//Hs.77705:U07563
 F-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//1.4e-110:625:91//Hs.80019:AF035606
 F-PLACE1004681//EST//0.00092:303:61//Hs.149560:AI281589
 F-PLACE1004686//ESTs//3.0e-31:186:76//Hs.139130:AA704561
 F-PLACE1004691//Homo sapiens clone 23963 mRNA sequence//0.54:242:61//Hs.48483:AF007131
 F-PLACE1004693//ESTs, Weakly similar to pot. ORF III [H.sapiens]//0.56:96:71//Hs.125740:AA884845

【0887】

【表586】

F-PLACE1004716//ESTs//2.0e-79:388:98//Hs.150999:AI306542	F-PLACE1005266//Kallmann syndrome 1 sequence//7.8e-06:484:60//Hs.89591:M97252
F-PLACE1004722//ESTs//7.5e-06:105:72//Hs.128796:AA485891	F-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds//5.1e-150:706:98//Hs.118087:AB011182
F-PLACE1004736//ESTs//1.7e-27:203:86//Hs.119593:AA700148	F-PLACE1005287//ESTs//8.1e-107:501:99//Hs.145703:AA447947
F-PLACE1004740//ESTs//1.0e-25:174:89//Hs.29696:AA910680	F-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL//4.4e-37:597:66//Hs.101642:X60673
F-PLACE1004743	F-PLACE1005308//High-mobility group (nonhistone chromosomal) protein 2//0.83:239:62//Hs.80684:X62534
F-PLACE1004751//ESTs. Highly similar to CMP-N-ACETYLNEURAMINATE-6-ETA-1,4-GALACTOSIDE ALPHA-2,3-SIALYLTRANSFERASE [Rattus norvegicus]//2.0e-41:260:90//Hs.6863:W52470	F-PLACE1005313
F-PLACE1004773//Homo sapiens invasin protein mRNA, complete cds//1.7e-172:828:97//Hs.104715:AF084367	F-PLACE1005327//ESTs. Weakly similar to No definition line found [C.elegans]//6.0e-81:459:91//Hs.146177:R51650
F-PLACE1004777//Human myosin-Ix beta mRNA, complete cds//1.0e-29:556:63//Hs.159629:U42391	F-PLACE1005331//Homo sapiens chromosome 19, cosmid F20569//3.7e-66:412:88//Hs.134031:AC004794
F-PLACE1004793	F-PLACE1005335//Homo sapiens mRNA for KIAA0754 protein, partial cds//0.96:510:56//Hs.159183:AB018297
F-PLACE1004804	F-PLACE1005373
F-PLACE1004813//EST//2.8e-42:296:83//Hs.155725:AI310340	F-PLACE1005374//ESTs//7.5e-77:437:91//Hs.143266:AI141348
F-PLACE1004814//ESTs. Weakly similar to U1 SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus laevis]//2.4e-78:415:95//Hs.80965:AA493284	F-PLACE1005409//ESTs//2.4e-05:267:63//Hs.163307:AA856751
F-PLACE1004815//Human mRNA for KIAA0364 gene, complete cds//4.3e-14:294:69//Hs.22111:AB002362	F-PLACE1005453//ESTs//0.12:333:58//Hs.134672:AI087951
F-PLACE1004824//ESTs//0.0072:128:69//Hs.164062:AA934047	F-PLACE1005467//HOMEBOX/POU DOMAIN PROTEIN RDC-1//0.0043:148:67//Hs.74095:L20433
F-PLACE1004827//ESTs//0.7e-38:100//Hs.18925:W30943	F-PLACE1005471//ESTs//3.4e-24:135:97//Hs.49275:M66925
F-PLACE1004836//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.78:338:57//Hs.8546:U97659	F-PLACE1005477//Human Line-1 repeat mRNA with 2 open reading frame s//3.5e-126:744:87//Hs.23094:M19503
F-PLACE1004838	F-PLACE1005480//ESTs//3.7e-26:184:70//Hs.113198:M39323
F-PLACE1004840//Protein phosphatase 1, catalytic subunit, beta isoform//0.89:200:66//Hs.21537:X09910	F-PLACE1005481//EST//0.27:153:64//Hs.120066:AA707973
F-PLACE1004868	F-PLACE1005494//ESTs//2.4e-50:257:98//Hs.159003:AA633029
F-PLACE1004885//ESTs//0.41:181:61//Hs.116796:AA633772	F-PLACE1005502//ESTs//0.15:408:57//Hs.45106:AA504105
F-PLACE1004900	F-PLACE1005526//ESTs//3.2e-61:305:98//Hs.122574:AA776747
F-PLACE1004902//ESTs//4.7e-72:367:96//Hs.54971:AI424382	F-PLACE1005528//ESTs//9.9e-32:249:78//Hs.142531:N91572
F-PLACE1004913//ESTs//0.031:166:63//Hs.130110:AA904929	F-PLACE1005530//ESTs//1.0e-94:491:95//Hs.131731:AI339335
F-PLACE1004918//Human tumor susceptibility protein (TSG101) mRNA, complete cds//4.1e-24:402:64//Hs.118910:U82130	F-PLACE1005550//ESTs//0.084:290:58//Hs.157775:AI359385
F-PLACE1004930//Homo sapiens TNF-induced protein GC2-1 mRNA, complete cds//9.7e-86:519:88//Hs.17839:AF099936	F-PLACE1005554//EST//0.38:213:58//Hs.102749:N64144
F-PLACE1004934//ESTs//7.2e-43:231:78//Hs.133503:AA628592	F-PLACE1005557//ESTs. Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR [Saccharomyces cerevisiae]//4.5e-51:258:97//Hs.7736:M81261
F-PLACE1004937//ESTs//0.97:80:68//Hs.144264:C00851	F-PLACE1005574//ESTs//3.2e-09:236:66//Hs.146884:AI160278
F-PLACE1004969	F-PLACE1005584//Fragile X mental retardation 2//1.2e-05:151:69//Hs.54472:U48436
F-PLACE1004972//Human retinoic acid- and interferon-inducible 58K protein R158 mRNA, complete cds//0.031:235:60//Hs.27610:U34605	F-PLACE1005595//ESTs//2.1e-98:512:95//Hs.118552:W74594
F-PLACE1004979//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-43:331:83//Hs.153468:AB011147	F-PLACE1005603//EST//1.0:90:66//Hs.111204:AA211851
F-PLACE1004982//ESTs//0.020:148:63//Hs.129377:AI218520	F-PLACE1005611//ESTs. Weakly similar to B0035.14 [C.elegans]//3.5e-32:197:92//Hs.8241:AA283057
F-PLACE1004985//ESTs//7.9e-05:372:61//Hs.87606:AA242831	F-PLACE1005623//ESTs//3.0e-30:191:92//Hs.77570:M48234
F-PLACE1005026//ESTs//4.6e-29:212:89//Hs.137451:AA351459	F-PLACE1005630//ESTs//2.3e-32:175:97//Hs.122278:AA781867
F-PLACE1005027//ESTs//6.5e-91:455:97//Hs.30890:HI5159	F-PLACE1005639//ESTs//0.88:218:58//Hs.117389:AA701991
F-PLACE1005046//ESTs//3.7e-56:250:96//Hs.152730:AI308943	F-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//2.1e-151:721:98//Hs.8765:AF083255
F-PLACE1005052//EST//1.8e-36:370:73//Hs.123424:AA813594	F-PLACE1005656//Ribonucleotide reductase M2 polypeptide//3.9e-53:480:74//Hs.75319:X59618
F-PLACE1005055//Homo sapiens mRNA for KIAA0576 protein, partial cds//6.2e-161:761:98//Hs.14687:AB011148	F-PLACE1005666//Homo sapiens mRNA for KIAA0448 protein, complete cds//0.086:223:59//Hs.27349:AB007917
F-PLACE1005066//Homo sapiens actin binding protein MAYVEM mRNA, complete cds//3.0e-11:757:56//Hs.122967:AF059569	F-PLACE1005698//Human membrane-associated lectin type-C mRNA//6.1e-65:374:85//Hs.23759:M98457
F-PLACE1005077//EST//0.79:283:59//Hs.89276:AA283899	F-PLACE1005727//ESTs//8.7e-65:330:96//Hs.127027:AA935437
F-PLACE1005085//ESTs//3.5e-18:231:72//Hs.142654:AA324740	F-PLACE1005730//ESTs//2.9e-14:270:67//Hs.28589:AI004944
F-PLACE1005086//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.9e-49:401:80//Hs.153468:AB011147	F-PLACE1005739//Homo sapiens mRNA for serin protease with IGF-binding motif, complete cds//0.75:289:59//Hs.75111:D87258
F-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds//8.2e-20:194:80//Hs.75437:L40401	F-PLACE1005755//Insulin-like growth factor binding protein 2//3.6e-05:377:62//Hs.162:X16302
F-PLACE1005102//Homo sapiens HIV-1 inducer of short transcripts binding protein (FBI1) mRNA, complete cds//8.9e-18:538:62//Hs.104640:AF000561	F-PLACE1005763//ESTs. Highly similar to S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN [Rattus norvegicus]//5.7e-49:252:88//Hs.24309:AI125696
F-PLACE1005108//Trescher Collins syndrome susceptibility protein//0.73:405:57//Hs.73166:U76366	F-PLACE1005799//ESTs//5.2e-13:392:58//Hs.110530:AA191493
F-PLACE1005111//ESTs//0.66:191:63//Hs.106446:N93227	F-PLACE1005802
F-PLACE1005128//Breakpoint cluster region protein BCR//5.6e-08:291:63//Hs.2557:Y00661	F-PLACE1005803
F-PLACE1005146//ESTs. Weakly similar to hypothetical protein II [H.sapiens]//4.8e-12:360:63//Hs.142177:HI1741	F-PLACE1005804//Homo sapiens alpha 1,2-mannosidase 1B mRNA, complete cds//4.5e-128:636:96//Hs.125315:AF027156
F-PLACE1005162//Human mRNA for KIAA0118 gene, partial cds//3.9e-49:563:72//Hs.154326:D42087	F-PLACE1005813//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//8.4e-156:739:98//Hs.11183:AF065482
F-PLACE1005176//Homo sapiens mRNA for KIAA0641 protein, complete cds//0.82:259:60//Hs.128316:AB014541	F-PLACE1005828//ESTs. Weakly similar to !!! ALU SUBFAMILY J. WARNING ENTRY !!! [H.sapiens]//4.1e-42:327:81//Hs.138404:R70986
F-PLACE1005181//ESTs. Weakly similar to No definition line found [C.elegans]//4.4e-126:583:99//Hs.25347:AI138605	F-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)//0.038:436:58//Hs.75770:L41870
F-PLACE1005187//ESTs//6.2e-34:222:90//Hs.124265:M70417	F-PLACE1005845//ESTs//4.8e-50:309:89//Hs.107149:AI379497
F-PLACE1005206//EST//0.089:167:62//Hs.140487:AA767009	F-PLACE1005850//ESTs//7.1e-40:253:79//Hs.158096:AA186905
F-PLACE1005232//ESTs. Weakly similar to synapse-associated protein sap47-1 [D.melanogaster]//0.56:192:60//Hs.47334:W72370	F-PLACE1005851//ESTs//7.6e-93:483:95//Hs.135608:AA732242
F-PLACE1005243	F-PLACE1005876//ESTs//0.97:282:60//Hs.98664:AI381487
F-PLACE1005261//ESTs//0.52:245:58//Hs.6682:T76941	F-PLACE1005884//ESTs//0.070:276:60//Hs.106057:AI031552

【0888】

【表587】

F-PLACE1005890//ESTs//1.5e-91:500:93//Hs.136993:AA843300
 F-PLACE1005898
 F-PLACE1005921
 F-PLACE1005923//ESTs//0.50:308:58//Hs.52489:R61504
 F-PLACE1005925//ESTs//0.024:93:68//Hs.149868:A1288274
 F-PLACE1005932//TYROSINE-PROTEIN KINASE RECEPTOR EPH PRECURSOR//0.97:342:57//Hs.89839:M18391
 F-PLACE1005934//ESTs//8.6e-10:74:93//Hs.25092:AA922142
 F-PLACE1005936//DNA excision repair protein ERCC5//1.0:144:63//Hs.48576:X69978
 F-PLACE1005951//B94 PROTEIN//0.00025:371:61//Hs.75522:M92357
 F-PLACE1005953//ESTs//2.8e-06:290:61//Hs.140996:R73468
 F-PLACE1005955//ESTs. Weakly similar to Y53C12A.3 [C.elegans]//0.15:136:66//Hs.107747:A1357868
 F-PLACE1005966//Human zinc finger/leucine zipper protein (AF10) mRNA, complete cds//1.0:215:63//Hs.7885:U13948
 F-PLACE1005968
 F-PLACE1005990
 F-PLACE1006002//Putative mismatch repair/binding protein hMSH3//1.9e-48:312:77//Hs.42674:U61981
 F-PLACE1006003//EST//0.00018:171:67//Hs.138882:W73256
 F-PLACE1006011
 F-PLACE1006017//ESTs//3.1e-21:159:88//Hs.142173:AA757743
 F-PLACE1006037//Homo sapiens mRNA for KIAA0789 protein, complete cds//0.021:202:64//Hs.158319:AB018332
 F-PLACE1006040//Homo sapiens mRNA for alpha endosulfine//1.1e-148:719:97//Hs.98782:X99906
 F-PLACE1006076//EST//0.29:92:64//Hs.161536:M80395
 F-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds//4.1e-147:679:99//Hs.4976:AF039023
 F-PLACE1006129
 F-PLACE1006139
 F-PLACE1006143//Human mRNA for KIAA0355 gene, complete cds//9.3e-43:357:79//Hs.153014:AB002353
 F-PLACE1006157//ESTs. Weakly similar to ETX1 (alternatively splice d) [H.sapiens]//2.9e-12:119:84//Hs.23153:R92857
 F-PLACE1006159//ESTs//2.3e-87:443:96//Hs.23740:H17868
 F-PLACE1006164//ESTs//0.099:223:60//Hs.8108:AA902721
 F-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149//1.1e-68:333:92//Hs.152894:AC005239
 F-PLACE1006170//ESTs//0.081:171:67//Hs.135187:A1074005
 F-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//1.2e-150:694:99//Hs.30464:AF091433
 F-PLACE1006195//ESTs//8.9e-14:229:70//Hs.141470:M49608
 F-PLACE1006196//ESTs. Weakly similar to protein synthesis initiation factor 4A-II homolog//3.5e-59:369:88//Hs.135623:AA134719
 F-PLACE1006205
 F-PLACE1006223//ESTs. Weakly similar to TERATOCARCINOMA-DERIVED GROWTH FACTOR 1 [H.sapiens]//0.0089:166:63//Hs.127179:A1279486
 F-PLACE1006225
 F-PLACE1006236//EST//0.060:89:69//Hs.136977:AA830668
 F-PLACE1006239//ESTs//0.028:105:66//Hs.142336:AA358185
 F-PLACE1006246//ESTs//0.060:330:60//Hs.105695:A1085802
 F-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//7.3e-168:791:98//Hs.131921:AB014548
 F-PLACE1006262
 F-PLACE1006288//Homo sapiens mRNA for Pex3 protein//4.8e-37:186:100//Hs.7277:AJ001625
 F-PLACE1006318
 F-PLACE1006325//ESTs//3.7e-25:206:83//Hs.102319:A1246503
 F-PLACE1006335//ESTs//2.0e-27:161:95//Hs.163529:A1361492
 F-PLACE1006357//ESTs//0.013:268:61//Hs.105775:AA526249
 F-PLACE1006360//ESTs//4.8e-27:146:98//Hs.100739:Z98481
 F-PLACE1006368//Homo sapiens clone 24540 mRNA sequence//0.65:272:59//Hs.153529:AF070581
 F-PLACE1006371//Homo sapiens jerky gene product homolog mRNA, complete cds//2.6e-07:403:61//Hs.105940:AF004715
 F-PLACE1006382//EST//0.98:77:68//Hs.136933:AA814693
 F-PLACE1006385//Homo sapiens epsilon 2b mRNA, complete cds//1.6e-111:539:97//Hs.22396:AF062085
 F-PLACE1006412//Human mRNA for KIAA0298 gene, complete cds//1.0e-36:424:74//Hs.21560:AB002296
 F-PLACE1006414//Homo sapiens PCAF associated factor 65 alpha mRNA, complete cds//4.3e-111:525:98//Hs.131846:AF069735
 F-PLACE1006438//Homo sapiens mRNA for KIAA0557 protein, partial cds//2.2e-24:531:65//Hs.101414:AB011129
 F-PLACE1006445//Homo sapiens chromosome 16 zinc finger protein ZNF200 (ZNF200) mRNA, complete cds//1.0:248:60//Hs.88219:AF060866
 F-PLACE1006469//Human SA mRNA for SA gene product, complete cds//0.24:210:62//Hs.89659:AC004381

F-PLACE1006470
 F-PLACE1006482//Homo sapiens basic-leucine zipper transcription factor MafK (MAFK) mRNA, complete cds//5.0e-46:520:71//Hs.131953:AF059194
 F-PLACE1006488//ESTs//6.2e-47:239:97//Hs.158161:AA312511
 F-PLACE1006492//ESTs//0.82:37:100//Hs.160417:AA488493
 F-PLACE1006506//HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 ENHANCER-BINDING PROTEIN 2//0.98:505:56//Hs.75063:AL023584
 F-PLACE1006521//ESTs//0.032:222:63//Hs.23171:AA706542
 F-PLACE1006531//EST//2.1e-53:258:100//Hs.117316:AA699358
 F-PLACE1006534//EST//1.8e-07:78:89//Hs.157551:A1356219
 F-PLACE1006540//Homo sapiens mRNA for cadherin-6, complete cds//0.96:383:58//Hs.32963:D31784
 F-PLACE1006552//Human (clone N5-4) protein p84 mRNA, complete cds//0.058:464:57//Hs.1540:L36529
 F-PLACE1006598//Homo sapiens mRNA for KIAA0737 protein, complete cds//4.1e-17:372:65//Hs.17630:AB018280
 F-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//2.2e-168:781:99//Hs.155377:U97670
 F-PLACE1006617//ESTs//6.0e-08:354:60//Hs.42624:H99088
 F-PLACE1006626//NUCLEOLIN//0.0044:186:66//Hs.79110:M60858
 F-PLACE1006629//Homo sapiens (clone s22171) mRNA fragment//0.097:29:63//Hs.26956:L40396
 F-PLACE1006640//ESTs//0.00019:380:59//Hs.13672:A1131473
 F-PLACE1006673//ESTs. Weakly similar to T1484.2 gene product [C.elegans]//1.6e-12:113:83//Hs.3385:M25917
 F-PLACE1006678
 F-PLACE1006704//Homo sapiens ALR mRNA, complete cds//0.16:284:60//Hs.153638:AF010403
 F-PLACE1006731//Homo sapiens SOX22 protein (SOX22) mRNA, complete cds//1.6e-05:382:63//Hs.43627:U35612
 F-PLACE1006754//Biliary glycoprotein//8.9e-27:305:72//Hs.50964:X16354
 F-PLACE1006760//ESTs//0.10:207:62//Hs.152589:AA954152
 F-PLACE1006779//Kallmann syndrome 1 sequence//0.00025:251:64//Hs.89591:M97252
 F-PLACE1006782//ESTs//1.2e-90:423:100//Hs.132826:A1075783
 F-PLACE1006792//ESTs//1.5e-10:439:58//Hs.138501:A1051228
 F-PLACE1006795//TYROSINE-PROTEIN KINASE RECEPTOR ETK1 PRECURSOR//4.5e-10:84:95//Hs.123642:M83941
 F-PLACE1006800//ESTs//0.00068:360:61//Hs.157876:A1422017
 F-PLACE1006805//ESTs//4.6e-103:491:98//Hs.140465:AA769892
 F-PLACE1006815//Homo sapiens mRNA for KIAA0618 protein, complete cds//0.47:403:56//Hs.15832:AB014518
 F-PLACE1006819//Human Line-1 repeat mRNA with 2 open reading frames s//3.7e-103:619:87//Hs.23094:M19503
 F-PLACE1006829//ESTs//1.5e-22:141:94//Hs.142988:AA142876
 F-PLACE1006860//EST//0.0062:206:65//Hs.158793:A1376773
 F-PLACE1006867//ESTs//0.068:218:62//Hs.91166:AA551273
 F-PLACE1006878//Homo sapiens mRNA for KIAA0711 protein, complete cds//1.0:268:58//Hs.5333:AB018254
 F-PLACE1006883//ESTs//1.6e-75:398:94//Hs.119544:T95601
 F-PLACE1006901//ESTs//1.6e-13:87:96//Hs.134737:A1089187
 F-PLACE1006904//EST//1.0:91:70//Hs.148270:AA906443
 F-PLACE1006917
 F-PLACE1006932//ESTs//0.98:110:70//Hs.100855:A1423913
 F-PLACE1006935//EST//1.0:92:65//Hs.124554:AA847211
 F-PLACE1006956//PERIPHERIN//0.13:443:57//Hs.37044:L14565
 F-PLACE1006958//Heat shock 70kD protein 4//6.4e-40:456:70//Hs.12712723
 F-PLACE1006961//ESTs. Highly similar to RSP5 PROTEIN [Saccharomyces cerevisiae]//3.2e-07:67:98//Hs.21806:AA630312
 F-PLACE1006962//H.sapiens iRiB mRNA//2.3e-16:202:71//Hs.135202:X63417
 F-PLACE1006966//Homo sapiens syntaxin 4 binding protein UNC-18c (UNC-18c) mRNA, complete cds//0.14:191:67//Hs.8813:AF032922
 F-PLACE1006989//Cyclin B1//0.99:224:59//Hs.23960:M25753
 F-PLACE1007014//Homo sapiens NBMPR-insensitive nucleoside transporter ei (ENT2) mRNA, complete cds//3.1e-05:594:58//Hs.32951:AF034102
 F-PLACE1007021//ESTs//7.2e-89:446:96//Hs.7111:U55971
 F-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frames s//1.0e-117:775:84//Hs.23094:M19503
 F-PLACE1007053//Homo sapiens mRNA for ARN03 protein//0.35:63:82//Hs.129811:AJ223957
 F-PLACE1007068//Polycystic kidney disease 1 (autosomal dominant)//0.22:361:60//Hs.75813:L33243
 F-PLACE1007097//ESTs//2.9e-25:197:83//Hs.105665:H78987
 F-PLACE1007105//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase

【0889】

【表588】

(glycogen debranching enzyme, glycogen storage disease type III) // 0.18:268:63//Hs.904:U84010
 F-PLACE1007111//EST//0.0066:260:60//Hs.147903:A1223385
 F-PLACE1007112
 F-PLACE1007132//ESTs//3.1e-30:195:76//Hs.46158:A1160121
 F-PLACE1007140//TRANSCRIPTION ELONGATION FACTOR S-1//0.13:302:60//Hs.78869:M81601
 F-PLACE1007178//ESTs//9.6e-54:289:95//Hs.12251:H12965
 F-PLACE1007226//Homo sapiens Notch3 (NOTCH3) mRNA, complete cds//0.0090:412:59//Hs.8546:U97669
 F-PLACE1007238//Human plectin (PLEC1) mRNA, complete cds//1.4e-07:492:64//Hs.79706:U53204
 F-PLACE1007239//Human mRNA for transcription elongation factor S-1, hS-11-T1, complete cds//2.0e-58:405:87//Hs.80598:D50495
 F-PLACE1007242//EST//0.014:55:89//Hs.88432:AA262141
 F-PLACE1007243//ESTs//2.0e-43:227:97//Hs.124775:AA648467
 F-PLACE1007257//Homo sapiens mRNA for dia-156 protein//3.7e-144:677:98//Hs.121556:Y15909
 F-PLACE1007274
 F-PLACE1007276//ATPase, Cutt transporting, alpha polypeptide (Menkes syndrome) //0.94:167:64//Hs.606:L06133
 F-PLACE1007282
 F-PLACE1007286//ESTs//1.0e-25:333:71//Hs.134860:A1091436
 F-PLACE1007301//EST//0.78:171:61//Hs.160990:H52412
 F-PLACE1007317//Homo sapiens oxysterol 7alpha-hydroxylase (CYP7B1) mRNA, complete cds//0.88:298:58//Hs.144877:AF029403
 F-PLACE1007342
 F-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds//1.7e-121:567:98//Hs.76596:AF096870
 F-PLACE1007367//H. sapiens mRNA for MACH-alpha-2 protein//2.2e-55:532:77//Hs.19949:X98173
 F-PLACE1007375
 F-PLACE1007386//ESTs//0.00086:61:91//Hs.149318:A1248642
 F-PLACE1007402//EST//1.7e-06:193:65//Hs.132124:A1041287
 F-PLACE1007409//Homo sapiens mitoxanthrone resistance protein 1 mRNA, partial sequence//3.8e-18:128:92//Hs.14387:AF093771
 F-PLACE1007416
 F-PLACE1007450//ESTs//2.6e-36:194:97//Hs.22359:A1024436
 F-PLACE1007452//EST//1.8e-34:197:94//Hs.134795:A1090359
 F-PLACE1007454//Homo sapiens (clone s153) mRNA fragment//2.6e-53:317:93//Hs.6445:L40391
 F-PLACE1007460//ESTs//0.0012:168:64//Hs.151708:AA554714
 F-PLACE1007478//ESTs//1.0e-42:440:74//Hs.141722:AA769103
 F-PLACE1007484//ESTs//7.1e-18:127:91//Hs.100251:AA535975
 F-PLACE1007488
 F-PLACE1007507//ESTs//1.2e-99:274:98//Hs.123462:AA903385
 F-PLACE1007511//Keratin 19//4.2e-31:586:64//Hs.23761:Y00503
 F-PLACE1007524//ESTs//6.8e-71:356:97//Hs.163067:AA897296
 F-PLACE1007525//ESTs//0.073:242:59//Hs.128711:AA856979
 F-PLACE1007537//Homo sapiens PYRIN (MEFY) mRNA, complete cds//0.93:468:57//Hs.113283:AF018080
 F-PLACE1007544//ESTs//1.7e-74:360:98//Hs.128632:A1076755
 F-PLACE1007547//Homo sapiens mRNA for KIAA0661 protein, complete cds//1.0e-70:733:71//Hs.65238:AB014581
 F-PLACE1007557//EST//0.58:80:72//Hs.130267:A1001863
 F-PLACE1007583//ESTs//1.8e-46:234:98//Hs.155071:AA584257
 F-PLACE1007598//ESTs//1.7e-83:400:99//Hs.120206:A1089163
 F-PLACE1007618//Homo sapiens mRNA for KIAA0633 protein, partial cds//7.2e-12:778:56//Hs.33010:AB014533
 F-PLACE1007621
 F-PLACE1007632//ESTs//1.7e-32:175:97//Hs.122278:AA781867
 F-PLACE1007645
 F-PLACE1007649
 F-PLACE1007677//ESTs//3.0e-13:125:82//Hs.143382:AA476266
 F-PLACE1007688//ESTs//6.8e-06:311:61//Hs.132926:A1027055
 F-PLACE1007690//ESTs//1.9e-13:83:98//Hs.150088:A1348503
 F-PLACE1007697//TRANSFORMING GROWTH FACTOR BETA 1 PRECURSOR//0.99:216:63//Hs.1103:X02812
 F-PLACE1007705//Human mRNA for RTP, complete cds//4.8e-58:637:70//Hs.75789:D87953
 F-PLACE1007706//Homo sapiens metalloprotease 1 (MPI) mRNA, complete cds//4.1e-149:709:97//Hs.4812:AF061243
 F-PLACE1007725//ESTs. Weakly similar to No definition line found [C.elegans]//4.5e-36:233:89//Hs.108797:AA476815
 F-PLACE1007729//ESTs. Moderately similar to RETROVIRUS-RELATED PROTEASE [H.sapiens]//0.00033:270:64//Hs.104129:AA923278
 F-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//2.6e-156:728:98//Hs.153121:AB014585
 F-PLACE1007737//Coagulation factor II (thrombin) receptor//1.1e-18:364:68//Hs.159347:M62424
 F-PLACE1007743//ESTs//0.029:421:58//Hs.106090:AA457030
 F-PLACE1007746//ESTs//5.7e-55:330:89//Hs.153392:A1089469
 F-PLACE1007791//EST//0.39:261:62//Hs.145991:A1277656
 F-PLACE1007807//ESTs//2.0e-54:385:83//Hs.163930:AA640504
 F-PLACE1007810//ESTs//6.1e-53:416:81//Hs.152395:AA533107
 F-PLACE1007829//EST//0.28:271:61//Hs.125514:AA883841
 F-PLACE1007843//EST//0.020:307:59//Hs.145535:A1261635
 F-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frame s//6.3e-38:396:77//Hs.23094:M19503
 F-PLACE1007852
 F-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//1.3e-190:894:98//Hs.28020:AB018309
 F-PLACE1007866//ESTs//3.0e-50:333:86//Hs.15792:A1038387
 F-PLACE1007877
 F-PLACE1007897//EST//1.0:59:72//Hs.138770:M70943
 F-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//7.3e-156:755:97//Hs.92381:AB007956
 F-PLACE1007946//ESTs//8.9e-16:250:68//Hs.88527:M24002
 F-PLACE1007954//ESTs//1.6e-05:76:90//Hs.63314:AA056538
 F-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//8.9e-173:813:98//Hs.5671:AF084530
 F-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//8.2e-155:730:98//Hs.78106:AF079529
 F-PLACE1007969//ESTs. Weakly similar to hnRNA-binding protein M4 [H.sapiens]//5.1e-45:264:92//Hs.42222:W28567
 F-PLACE1007990//ESTs//1.2e-104:493:99//Hs.118445:A1097043
 F-PLACE1008000//Homo sapiens vcl1 mRNA, complete cds//5.7e-63:578:74//Hs.150380:AF087693
 F-PLACE1008002//ESTs//0.52:236:59//Hs.134292:AA603031
 F-PLACE1008044
 F-PLACE1008045//COL10A1//0.29:221:58//Hs.37075:X60382
 F-PLACE1008080//Human homeodomain protein (Prox 1) mRNA, complete cds//0.00037:151:71//Hs.159437:U44060
 F-PLACE1008095//Human hybrid receptor gp250 precursor mRNA, complete cds//1.0:461:58//Hs.155494:U60975
 F-PLACE1008111//Homo sapiens B lymphocyte chemoattractant BLC mRNA, complete cds//0.034:497:58//Hs.100431:AF044197
 F-PLACE1008122//ESTs//0.95:198:60//Hs.126776:N28769
 F-PLACE1008129//ESTs//1.1e-99:499:96//Hs.131807:AA778874
 F-PLACE1008132//EST//3.3e-27:218:83//Hs.145258:A1218683
 F-PLACE1008177//ESTs. Moderately similar to meiosis-specific nuclear structural protein 1 [M.musculus]//5.1e-20:124:95//Hs.146238:A1263135
 F-PLACE1008181//ESTs//0.018:285:61//Hs.88843:AA281427
 F-PLACE1008198//ESTs//5.9e-07:410:60//Hs.63348:AA643524
 F-PLACE1008201
 F-PLACE1008209
 F-PLACE1008231//ESTs//0.40:188:61//Hs.130266:A1001856
 F-PLACE1008244//Miller-Dieker syndrome chromosome region//0.22:247:61//Hs.77318:L13385
 F-PLACE1008273
 F-PLACE1008275//EST//0.77:74:71//Hs.145907:A1275113
 F-PLACE1008280//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//2.6e-25:389:70//Hs.159897:AB007970
 F-PLACE1008309//Homo sapiens serine phosphatase FCPIa (FCPI) mRNA, complete cds//0.16:263:63//Hs.4076:AF081287
 F-PLACE1008329//EST//1.3e-09:94:85//Hs.144135:R82071
 F-PLACE1008330//Homo sapiens mRNA for KIAA0557 protein, partial cds//1.5e-45:291:83//Hs.101414:AB011129
 F-PLACE1008331//ESTs. Weakly similar to ORF2-like protein [H.sapiens]//5.4e-74:356:98//Hs.105382:AA496362
 F-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//3.4e-139:659:98//Hs.5734:AB014579
 F-PLACE1008368//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.011:355:60//Hs.122967:AF059569
 F-PLACE1008369//ESTs//0.00074:443:61//Hs.102756:AA526911
 F-PLACE1008392//EST//7.4e-08:324:60//Hs.149930:A1289171
 F-PLACE1008398
 F-PLACE1008401//Homo sapiens methyl-CpG binding protein MBD2 (MBD2) mRNA, complete cds//2.5e-09:461:62//Hs.25674:AF072242
 F-PLACE1008402//Homo sapiens mRNA for p115, complete cds//1.4e-149:711:98//Hs.7763:D86326
 F-PLACE1008405//ESTs//2.8e-102:529:95//Hs.116278:AA628943
 F-PLACE1008424//Human DNA sequence from clone 753P9 on chromosome Xq25-26.1. Contains the gene coding for Aminopeptidase P (EC 3.4.11.9, XAA-Pro-X-Pro/Proline/Aminoacylproline Aminopeptidase) and a novel gene. Contains ESTs, STSs, GSSs and a gaa repeat polymorphism//0.98:113:67//Hs.57922:AL023653
 F-PLACE1008426//ESTs//3.2e-77:393:95//Hs.37585:W28499
 F-PLACE1008429//Orf1 5' to PD-ECGF/TP...orf2 5' to PD-ECGF/TP [hum

【0890】

【表589】

an, epidermoid carcinoma cell line A431, mRNA, 3 genes, 1718 nt]]/ 0.019:530:58//Hs.72248:S72487	F-PLACE1009110//ESTs//2.6e-91:453:96//Hs.143756:A1040890
F-PLACE1008437	F-PLACE1009111//ESTs//2.7e-15:159:77//Hs.146811:AA410788
F-PLACE1008455//ESTs//0.51:279:61//Hs.122319:AA782335	F-PLACE1009113//Homo sapiens X-ray repair cross-complementing prot ein 3 (XRCC3) mRNA, complete cds//1.1e-139:671:97//Hs.99742:AF0355
F-PLACE1008457//ESTs//3.0e-30:229:75//Hs.60740:AA053901	86
F-PLACE1008465//Human mRNA for KIAA0383 gene, partial cds//0.0084: 210:63//Hs.27590:AB002381	F-PLACE1009130//Human mRNA for KIAA0032 gene, complete cds//1.1e-2 4:718:59//Hs.35804:025215
F-PLACE1008488//Human density enhanced phosphatase-1 mRNA, complet e cds//6.8e-07:469:60//Hs.1177:U10886	F-PLACE1009150//Human HsLIM15 mRNA for HsLIM15, complete cds//1.7 e-50:440:78//Hs.37181:D64108
F-PLACE1008524//Homo sapiens TWIK-related acid-sensitive K ⁺ channe l (TASK) mRNA, complete cds//1.0:304:60//Hs.24040:AF006823	F-PLACE1009155//Homo sapiens mRNA, chromosome 1 specific transcrip t KIAA0484//4.0e-46:440:69//Hs.158095:AB007953
F-PLACE1008531//ESTs//1.1e-17:190:76//Hs.156041:A1274697	F-PLACE1009158//Human growth/differentiation factor 1 (GDF-1) mRN A, complete cds//0.28:245:61//Hs.92614:M62302
F-PLACE1008532//Thromboxane A2 receptor//5.6e-17:231:71//Hs.89887: D38081	F-PLACE1009166//EST//0.98:114:67//Hs.137706:AA977250
F-PLACE1008533//Homo sapiens PAC clone DJ130H16 from 22q12.1-qter/ 1.1e-45:507:71//Hs.8003:AC004997	F-PLACE1009172//EST//6.2e-34:257:84//Hs.161081:M22770
F-PLACE1008568//Homo sapiens mRNA for neuronatin alpha, complete c ds//1.0:95:71//Hs.117546:U31767	F-PLACE1009174//ESTs//6.0e-24:234:77//Hs.155196:A1282821
F-PLACE1008584//ESTs//1.4e-13:252:68//Hs.153429:A1283069	F-PLACE1009183//EST//0.021:261:62//Hs.144222:N90100
F-PLACE1008603//Homo sapiens mRNA for KIAA0791 protein, complete c ds//3.9e-175:812:98//Hs.23255:AB018334	F-PLACE1009186//ESTs. Weakly similar to No definition line found [C.elegans]//3.6e-117:588:95//Hs.54943:Z78396
F-PLACE1008621//ESTs. Weakly similar to reverse transcriptase [H.s apiens]//1.2e-15:350:66//Hs.151087:AA649326	F-PLACE1009190//EST//0.046:95:70//Hs.131646:A1025689
F-PLACE1008625//ESTs//0.86:269:57//Hs.94998:M26794	F-PLACE1009200//EST//2.5e-41:195:78//Hs.162404:AA573131
F-PLACE1008626//ESTs//0.55:69:71//Hs.92096:F10560	F-PLACE1009230//CARCINOEMBRYONIC ANTIGEN PRECURSOR//5.3e-29:157:77 //Hs.146403:M29540
F-PLACE1008627//ESTs//3.0e-62:302:99//Hs.120766:H82458	F-PLACE1009246//EST//0.13:178:62//Hs.23298:R22575
F-PLACE1008629//EST//0.0012:174:67//Hs.121195:AA757211	F-PLACE1009298//ESTs. Highly similar to VACUOLAR SORTING PROTEIN 35 [Saccharomyces cerevisiae]//1.9e-21:121:98//Hs.124768:AA307735
F-PLACE1008630//ESTs//4.5e-77:371:99//Hs.132960:AA252394	F-PLACE1009308//SERUM PROTEIN MSE55//0.44:195:62//Hs.148101:M88338
F-PLACE1008643//Human mRNA for PK-120//4.7e-25:299:64//Hs.76415:D3 8535	F-PLACE1009319//Homo sapiens post-synaptic density protein 95 (PSD 95) mRNA, complete cds//9.7e-08:411:59//Hs.23731:U83192
F-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds//3.5e-135:622:99//Hs.147967:AF044333	F-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frame s//2.3e-91:594:86//Hs.23094:M19503
F-PLACE1008693//EST//0.19:36:94//Hs.138817:M93728	F-PLACE1009335//EST//0.037:169:63//Hs.148875:A1240767
F-PLACE1008696//Human mitochondrial NADH dehydrogenase-ubiquinone Fe-S protein 8, 23 kDa subunit precursor (NDUFS8) nuclear mRNA enc oding mitochondrial protein, complete cds//8.3e-25:137:97//Hs.9044 3:AF038406	F-PLACE1009338//ESTs//5.7e-22:123:98//Hs.66783:AA059473
F-PLACE1008715//Homo sapiens mRNA for matrilin-3//0.99:183:63//Hs. 119534:AJ224741	F-PLACE1009368
F-PLACE1008748//ESTs//0.88:204:63//Hs.15139:AA527080	F-PLACE1009375
F-PLACE1008757//ESTs. Weakly similar to unknown protein [R.norvegi cus]//4.3e-17:285:69//Hs.35460:H65503	F-PLACE1009388//Homo sapiens KIAA0395 mRNA, partial cds//1.7e-41:3 17:81//Hs.43681:AL022394
F-PLACE1008790//Homo sapiens importin alpha 7 subunit mRNA, comple te cds//1.4e-121:503:97//Hs.6458:AF060543	F-PLACE1009398//Zinc finger protein 84 (HPF2)//1.4e-79:730:74//Hs. 9450:M27878
F-PLACE1008798//ESTs. Weakly similar to putative p150 [H.sapiens]/ 0.30:127:68//Hs.111380:AA258772	F-PLACE1009404//MICROTUBULE-ASSOCIATED PROTEIN TAU//0.099:207:61// Hs.101174:AF047863
F-PLACE1008807//ESTs//0.81:346:58//Hs.116901:AA663542	F-PLACE1009410//Homo sapiens BAF57 (BAF57) gene, complete cds//1.4 e-27:210:86//Hs.3404:AF035262
F-PLACE1008808//Homo sapiens putative checkpoint control protein H RAD1 mRNA, complete cds//6.7e-104:376:98//Hs.1179:AF011905	F-PLACE1009434//Human mRNA for KIAA0005 gene, complete cds//2.8e-4 5:599:68//Hs.155291:D13630
F-PLACE1008813//Glutamate decarboxylase 1 (brain, 67kD)//0.17:318: 61//Hs.75668:M81883	F-PLACE1009443//H.sapiens ST4 gene for ST4 Oncofetal antigen//0.1 1:350:58//Hs.82128:AJ012159
F-PLACE1008851//ESTs. Highly similar to CELL DIVISION CONTROL PRO TEIN 2 HOMOLOG [Plasmodium falciparum (isolate kl / thailand)]//0. 73:354:59//Hs.26322:AA156858	F-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//1.5e-22:146:9 3//Hs.76987:AF012872
F-PLACE1008854//ESTs//3.0e-26:391:66//Hs.133260:A1052728	F-PLACE1009459//H.sapiens garp gene mRNA, complete CDS//1.0:241:60 //Hs.151641:Z24680
F-PLACE1008867//ESTs//5.9e-08:64:93//Hs.91115:A1221563	F-PLACE1009468//1-PHOSPHATIDYLINOSITOL-4, 5-BISPHOSPHATE PHOSPHODIE STERASE BETA 2//0.00039:347:60//Hs.994:M95678
F-PLACE1008887//Human Line-1 repeat mRNA with 2 open reading frame s//5.5e-51:701:68//Hs.23094:M19503	F-PLACE1009476//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-67 A1//4.1e-91:464:96//Hs.155049:AC004531
F-PLACE1008902//EST//0.85:425:60//Hs.140573:AA826323	F-PLACE1009477//ESTs//0.30:221:61//Hs.107287:A1308839
F-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cd s//2.1e-159:753:98//Hs.62318:AB018308	F-PLACE1009493//Homo sapiens mRNA for LAK-4p, complete cds//1.6e-3 0:608:63//Hs.16165:AB002405
F-PLACE1008925//ESTs//0.025:133:67//Hs.103218:M84771	F-PLACE1009524//Human Sec7p-like protein mRNA, partial cds//2.3e-6 8:526:78//Hs.8517:U70728
F-PLACE1008934//ESTs//0.27:307:59//Hs.135168:A1394026	F-PLACE1009539//ESTs//3.3e-18:186:83//Hs.71922:AA148417
F-PLACE1008941//ESTs//3.3e-53:266:98//Hs.108677:AA488937	F-PLACE1009542//EST//7.8e-11:265:65//Hs.159692:A1416956
F-PLACE1008947//Human TBP-associated factor (hTAF1130) mRNA, part ial cds//2.4e-13:625:58//Hs.24644:U75308	F-PLACE1009571//ESTs//6.1e-15:94:97//Hs.151458:AA600866
F-PLACE1009020//ESTs//3.3e-11:122:81//Hs.131777:A1024950	F-PLACE1009581//Microtubule-associated protein 1A//1.0:196:59//Hs. 147918:U38291
F-PLACE1009027//Homo sapiens mRNA for doublecortin//1.2e-151:763:9 6//Hs.34780:AJ003112	F-PLACE1009595//EST//1.8e-28:179:92//Hs.60090:AA004806
F-PLACE1009039//EST//0.76:111:63//Hs.160997:H55762	F-PLACE1009596//ESTs. Weakly similar to LIS-1 protein [H.sapiens]/ /4.1e-16:281:66//Hs.13889:A1341394
F-PLACE1009045//ESTs//2.2e-76:399:95//Hs.114919:AA457689	F-PLACE1009607//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.9 e-52:313:79//Hs.113283:AF018080
F-PLACE1009048//GLYCOPROTEIN HORMONES ALPHA CHAIN PRECURSOR//2.6e- 16:93:100//Hs.119689:S70585	F-PLACE1009613//ESTs//0.50:297:60//Hs.25114:A1074011
F-PLACE1009050//ESTs//1.4e-92:451:98//Hs.66373:A1239698	F-PLACE1009621//ESTs//1.4e-98:470:98//Hs.124695:A1094085
F-PLACE1009060//ESTs//1.4e-14:86:100//Hs.131725:A1090525	F-PLACE1009622//ESTs//9.8e-14:94:93//Hs.117227:AA682773
F-PLACE1009090//ESTs//2.7e-20:198:78//Hs.110044:AA181800	F-PLACE1009637//ESTs//4.9e-92:440:98//Hs.126587:AA917087
F-PLACE1009091//ESTs//0.99:342:57//Hs.46903:A1093091	F-PLACE1009639
F-PLACE1009094//ESTs//1.0:225:63//Hs.120374:A1337031	F-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete c ds//4.4e-173:816:98//Hs.21862:AB011159
F-PLACE1009099//H.sapiens ZNF81 gene//2.2e-79:733:74//Hs.104020:16 8011	F-PLACE1009665//ESTs//9.1e-45:383:79//Hs.61199:AA024494
	F-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//8.1 e-149:701:98//Hs.109590:AF062534

【0891】

【表590】

F-PLACE1009708//ESTs. Weakly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN HXT14-PHA2 INTERGENIC REGION [S. cerevisiae]//7.5e-51:295:92//Hs.48541:AA827926
 F-PLACE1009721//EST//0.18:467:58//Hs.124358:AA830650
 F-PLACE1009731//ESTs//1.0:207:63//Hs.60440:AA195789
 F-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//1.3e-126:602:98//Hs.154320:AF046024
 F-PLACE1009794//ESTs//4.0e-41:252:91//Hs.42927:N20989
 F-PLACE1009798//Human DNA sequence from clone 1189824 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.99.3, C1-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and GSSs//5.5e-130:600:95//Hs.16411:AL030996
 F-PLACE1009845
 F-PLACE1009861
 F-PLACE1009879//ESTs//5.3e-12:293:66//Hs.147071:A1200021
 F-PLACE1009886
 F-PLACE1009888//EST//0.044:255:58//Hs.160695:A1282889
 F-PLACE1009908
 F-PLACE1009921//Apoptosis (APO-1) antigen 1//0.62:407:57//Hs.82359:X63717
 F-PLACE1009924//EST//2.9e-29:155:99//Hs.162937:AA634379
 F-PLACE1009925
 F-PLACE1009935//CATHEPSIN K PRECURSOR//0.43:153:66//Hs.83942:X82153
 F-PLACE1009947//ESTs//1.8e-07:56:100//Hs.149940:A1306446
 F-PLACE1009971//Acyl-Coenzyme A dehydrogenase, C-2 to C-3 short chain//0.89:243:61//Hs.127610:Z80345
 F-PLACE1009992//ESTs//0.99:123:68//Hs.91202:A1139114
 F-PLACE1009995//ESTs. Weakly similar to C01A2.4 [C. elegans]//3.3e-24:174:88//Hs.11449:A1201540
 F-PLACE1009997//Homo sapiens mRNA for KIAA0629 protein, partial cds//3.7e-36:196:96//Hs.153545:AB014529
 F-PLACE1010023
 F-PLACE1010031//ESTs//1.3e-16:132:87//Hs.46847:M02878
 F-PLACE1010053//ESTs. Moderately similar to M-phase phosphoprotein 4 [H. sapiens]//5.2e-63:312:98//Hs.142151:AA984061
 F-PLACE1010069//ESTs//6.6e-33:171:98//Hs.128844:AA977596
 F-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//5.9e-168:792:98//Hs.11183:AF065482
 F-PLACE1010076//ESTs//0.88:379:55//Hs.5884:N21424
 F-PLACE1010083//Homo sapiens mRNA for KIAA0456 protein, partial cds//9.6e-154:727:98//Hs.5003:AB007925
 F-PLACE1010089//ESTs. Highly similar to PROBABLE UBQUITIN CARBOXYL-TERMINAL HYDROLASE [Mus musculus]//1.8e-38:212:95//Hs.98067:AA236822
 F-PLACE1010096//ESTs. Highly similar to hypothetical protein, 100K [R. norvegicus]//1.8e-08:100:89//Hs.11469:U69567
 F-PLACE1010102//Homo sapiens stimulator of Fe transport mRNA, complete cds//0.0035:339:60//Hs.129683:AF020761
 F-PLACE1010105//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//1.2e-26:728:60//Hs.122967:AF059569
 F-PLACE1010106//EST//8.5e-28:394:70//Hs.142044:AA166682
 F-PLACE1010134//H. sapiens hbrn mRNA//1.2e-14:380:64//Hs.77590:X72889
 F-PLACE1010148//Human trans-Golgi p230 mRNA, complete cds//0.26:708:57//Hs.158245:U41740
 F-PLACE1010152
 F-PLACE1010181//EST//1.3e-21:312:71//Hs.141501:N50792
 F-PLACE1010194//ESTs//2.6e-55:284:97//Hs.155940:AA459582
 F-PLACE1010202//ESTs. Weakly similar to No definition line found [C. elegans]//2.3e-72:391:94//Hs.35225:M69637
 F-PLACE1010231
 F-PLACE1010261//Homo sapiens mRNA for KIAA0448 protein, complete cds//1.9e-146:693:97//Hs.27349:AB007917
 F-PLACE1010270//ESTs//2.0e-104:514:98//Hs.124062:H04590
 F-PLACE1010274//ESTs. Weakly similar to C01A2.4 [C. elegans]//6.8e-25:149:93//Hs.11449:A1201540
 F-PLACE1010293//EST//4.5e-36:358:74//Hs.162398:AA572813
 F-PLACE1010310//HOMEBOX/POU DOMAIN PROTEIN RDC-1//2.1e-10:352:62//Hs.74095:L20433
 F-PLACE1010321//Human hSIAH2 mRNA, complete cds//0.071:604:58//Hs.20191:U76248
 F-PLACE1010324//ESTs//0.22:286:58//Hs.130853:A1367875
 F-PLACE1010329//EST//5.7e-05:351:60//Hs.120644:AA742659
 F-PLACE1010341//EST//4.5e-16:255:72//Hs.141206:H53117
 F-PLACE1010362//ESTs//1.9e-41:246:92//Hs.128771:AA236855
 F-PLACE1010364//EST//0.11:282:58//Hs.135771:A1005648

F-PLACE1010383//EST//6.1e-08:107:76//Hs.136441:AA564986
 F-PLACE1010401
 F-PLACE1010481//Human BLU protein (BLU) mRNA, complete cds//0.94:254:61//Hs.125257:U70824
 F-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds//7.2e-152:702:99//Hs.13313:AF039081
 F-PLACE1010492//ESTs//1.0:201:60//Hs.146036:A1038500
 F-PLACE1010522//ESTs//3.9e-52:263:97//Hs.125149:A1302100
 F-PLACE1010529//Homo sapiens chromodomain-helicase-DNA-binding protein mRNA, complete cds//1.0:175:64//Hs.159273:AF054177
 F-PLACE1010547//ESTs//0.96:288:57//Hs.87156:AA233472
 F-PLACE1010562//EST//1.0:164:66//Hs.147868:A1222979
 F-PLACE1010579//EST//0.39:279:58//Hs.158960:A1380148
 F-PLACE1010580//ESTs. Moderately similar to PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06 [Schizosaccharomyces pombe]//3.8e-31:193:91//Hs.145229:N44661
 F-PLACE1010599//Homo sapiens peroxisomal membrane anchor protein HsPex14p (PEX14) mRNA, complete cds//9.9e-148:707:97//Hs.19851:AF045186
 F-PLACE1010616//EST//3.1e-43:213:100//Hs.128215:AA972394
 F-PLACE1010622//NUCLEOLIN//0.00040:282:60//Hs.7910:M60858
 F-PLACE1010624//Homo sapiens Jagged 2 mRNA, complete cds//1.2e-05:516:61//Hs.106387:AF029778
 F-PLACE1010628//EST. Weakly similar to line-1 protein ORF2 [H. sapiens]//0.012:258:62//Hs.144375:AA484200
 F-PLACE1010629//EST//8.3e-23:218:79//Hs.161975:AA501461
 F-PLACE1010630//EST//0.29:319:58//Hs.137277:M62225
 F-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//9.5e-66:363:95//Hs.10801:AB011102
 F-PLACE1010661//ESTs//3.9e-89:504:92//Hs.122666:M27076
 F-PLACE1010662
 F-PLACE1010702//Human repressor transcriptional factor (ZNF85) mRNA, complete cds//1.1e-74:697:74//Hs.37138:U35376
 F-PLACE1010714//EST//0.018:253:59//Hs.148028:A1270027
 F-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//6.1e-77:393:96//Hs.50758:AF092564
 F-PLACE1010739//Homo sapiens mRNA for Sec24 protein (Sec24A isoform), partial//0.97:314:59//Hs.14574:AJ131244
 F-PLACE1010743//Human myosin-IXb mRNA, complete cds//2.4e-56:409:86//Hs.159629:U42391
 F-PLACE1010761//ESTs. Weakly similar to UI SMALL NUCLEAR RIBONUCLEOPROTEIN 70 KD [Xenopus laevis]//5.1e-80:407:96//Hs.80965:AA493284
 F-PLACE1010771//ESTs. Highly similar to TRANSCRIPTIONAL REGULATOR PROTEIN HCNGP [Mus musculus]//6.0e-45:251:94//Hs.11379:AA594140
 F-PLACE1010786
 F-PLACE1010800
 F-PLACE1010802//EST//0.94:128:64//Hs.120366:AA719157
 F-PLACE1010811//ESTs//0.89:339:59//Hs.127314:M48085
 F-PLACE1010833//ESTs. Weakly similar to allograft inflammatory factor-1 [H. sapiens]//2.9e-28:245:79//Hs.132736:AA583494
 F-PLACE1010856//ESTs//1.5e-06:95:87//Hs.17401:M01048
 F-PLACE1010857//ESTs. Weakly similar to KIAA0157 gene product is novel. [H. sapiens]//5.8e-67:336:97//Hs.130135:AA905493
 F-PLACE1010870//Zinc finger protein 43 (HTF6)//9.7e-40:498:69//Hs.74107:X59244
 F-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//3.7e-149:694:98//Hs.118087:AB011182
 F-PLACE1010891//ESTs//6.9e-54:377:87//Hs.24453:R31671
 F-PLACE1010896//Human homologue of yeast sec7 mRNA, complete cds//0.64:167:65//Hs.1050:M85169
 F-PLACE1010900
 F-PLACE1010916//EST//0.55:151:66//Hs.145800:A1269981
 F-PLACE1010917
 F-PLACE1010925//ESTs//2.6e-81:437:94//Hs.5876:M26537
 F-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//3.1e-139:653:98//Hs.74750:AB011126
 F-PLACE1010942//Homo sapiens intersectin short form mRNA, complete cds//2.9e-91:437:98//Hs.66392:AF064244
 F-PLACE1010944//ESTs//1.3e-17:117:91//Hs.29444:M30985
 F-PLACE1010947//EST//0.97:93:72//Hs.162299:AA555154
 F-PLACE1010954//Apolipoprotein B (including Ag(x) antigen)//0.28:44:59//Hs.585:X04506
 F-PLACE1010960//ESTs//0.98:238:60//Hs.163674:AA506632
 F-PLACE1010965//ESTs//3.1e-74:376:96//Hs.115679:A1379721
 F-PLACE1011026//EST//0.022:222:60//Hs.47154:M50931
 F-PLACE1011032//EST//1.1e-05:88:79//Hs.118024:N34032
 F-PLACE1011041//Human density enhanced phosphatase-1 mRNA, complete cds//0.28:179:67//Hs.1177:U10886
 F-PLACE1011046//1-PHOSPHATIDYLINOSITOL-4,5-BISPHOSPHATE PHOSPHODIESTERASE BETA 2//6.2e-11:207:68//Hs.994:M95678

【0892】

【表591】

F-PLACE1011054//H.sapiens OBF-1 mRNA for octamer binding factor 1/ 6.1e-35:310:78//Hs.2407:Z49194	F-PLACE1011858//Human novel homeobox mRNA for a DNA binding protei n//8.9e-05:477:59//Hs.37035:U07664
F-PLACE1011056//Human putative serine/threonine protein kinase PRK (prk) mRNA, complete cds//0.74:228:61//Hs.153640:U56998	F-PLACE1011874//EST//0.20:118:66//Hs.127351:AA954775
F-PLACE1011057//EST//2.5e-80:388:98//Hs.126466:AA913320	F-PLACE1011875//Homo sapiens mRNA for KIAA0580 protein, partial cd s//5.3e-110:526:98//Hs.22572:AB011152
F-PLACE1011090//ESTs//1.4e-94:469:97//Hs.106448:R76663	F-PLACE1011891//ESTs//1.8e-58:397:88//Hs.84698:AA725913
F-PLACE1011109//ESTs//0.13:303:62//Hs.49294:AA418037	F-PLACE1011896//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//9.4 e-09:478:56//Hs.107747:A1357868
F-PLACE1011114//ESTs//5.8e-12:75:100//Hs.147422:A1214317	F-PLACE1011922//ESTs//0.49:249:62//Hs.152627:AA595817
F-PLACE1011133//ESTs//0.17:225:62//Hs.132853:A1370857	F-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//3.7e-140:664:98//Hs.3838:AF059617
F-PLACE1011143//ESTs//0.013:264:63//Hs.115368:AA629949	F-PLACE1011962//EST//1.7e-07:81:85//Hs.104333:AA250763
F-PLACE1011160	F-PLACE1011964//EST//6.6e-38:412:74//Hs.140562:AA826514
F-PLACE1011165//Galactokinase 2//2.7e-32:194:92//Hs.129228:M84443	F-PLACE1011982//ESTs//0.40:405:60//Hs.127743:A1261591
F-PLACE1011185//EST//1.4e-34:261:83//Hs.140250:AA708114	F-PLACE1011995//ESTs//1.7e-22:486:64//Hs.105157:AA527514
F-PLACE1011203//Homo sapiens chromosome 18q11 beta-1,4-galactosyl t ransferase mRNA, complete cds//6.9e-124:576:99//Hs.159140:AF038664	F-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cd s//4.0e-148:690:98//Hs.88756:AB018256
F-PLACE1011214//ESTs, Weakly similar to B0035.14 [C.elegans]//9.7 e-101:469:99//Hs.8241:AA283057	F-PLACE2000003//Homo sapiens mRNA, chromosome 1 specific transcrip t KIAA0487//6.5e-54:290:81//Hs.92381:AB007956
F-PLACE1011219//ESTs, Weakly similar to coded for by C. elegans cD NA CEESL70F [C.elegans]//2.6e-62:221:88//Hs.101821:W27452	F-PLACE2000006//ESTs//0.067:224:62//Hs.144100:A1205503
F-PLACE1011221//EST//0.46:238:62//Hs.32853:AA015751	F-PLACE2000007//ESTs//8.1e-23:147:91//Hs.128530:AA325330
F-PLACE1011229//Homo sapiens mRNA for KIAA0529 protein, partial cd s//1.4e-147:675:99//Hs.23168:AB011101	F-PLACE2000011//Interleukin 10//4.2e-42:362:78//Hs.2180:M57627
F-PLACE1011263//Homo sapiens BAC clone GS166A23 from Tp21//5.9e-7 1:350:98//Hs.15144:AC005014	F-PLACE2000014//EST//0.10:214:61//Hs.160247:A1138831
F-PLACE1011273//EST//1.0:222:59//Hs.35274:AA495803	F-PLACE2000015//Interleukin 10//1.4e-44:393:78//Hs.2180:M57627
F-PLACE1011291//Homo sapiens clone 24712 unknown mRNA, partial cds //3.4e-09:191:65//Hs.140950:AF070637	F-PLACE2000017
F-PLACE1011296//ESTs//0.019:137:63//Hs.140654:AA865915	F-PLACE2000021//Homo sapiens TRF1-interacting ankyrin-related ADP- ribose polymerase mRNA, partial cds//5.7e-85:844:72//Hs.7928:AF082 557
F-PLACE1011310//EST//0.066:336:58//Hs.162529:AA584160	F-PLACE2000030
F-PLACE1011325//ESTs//7.4e-43:229:96//Hs.21081:H08310	F-PLACE2000033//Human adhesion molecule ninjurin mRNA, complete cd s//0.85:234:66//Hs.11342:U91512
F-PLACE1011332//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.8e-151:696:99//Hs.5819:AF102265	F-PLACE2000034//Homo sapiens mRNA for KIAA0607 protein, partial cd s//0.058:348:62//Hs.94653:AB011179
F-PLACE1011340//Homo sapiens mRNA, chromosome 1 specific transcrip t KIAA0501//1.5e-20:120:81//Hs.159897:AB007970	F-PLACE2000039//Human plectin (PLEC1) mRNA, complete cds//0.0058:4 73:59//Hs.79706:U53204
F-PLACE1011371//Human mRNA for PK-120//9.5e-35:684:63//Hs.76415:D3 8535	F-PLACE2000047//ESTs//4.9e-32:328:75//Hs.141024:H07128
F-PLACE1011375//ESTs, Moderately similar to potassium channel prot ein Raw3 [R.norvegicus]//6.7e-68:325:99//Hs.107245:AA627053	F-PLACE2000050//ESTs//3.0e-36:270:83//Hs.155512:AA663966
F-PLACE1011399//EST//6.6e-05:285:61//Hs.130105:AA904868	F-PLACE2000061
F-PLACE1011419//ESTs//0.70:240:62//Hs.159650:M95552	F-PLACE2000062//Human membrane-associated lectin type-C mRNA//2.9 e-114:662:86//Hs.23759:M98457
F-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cd s//1.5e-158:743:98//Hs.10801:AB011102	F-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//7.1e-135:631:98//Hs.9443:AF027219
F-PLACE1011452//Human Line-1 repeat mRNA with 2 open reading frame s//1.9e-53:557:72//Hs.23094:M19503	F-PLACE2000097//ESTs//0.021:117:70//Hs.132811:A1034333
F-PLACE1011465//EST//3.1e-58:380:85//Hs.131605:A1025204	F-PLACE2000100
F-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete c ds//1.5e-152:703:99//Hs.111138:AB018255	F-PLACE2000103//ESTs//1.1e-56:284:98//Hs.144786:A1219219
F-PLACE1011477//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.7e-146:675:99//Hs.11183:AF065482	F-PLACE2000111//H.sapiens mRNA for 1-acylglycerol-3-phosphate O-ac yltransferase//0.76:215:65//Hs.6587:U56417
F-PLACE1011492//ESTs//2.0e-35:186:98//Hs.125886:AA884264	F-PLACE2000115
F-PLACE1011503//EST//0.67:149:65//Hs.149774:A1285997	F-PLACE2000124//Human mRNA for KIAA0355 gene, complete cds//2.8e-4 9:400:79//Hs.153014:AB002353
F-PLACE1011520//ESTs//0.00014:213:64//Hs.119889:AA705319	F-PLACE2000132
F-PLACE1011563//ESTs//2.2e-61:394:85//Hs.117718:AA883476	F-PLACE2000136//ESTs, Moderately similar to hypothetical protein [H.sapiens]//1.2e-08:245:64//Hs.140343:AA718911
F-PLACE1011567//Homo sapiens DEC-205 mRNA, complete cds//3.1e-46:3 25:84//Hs.153563:AF011333	F-PLACE2000140//Adenylate kinase 2 (adk2)//3.7e-24:162:90//Hs.8383 3:U54645
F-PLACE1011576//Homo sapiens hematopoietic cell derived zinc finger r protein mRNA, complete cds//4.3e-67:268:86//Hs.86371:AF054180	F-PLACE2000164
F-PLACE1011586//Homo sapiens hLRp105 mRNA for LDL receptor related protein 105, complete cds//0.98:153:65//Hs.143641:AB009462	F-PLACE2000170
F-PLACE1011635//Homo sapiens Jagged 2 mRNA, complete cds//0.00029: 585:57//Hs.106387:AF029778	F-PLACE2000172//ESTs//0.64:239:62//Hs.31175:A1219179
F-PLACE1011641	F-PLACE2000176
F-PLACE1011643//Homo sapiens mRNA for KIAA0293 gene, partial cds// 0.00058:499:58//Hs.12784:AB006631	F-PLACE2000187
F-PLACE1011646//EST//3.2e-26:201:68//Hs.140349:AA757661	F-PLACE2000216
F-PLACE1011649//ESTs//0.25:145:64//Hs.23033:R46086	F-PLACE2000223//EST//0.0092:171:60//Hs.162830:AA643933
F-PLACE1011650//ESTs//0.041:96:77//Hs.119351:AA447745	F-PLACE2000235//Human mRNA for KIAA0298 gene, complete cds//1.6e-3 8:792:63//Hs.21560:AB002296
F-PLACE1011664//Human mRNA for stac, complete cds//1.0:245:60//Hs. 56045:D86640	F-PLACE2000246//Homo sapiens mRNA for KIAA0795 protein, partial cd s//1.5e-74:367:98//Hs.22926:AB018338
F-PLACE1011675//Cell division cycle 27//0.098:448:57//Hs.73151:S78 234	F-PLACE2000264//Homo sapiens mRNA for KIAA0792 protein, complete c ds//2.0e-29:366:73//Hs.119387:AB007958
F-PLACE1011682//EST//9.6e-06:119:72//Hs.93664:M23366	F-PLACE2000274//Homo sapiens mRNA for dynein heavy chain//1.0e-23: 650:62//Hs.144672:AJ000522
F-PLACE1011719//Human mRNA for KIAA0352 gene, complete cds//0.92:3 65:60//Hs.17262:AB002350	F-PLACE2000302//ESTs//1.7e-05:66:89//Hs.55572:W37560
F-PLACE1011725	F-PLACE2000305//ESTs//1.6e-78:382:98//Hs.136731:AA745869
F-PLACE1011729//EST//0.56:304:58//Hs.86378:AA210853	F-PLACE2000317
F-PLACE1011749//ESTs//4.3e-88:443:96//Hs.132850:AA779891	F-PLACE2000335//Fc fragment of IgE, high affinity I. receptor for; beta polypeptide//6.1e-24:295:76//Hs.30:M89796
F-PLACE1011762//ESTs//0.012:149:68//Hs.145075:A1208240	F-PLACE2000341//Human sodium iodide symporter mRNA, complete cds// 6.8e-21:593:61//Hs.103983:U66088
F-PLACE1011778//ESTs//0.00016:199:64//Hs.160395:A1393693	F-PLACE2000342//Centromere protein B (BokD)//1.4e-06:326:61//Hs.85 004:X05299
F-PLACE1011783//EST//1.0:119:66//Hs.162191:AA534660	F-PLACE2000347//ESTs, Moderately similar to F18547_1 [H.sapiens]//

【0893】

【表592】

3.7e-16:139:82//Hs.28209:A1073817
 F-PLACE2000359//ESTs//5.0e-19:251:71//Hs.58272:W76645
 F-PLACE2000366//ESTs//1.7e-37:399:75//Hs.136646:AA748045
 F-PLACE2000371//EST//0.65:107:65//Hs.157677:A158861
 F-PLACE2000373//ESTs//0.30:207:59//Hs.143902:A1131032
 F-PLACE2000379//ESTs//1.3e-64:402:87//Hs.146307:AA584638
 F-PLACE2000394//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0484//1.0e-87:694:80//Hs.158095:AB007953
 F-PLACE2000398
 F-PLACE2000399
 F-PLACE2000404
 F-PLACE2000411
 F-PLACE2000419//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.0e-52:463:74//Hs.113283:AF018080
 F-PLACE2000425//EST//0.44:168:62//Hs.44677:N34966
 F-PLACE2000427
 F-PLACE2000433//ESTs//4.7e-18:213:74//Hs.110187:AA699719
 F-PLACE2000435//EST//4.7e-05:159:64//Hs.123604:AA815257
 F-PLACE2000438//H. sapiens mRNA for UDP-GalNAc:polypeptide N-acetyl galactosaminyltransferase (T2)//1.9e-20:418:64//Hs.130181:X85019
 F-PLACE2000450//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.0e-83:324:81//Hs.113283:AF018080
 F-PLACE2000455//ESTs. Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H. sapiens]//4.0e-05:100:73//Hs.104239:AA488082
 F-PLACE2000458//H. sapiens mRNA for hFat protein//0.0010:545:57//Hs.91107:X87241
 F-PLACE2000465//ESTs//4.4e-38:377:75//Hs.55855:AA621381
 F-PLACE2000477//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.8e-68:520:81//Hs.113283:AF018080
 F-PLACE2000004//Human EYA3 homolog (EYA3) mRNA, complete cds//3.9e-14:204:73//Hs.46925:Y10262
 F-PLACE2000009//Human mRNA for KIAA0386 gene, complete cds//4.8e-59:696:69//Hs.101359:AB002384
 F-PLACE2000020//Prostaglandin I2 (prostaglandin) receptor (IP)//0.0081:500:61//Hs.393:D38128
 F-PLACE2000029
 F-PLACE2000059//ESTs//0.0026:49:100//Hs.42913:A1082248
 F-PLACE2000070//EST//5.6e-15:202:74//Hs.154993:AA142842
 F-PLACE2000103//Homo sapiens cofactor of initiator function (CIF15) mRNA, complete cds//1.0:186:62//Hs.122752:AF026445
 F-PLACE2000119//Homo sapiens mRNA for KIAA0752 protein, partial cds//2.8e-48:283:83//Hs.23711:AB018295
 F-PLACE2000121
 F-PLACE2000124//Thromboxane A2 receptor//1.1e-55:195:83//Hs.89887:D38081
 F-PLACE2000136//Homo sapiens mRNA for KIAA0703 protein, complete cds//1.0:194:59//Hs.6168:AB014603
 F-PLACE2000142//EST//0.41:179:59//Hs.137438:AA282243
 F-PLACE2000145//EST//3.5e-25:145:96//Hs.163950:AA683016
 F-PLACE2000147//EST//5.0e-43:285:86//Hs.160895:A1365871
 F-PLACE2000148
 F-PLACE2000155//Homo sapiens mRNA for KIAA0672 protein, complete cds//5.6e-80:382:99//Hs.6336:AB014572
 F-PLACE2000156//ESTs//0.00015:277:62//Hs.156834:A1336023
 F-PLACE2000157//Calcium channel, voltage-dependent, P/Q type, alpha 1A subunit//0.54:320:60//Hs.96253:U79666
 F-PLACE2000158//Homo sapiens mRNA for KIAA0575 protein, complete cds//4.9e-66:319:88//Hs.153468:AB011147
 F-PLACE2000160
 F-PLACE2000169//Small inducible cytokine A5 (RANTES)//1.3e-64:501:80//Hs.155464:AF088219
 F-PLACE2000194
 F-PLACE2000197
 F-PLACE2000199//EST//1.0:108:68//Hs.98488:AA426546
 F-PLACE2000207//EST//1.0e-32:184:75//Hs.160146:A1049975
 F-PLACE2000208//CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN PRECURSOR//1.0:271:61//Hs.77522:X62744
 F-PLACE2000218//EST//1.3e-46:317:84//Hs.162197:AA535216
 F-PLACE2000220//EST//9.3e-95:443:99//Hs.112702:AA609377
 F-PLACE2000221//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//9.2e-56:200:85//Hs.133089:AF064019
 F-PLACE2000226
 F-PLACE2000230//EST//6.1e-16:173:72//Hs.148578:A1201568
 F-PLACE2000242//Human DNA sequence from clone 1409 on chromosome X p11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8032//1.2e-54:434:80//Hs.4943:Z98046
 F-PLACE2000244

F-PLACE2000254//NUCLEOLIN//2.6e-05:445:60//Hs.79110:M60858
 F-PLACE2000271//ESTs//1.6e-25:195:72//Hs.108452:H78650
 F-PLACE2000276//ESTs//1.0e-13:274:66//Hs.28589:A1004944
 F-PLACE2000304//EST//0.043:210:61//Hs.132378:A1026770
 F-PLACE2000310
 F-PLACE2000320//EST//1.2e-12:188:70//Hs.145771:A1269586
 F-PLACE2000322//Small inducible cytokine A5 (RANTES)//4.7e-29:252:80//Hs.155464:AF088219
 F-PLACE2000331
 F-PLACE2000339//Homo sapiens mRNA for KIAA0645 protein, complete cds//0.91:222:61//Hs.155987:AB014545
 F-PLACE2000341//EST//1.8e-05:394:58//Hs.112894:AA620741
 F-PLACE2000350//ESTs. Highly similar to SERINE/THREONINE-PROTEIN KINASE SULU [Caenorhabditis elegans]//2.9e-59:474:77//Hs.125850:AA885355
 F-PLACE2000352//H. sapiens OBF-1 mRNA for octamer binding factor 1//2.5e-48:442:78//Hs.2407:Z49194
 F-PLACE2000353//H. sapiens mRNA for UDP-GalNAc:polypeptide N-acetyl galactosaminyltransferase (T1)//0.78:234:63//Hs.7498:U41514
 F-PLACE2000362//EST//6.5e-25:302:73//Hs.140504:AA810441
 F-PLACE2000363
 F-PLACE2000365//ESTs//0.81:200:60//Hs.141556:N49928
 F-PLACE2000373//ESTs//0.0071:82:73//Hs.136310:AA442641
 F-PLACE2000388//ESTs//7.9e-16:235:71//Hs.44701:AA830432
 F-PLACE2000399//Clathrin, light polypeptide (Lcb)//5.2e-70:391:81//Hs.73919:X81637
 F-PLACE2000400//ESTs//0.53:162:66//Hs.49303:AA810785
 F-PLACE2000401//EST//2.3e-35:178:100//Hs.162851:AA632270
 F-PLACE2000402//ESTs//2.4e-84:425:96//Hs.148962:A1219715
 F-PLACE2000405//EST//2.1e-39:452:73//Hs.140414:AA778541
 F-PLACE2000406//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.9e-07:116:78//Hs.77579:AF013263
 F-PLACE2000413//ESTs. Weakly similar to methyl sterol oxidase [H. sapiens]//1.6e-51:260:98//Hs.122512:H61502
 F-PLACE2000416//Homo sapiens mRNA for KIAA0801 protein, complete cds//0.00020:630:57//Hs.17585:AB018344
 F-PLACE2000425//EST//3.8e-34:286:79//Hs.135301:A1039161
 F-PLACE2000455//Homo sapiens mRNA for cytochrome b small subunit of complex II, complete cds//3.6e-32:183:93//Hs.108326:AB006202
 F-PLACE2000475//ESTs//1.9e-09:422:61//Hs.145783:AA081874
 F-PLACE2000477//H. sapiens mRNA for chemokine receptor D6//1.0:426:54//Hs.117572:U94888
 F-PLACE2000009//TRICHOHYALIN//3.1e-09:692:60//Hs.82276:L09190
 F-PLACE2000014//Homo sapiens mRNA for KIAA0809 protein, partial cds//3.6e-118:331:100//Hs.105399:AB018352
 F-PLACE2000034//Homo sapiens Chromosome 16 BAC clone CIT987SK-A-69 G12//1.1e-06:244:63//Hs.154050:AC004131
 F-PLACE2000049//Homo sapiens clone 24519 mRNA sequence//4.3e-45:371:79//Hs.139088:AF070533
 F-PLACE2000052//Human ATP binding cassette transporter (ABCR) mRNA, complete cds//1.4e-53:669:67//Hs.40993:AF000148
 F-PLACE2000063
 F-PLACE2000089//ESTs//2.2e-10:121:85//Hs.49391:W00713
 F-PLACE2000093//ESTs//0.0053:273:60//Hs.136952:AA825819
 F-PLACE2000100//ESTs//8.0e-21:246:73//Hs.140207:N32058
 F-PLACE2000106//Homo sapiens mRNA for KIAA0462 protein, partial cds//3.8e-147:684:99//Hs.129937:AB007931
 F-PLACE2000128//Homo sapiens ES/130 mRNA, complete cds//0.23:398:60//Hs.98614:AF006751
 F-PLACE2000129
 F-PLACE2000131//ESTs//2.4e-13:194:72//Hs.41418:H90627
 F-PLACE2000147//ESTs//0.0060:324:60//Hs.85640:AA535856
 F-PLACE2000156//Zinc finger protein 136 (clone pHZ-20)//2.3e-89:764:76//Hs.69740:U09367
 F-PLACE2000192
 F-PLACE2000211
 F-PLACE2000222//EST//1.9e-15:317:66//Hs.149206:A1246594
 F-PLACE2000230//Human mRNA for KIAA0331 gene, complete cds//0.0048:258:60//Hs.146395:AB002329
 F-PLACE2000233//ESTs//4.4e-38:240:80//Hs.114605:A1304317
 F-PLACE2000247//Homo sapiens mitochondrial outer membrane protein (TOM40) mRNA, nuclear gene encoding mitochondrial protein, complete cds//0.0095:156:69//Hs.30928:AF043250
 F-PLACE2000250//ESTs//3.8e-72:377:94//Hs.124234:T89609
 F-PLACE2000252//ESTs//1.0:196:64//Hs.144869:AA493886
 F-PLACE2000259//Homo sapiens mRNA for KIAA0788 protein, partial cds//6.2e-27:191:87//Hs.2397:Z70200
 F-PLACE2000261
 F-PLACE2000269//ESTs. Weakly similar to coded for by C. elegans cDNA yk52b10.3 [C. elegans]//9.5e-41:202:100//Hs.118849:AA215645

【0894】

【表593】

F-PLACE4000270
F-PLACE4000300
F-PLACE4000320//FKBP-RAPAMYCIN ASSOCIATED PROTEIN//4.5e-23:135:96//
Hs.155952:U88966
F-PLACE4000323//EST//6.7e-09:180:68//Hs.116769:AA630365
F-PLACE4000326//ESTs//2.1e-94:453:98//Hs.103177:W72798
F-PLACE4000344//EST//6.4e-05:135:67//Hs.146729:A1147292
F-PLACE4000367
F-PLACE4000369
F-PLACE4000379//EST//3.9e-42:381:79//Hs.162335:AA564256
F-PLACE4000387//ESTs//0.19:93:69//Hs.154173:A1379823
F-PLACE4000392//ESTs//0.0015:381:59//Hs.120172:AA709046
F-PLACE4000401//Homo sapiens mRNA for KIAA0640 protein, partial cd
s//3.1e-47:605:71//Hs.153026:AB014540
F-PLACE4000411//ESTs. Moderately similar to plakophilin 2b [H.sapi
ens]//4.7e-33:159:81//Hs.154257:A1275982
F-PLACE4000431//Homo sapiens mRNA for KIAA0788 protein, partial cd
s//1.3e-45:263:92//Hs.2397:270200
F-PLACE4000445
F-PLACE4000450
F-PLACE4000465//ESTs//1.5e-11:273:65//Hs.145783:AA081874
F-PLACE4000487//Sialoporphin (gp115, leukosialin, CD43)//3.0e-14:1
89:71//Hs.80738:X52075
F-PLACE4000489//ESTs//0.94:104:68//Hs.125119:R38951
F-PLACE4000494//ESTs//1.0:185:60//Hs.143053:A1126289
F-PLACE4000521//ESTs//0.0027:161:70//Hs.135740:AA651731
F-PLACE4000522//ESTs. Highly similar to NEUROGENIC LOCUS NOTCH PR
OTEIN HOMOLOG 1 PRECURSOR [Homo sapiens]//0.047:119:65//Hs.129053:
AA767022
F-PLACE4000548
F-PLACE4000558//Homo sapiens mRNA for DFFRY protein, abundant tran
script//0.0035:510:59//Hs.39163:AF000986
F-PLACE4000581
F-PLACE4000590//ESTs. Highly similar to POL POLYPROTEIN [Friend m
urine leukemia virus (isolate 57)]//3.4e-13:275:68//Hs.113980:A103
4080
F-PLACE4000593//ESTs. Weakly similar to F2507.1 [C.elegans]//5.2e-
28:239:79//Hs.109084:A1004675
F-PLACE4000612//Keratin 9//0.27:207:64//Hs.2783:Z29074
F-PLACE4000638//Homo sapiens mRNA from chromosome 5q21-22, clone:s
F2//3.5e-47:562:69//Hs.129685:AB002446
F-PLACE4000650
F-PLACE4000654
F-PLACE4000670//ESTs//6.1e-88:411:100//Hs.130688:A1028132
F-SKNC1000011//Centromere protein B (80kD)//0.0013:243:62//Hs.850
04:X05299
F-SKNC1000013//ESTs. Highly similar to MULTIDRUG RESISTANCE PROT
EIN HOMOLOG 50 [Drosophila melanogaster]//2.5e-36:197:96//Hs.11863
4:U66688
F-SKNC1000046//Homo sapiens mRNA for KIAA0654 protein, partial cd
s//2.5e-148:706:98//Hs.109299:AB014554
F-SKNC1000050//Calpain, large polypeptide, L2//4.1e-53:330:90//Hs.
76288:M23254
F-SKNC1000091//ESTs//3.3e-64:420:88//Hs.90997:AA946877
F-THYR01000017//Human mRNA for KIAA0315 gene, partial cds//1.0:31
0:60//Hs.3989:AB002313
F-THYR01000026//H. sapiens OBF-1 mRNA for octamer binding factor 1/
2.9e-35:299:81//Hs.2407:Z49194
F-THYR01000034
F-THYR01000035//ESTs//4.1e-37:317:79//Hs.141254:A1334099
F-THYR01000040//ESTs//0.30:331:59//Hs.87176:A1148326
F-THYR01000070//Human mRNA for KIAA0347 gene, complete cds//0.069:
278:63//Hs.101996:AB002345
F-THYR01000072//Homo sapiens clone 23584 mRNA sequence//8.7e-86:72
2:77//Hs.6654:AB014557
F-THYR01000085
F-THYR01000092//ESTs//3.1e-100:469:99//Hs.132207:A1148065
F-THYR01000107
F-THYR01000111//Human Line-1 repeat mRNA with 2 open reading frame
s//6.8e-106:590:86//Hs.23094:M19503
F-THYR01000121
F-THYR01000124//Human mRNA for alanine aminotransferase//0.0026:42
0:58//Hs.103502:U70732
F-THYR01000129//Homo sapiens TED protein (TED) mRNA, complete cds/
2.8e-155:732:98//Hs.87619:AF087142
F-THYR01000132//ESTs//1.9e-35:164:79//Hs.139179:AA650203
F-THYR01000156//EST//0.32:102:68//Hs.139634:AA478416
F-THYR01000163//Small inducible cytokine A5 (RANTES)//5.2e-50:331:
85//Hs.155464:AF088219
F-THYR01000173//Human clathrin assembly protein 50 (AP50) mRNA, co

mplete cds//1.1e-05:261:61//Hs.152936:D63475
F-THYR01000186//H.sapiens mRNA for phosphoinositide 3-kinase//3.7
e-41:270:87//Hs.101238:Y11312
F-THYR01000187//EST//0.11:227:62//Hs.101773:H23270
F-THYR01000190//ESTs//0.82:194:63//Hs.128818:AA976883
F-THYR01000197//Homo sapiens mRNA for poly(A)-specific ribonuclea
se//2.4e-175:805:99//Hs.43445:AJ005698
F-THYR01000199//Homo sapiens mRNA for KIAA0652 protein, complete c
ds//4.0e-88:616:84//Hs.79672:AB014552
F-THYR01000206//EST//0.96:291:61//Hs.104962:AA443848
F-THYR01000221//Human clone 23589 mRNA sequence//0.035:242:62//Hs.
11506:U79297
F-THYR01000241//EST//0.48:102:69//Hs.160764:A1313322
F-THYR01000242//Zinc finger protein 84 (HPF2)//1.2e-42:534:64//Hs.
9450:M27878
F-THYR01000253//Homo sapiens mRNA for KIAA0690 protein, partial cd
s//0.61:211:64//Hs.60103:AB014590
F-THYR01000270
F-THYR01000279//ESTs//0.0020:104:72//Hs.121476:A1215500
F-THYR01000288//Homo sapiens mRNA for Hs Ste24p, complete cds//1.3
e-180:848:98//Hs.25846:AB016068
F-THYR01000320//ESTs. Weakly similar to Similar to glutamate decar
boxylase [C.elegans]//7.6e-92:431:99//Hs.122719:AA777803
F-THYR01000327//Autocrine motility factor receptor//2.8e-52:290:93
//Hs.80731:M63175
F-THYR01000343//Homo sapiens mRNA for KIAA0790 protein, partial cd
s//7.2e-164:763:98//Hs.12002:AB018333
F-THYR01000358//Human selenium-binding protein (hSBP) mRNA, comple
te cds//6.9e-34:177:84//Hs.7833:U29091
F-THYR01000368//ESTs//0.0011:55:96//Hs.34994:AA252919
F-THYR01000381//Homo sapiens mRNA for KIAA0562 protein, complete c
ds//0.081:240:62//Hs.118401:AB011134
F-THYR01000387//EST//3.6e-14:197:71//Hs.139399:AA416855
F-THYR01000394//ESTs. Weakly similar to No definition line found
[C.elegans]//5.8e-39:245:91//Hs.119095:T79413
F-THYR01000395//EST//5.8e-69:333:99//Hs.156524:AA724572
F-THYR01000401//ESTs//1.8e-24:132:98//Hs.54852:M26238
F-THYR01000438//EST//1.9e-05:217:63//Hs.115930:AA579773
F-THYR01000452//B cell lymphoma protein 6 (zinc finger protein 51)
//0.096:306:60//Hs.155024:U00115
F-THYR01000471//Tyrosine aminotransferase//5.6e-44:403:77//Hs.299
9:X52520
F-THYR01000484//EST. Weakly similar to putative p150 [H.sapiens]//
8.9e-22:248:76//Hs.162011:AA513663
F-THYR01000488
F-THYR01000501//H.sapiens Staf50 mRNA//3.2e-75:615:77//Hs.68054:X8
2200
F-THYR01000502//ESTs//1.0:350:57//Hs.119749:AA689298
F-THYR01000505//Interleukin 13//0.95:245:60//Hs.845:U31120
F-THYR01000558//EST//1.3e-24:351:64//Hs.142326:AA351877
F-THYR01000569//Homo sapiens mRNA for dihydropyrimidinase related
protein 4, complete cds//0.28:229:61//Hs.100058:AB006713
F-THYR01000570//EST//0.80:171:61//Hs.112790:AA609949
F-THYR01000585//Homo sapiens protein associated with Myc mRNA, com
plete cds//2.4e-168:808:97//Hs.151411:AF075587
F-THYR01000596//EST//9.5e-94:461:96//Hs.135397:A1056322
F-THYR01000602//EST//4.9e-06:80:80//Hs.162135:AA526331
F-THYR01000605//Guanylate cyclase 1, soluble, alpha 2//0.44:182:62
//Hs.2685:Z50053
F-THYR01000625//Thromboxane A2 receptor//4.5e-45:323:82//Hs.89887:
D38081
F-THYR01000637//ESTs//4.4e-24:255:75//Hs.101014:AA194941
F-THYR01000641//ESTs//0.00017:375:58//Hs.32703:AA054125
F-THYR01000658//CD4 receptor (exons 1 and 2) [human, T-lymphocyte,
mRNA, 3429 nt]//1.8e-09:127:77//Hs.116007:S79267
F-THYR01000662
F-THYR01000666//ESTs//1.9e-28:149:99//Hs.105187:A1394157
F-THYR01000676//CD4 receptor (exons 1 and 2) [human, T-lymphocyte,
mRNA, 3429 nt]//5.7e-49:281:77//Hs.116007:S79267
F-THYR01000684//ESTs. Weakly similar to band-6-protein [H.sapiens]
//0.46:368:57//Hs.26557:AA480380
F-THYR01000699//ESTs//1.6e-10:314:65//Hs.139212:AA243452
F-THYR01000712//ESTs//3.3e-42:211:99//Hs.69330:A1056324
F-THYR01000715//Human plectin (PLEC1) mRNA, complete cds//2.9e-06:
631:59//Hs.79706:U53204
F-THYR01000734//ESTs//8.4e-08:226:64//Hs.125754:AA806085
F-THYR01000748//Homo sapiens KIAA0411 mRNA, complete cds//3.1e-35:
339:74//Hs.7977:AB007871
F-THYR01000756//Homo sapiens protocadherin (PCDH8) mRNA, complete
cds//1.0:209:62//Hs.19492:AF061573

【0895】

【表594】

F-THYRO1000777//Human mRNA for KIAA0147 gene, partial cds//0.0006
9:636:57//Hs.158132:063481
F-THYRO1000783//Homo sapiens Arp2/3 protein complex subunit p41-Arc (ARC41) mRNA, complete cds//0.70:452:58//Hs.11538:AF006084
F-THYRO1000787
F-THYRO1000793
F-THYRO1000796
F-THYRO1000805//Homo sapiens mRNA from chromosome Sq21-22, clone:s
F2//9.4e-36:561:68//Hs.129685:AB002446
F-THYRO1000815//Human mRNA for KIAA0118 gene, partial cds//1.2e-4
5:465:75//Hs.154326:042087
F-THYRO1000829//ESTs//1.7e-66:361:95//Hs.7906:H16339
F-THYRO1000843
F-THYRO1000852//ESTs//6.2e-23:204:81//Hs.144452:AA838788
F-THYRO1000855//ESTs//0.049:159:64//Hs.163532:AI424170
F-THYRO1000865//ESTs. Weakly similar to !!!! ALU SUBFAMILY J WARNI
NG ENTRY !!!! [H.sapiens]//3.0e-33:190:75//Hs.133526:N21103
F-THYRO1000895//ESTs//3.8e-24:191:84//Hs.132722:AA618531
F-THYRO1000916//Homo sapiens mRNA, chromosome 1 specific transcrip
t KIAA0487//1.8e-43:318:79//Hs.92381:AB007956
F-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (P
DE8B) mRNA, partial cds//3.0e-179:839:98//Hs.78106:AF079529
F-THYRO1000934//PYRROLINE-5-CARBOXYLATE REDUCTASE//1.1e-33:759:63/
Hs.79217:M77836
F-THYRO1000951//MUELLERIAN INHIBITING FACTOR PRECURSOR//0.055:662:
56//Hs.112432:AC005263
F-THYRO1000952//Human mRNA for KIAA0208 gene, complete cds//0.98:1
77:55//Hs.83558:086963
F-THYRO1000974//Homo sapiens putative ATP-dependent mitochondrial
RNA helicase (SUV3) mRNA, nuclear gene encoding mitochondrial prot
ein, complete cds//2.7e-15:123:90//Hs.106469:AF042169
F-THYRO1000975//EST//0.45:172:62//Hs.105449:AA513907
F-THYRO1000983
F-THYRO1000984//EST//0.0075:119:65//Hs.150347:AA984646
F-THYRO1000988//ESTs//0.056:99:71//Hs.153409:AI224307
F-THYRO1001003
F-THYRO1001031//Thiopurine S-methyltransferase//3.8e-44:568:71//H
s.51124:AF019369
F-THYRO1001033//H.sapiens mRNA for cyclicin 11//0.0061:287:60//Hs.3
232:246788
F-THYRO1001062//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.2e-45:394:7
9//Hs.51048:X68830
F-THYRO1001093//Human mRNA for KIAA0355 gene, complete cds//3.4e-3
3:421:72//Hs.153014:AB002353
F-THYRO1001100//Human DNA-binding protein mRNA, 3' end//2.1e-74:74
1:74//Hs.159249:Z99130
F-THYRO1001120//Homo sapiens deltex (Dx) mRNA, complete cds//4.5e-
18:447:62//Hs.124024:AF053700
F-THYRO1001121//ESTs//0.92:257:61//Hs.118246:N95416
F-THYRO1001133//EST//1.1e-38:367:75//Hs.144175:HT0425
F-THYRO1001134//ESTs//1.4e-28:186:91//Hs.109468:W52074
F-THYRO1001142//ESTs//1.8e-44:332:82//Hs.146811:AA410788
F-THYRO1001173
F-THYRO1001177//ESTs//7.7e-40:240:84//Hs.155384:Z78385
F-THYRO1001189//ESTs//2.1e-36:323:76//Hs.120206:AI089163
F-THYRO1001204
F-THYRO1001213//Small inducible cytokine A5 (RANTES)//3.1e-43:256:
81//Hs.155464:AF088219
F-THYRO1001262//EST//7.9e-44:279:87//Hs.138856:H47461
F-THYRO1001271//Homo sapiens mRNA for synaptogyrin 3//0.0045:273:6
0//Hs.6467:AJ002309
F-THYRO1001287//Homo sapiens alpha 1,2-mannosidase IB mRNA, comple
te cds//0.014:178:66//Hs.125315:AF027156
F-THYRO1001290//ESTs//3.9e-43:145:99//Hs.147797:AA069836
F-THYRO1001313//ESTs//1.0e-244:61//Hs.127488:AA528182
F-THYRO1001320//ESTs//0.062:126:67//Hs.133296:AI311872
F-THYRO1001321//Homo sapiens DEC-205 mRNA, complete cds//2.5e-35:5
60:68//Hs.153563:AF011333
F-THYRO1001322//ESTs//0.12:238:61//Hs.29169:N66545
F-THYRO1001347//ESTs//7.5e-61:293:99//Hs.129962:AA927207
F-THYRO1001363//ESTs//1.0e-16:178:78//Hs.163954:N57939
F-THYRO1001365//Homo sapiens KIAA0417 mRNA, complete cds//3.6e-18:
187:79//Hs.12385:AB007877
F-THYRO1001374//Homo sapiens mRNA for KIAA0707 protein, partial cd
s//7.4e-157:740:97//Hs.138488:AB014607
F-THYRO1001401//EST//4.6e-14:171:76//Hs.157587:AI356993
F-THYRO1001403//ESTs//2.2e-50:464:79//Hs.118046:M49946
F-THYRO1001405//ESTs//1.7e-44:226:98//Hs.156667:AI347694
F-THYRO1001406//Hydroxysteroid (17-beta) dehydrogenase 3//2.8e-20:
459:62//Hs.477:U05659
F-THYRO1001411//ESTs//1.9e-41:342:78//Hs.146811:AA410788
F-THYRO1001426//Human ring zinc-finger protein (ZNF127-Xp) gene an
d 5' flanking sequence//4.6e-33:153:81//Hs.102877:U41315
F-THYRO1001434//ESTs//1.1e-07:274:60//Hs.151093:AI224099
F-THYRO1001458//Myosin, heavy polypeptide 9, non-muscle//6.2e-60:6
53:71//Hs.44782:Z82215
F-THYRO1001480//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.3e-42:370:7
8//Hs.51048:X68830
F-THYRO1001487//EST//1.0:88:71//Hs.160760:AI311943
F-THYRO1001534//ESTs//1.2e-94:457:98//Hs.125523:AA883904
F-THYRO1001537//ESTs//3.5e-94:469:97//Hs.106448:R76663
F-THYRO1001541//EST//1.4e-10:158:65//Hs.145159:AI150211
F-THYRO1001559//ESTs//1.4e-07:91:81//Hs.43507:M24046
F-THYRO1001570//ESTs//2.3e-41:280:80//Hs.119752:AA703335
F-THYRO1001573//Homo sapiens clone 24778 unknown mRNA//2.7e-105:54
6:95//Hs.25306:AF070572
F-THYRO1001584//Human RGP3 mRNA, complete cds//0.14:335:58//Hs.822
94:U27655
F-THYRO1001595//Human RSU-1/RSP-1 mRNA, complete cds//3.6e-35:165:
84//Hs.75551:L12535
F-THYRO1001602//ESTs//3.1e-42:350:80//Hs.138384:R72849
F-THYRO1001605//EST//0.11:426:57//Hs.151206:AI126071
F-THYRO1001617//ESTs//5.2e-43:345:81//Hs.8710:M07046
F-THYRO1001637//ESTs. Weakly similar to anion exchanger [H.sapien
s]//5.2e-13:108:86//Hs.141045:AA191659
F-THYRO1001656//Solute carrier family 2 (facilitated glucose trans
porter), member 4//0.099:540:55//Hs.95958:M91463
F-THYRO1001661//ESTs//0.12:53:92//Hs.151586:W45568
F-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthet
ase 59 kDa isoform//8.0e-166:780:98//Hs.118633:AJ225089
F-THYRO1001673//Von Hippel-Lindau syndrome//4.6e-25:212:73//Hs.781
60:AF010238
F-THYRO1001703//Homo sapiens clone 24767 mRNA sequence//0.27:421:5
7//Hs.122908:AF070552
F-THYRO1001706//ESTs//1.8e-24:142:95//Hs.112536:AI147691
F-THYRO1001721//ESTs. Highly similar to RING CANAL PROTEIN [Droso
phila melanogaster]//2.5e-51:296:92//Hs.3826:U69560
F-THYRO1001738//EST//6.9e-30:180:94//Hs.58641:W81229
F-THYRO1001745//ESTs//6.1e-49:244:98//Hs.97534:AA398813
F-THYRO1001746//EST//0.96:119:63//Hs.144107:AI053590
F-THYRO1001772//ESTs. Weakly similar to !!!! ALU SUBFAMILY J WARNI
NG ENTRY !!!! [H.sapiens]//2.2e-21:182:81//Hs.118053:N75725
F-THYRO1001793//ESTs//1.9e-93:439:99//Hs.150116:AI299324
F-THYRO1001809//Human mRNA for KIAA0297 gene, partial cds//0.47:16
8:67//Hs.11711:AB002295
F-THYRO1001828
F-THYRO1001854//EST//0.038:128:67//Hs.160649:AI241823
F-THYRO1001895//Intercellular adhesion molecule 1 (CD54), human rh
inovirus receptor//9.6e-13:288:65//Hs.51061:M24283
F-THYRO1001907//EST//1.9e-12:126:80//Hs.139296:AA350198
F-VESEN1000122
F-Y79AA1000013//ESTs//1.7e-72:369:96//Hs.97176:AA447885
F-Y79AA1000033
F-Y79AA1000037//Murine leukemia viral (bmi-1) oncogene homolog//7.
8e-21:230:66//Hs.431:L13689
F-Y79AA1000059//Homo sapiens immunophilin homolog ARA9 mRNA, compl
ete cds//7.3e-40:629:64//Hs.75305:U78521
F-Y79AA1000065//CD81 ANTIGEN//0.0050:241:60//Hs.54457:M33680
F-Y79AA1000131//Guanylate cyclase 1, soluble, alpha 2//0.078:477:5
8//Hs.2685:Z50053
F-Y79AA1000181//Fatty acid synthase (3' region) [human, breast and
HepG2 cells, mRNA Partial, 2237 nt]//0.0022:684:58//Hs.83190:U293
44
F-Y79AA1000202//ESTs//2.5e-17:143:86//Hs.76925:AA211860
F-Y79AA1000214//Homo sapiens histone H2A.F/Z variant (H2AV) mRNA,
complete cds//3.9e-73:345:100//Hs.9242:AF081192
F-Y79AA1000230//Polymeric immunoglobulin receptor//0.98:335:59//H
s.842:X73079
F-Y79AA1000231//ESTs//0.11:209:66//Hs.132184:AI278623
F-Y79AA1000258//Homo sapiens metase (MET-1) mRNA, complete cds//0.
30:444:61//Hs.99941:L23134
F-Y79AA1000268//Human mRNA for KIAA0367 gene, partial cds//9.1e-1
1:300:64//Hs.23311:AB002365
F-Y79AA1000313//Human mRNA for KIAA0129 gene, complete cds//0.89:7
44:56//Hs.44361:D50919
F-Y79AA1000328
F-Y79AA1000342//Homo sapiens OPA-containing protein mRNA, complete
cds//8.4e-15:223:75//Hs.85313:AF071309
F-Y79AA1000346
F-Y79AA1000349//ALPHA-2C-1 ADRENERGIC RECEPTOR//8.3e-06:180:73//H

【0896】

【表595】

s.123022:J03853
F-Y79AA1000355
F-Y79AA1000368//ESTs//0.0062:235:64//Hs.114777:AA782908
F-Y79AA1000405//ESTs//0.76:244:62//Hs.153027:AA648897
F-Y79AA1000410//Small inducible cytokine A5 (RANTES)//8.1e-31:229:83//Hs.155464:AF088219
F-Y79AA1000420//ESTs//1.1e-53:271:87//Hs.13056:AA181018
F-Y79AA1000469//Homo sapiens I-1 receptor candidate protein mRNA, complete cds//0.0047:315:66//Hs.26285:AF082516
F-Y79AA1000480
F-Y79AA1000538//ESTs//5.7e-09:110:77//Hs.98790:AA284871
F-Y79AA1000539//ESTs//2.6e-52:412:77//Hs.81648:W26521
F-Y79AA1000540//Homo sapiens chromosome 7q22 sequence//0.70:133:69//Hs.151555:AF053356
F-Y79AA1000560//Homo sapiens gamma2-adaptin (G2AD) mRNA, complete cds//1.2e-07:371:63//Hs.8991:AF068706
F-Y79AA1000574//Human mRNA for GC box binding protein, complete cds//0.95:258:62//Hs.150557:D31716
F-Y79AA1000589//Homo sapiens clone 614 unknown mRNA, complete sequence//2.8e-154:755:97//Hs.21811:AF091080
F-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//1.7e-136:644:98//Hs.60580:AF060503
F-Y79AA1000705//Homo sapiens CHD1 mRNA, complete cds//0.0023:523:59//Hs.22670:AF006513
F-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11b) mRNA, complete cds//1.6e-181:850:98//Hs.83023:AF093670
F-Y79AA1000748//ESTs//4.2e-12:95:90//Hs.33687:R85969
F-Y79AA1000752//ESTs//8.1e-114:551:97//Hs.153471:A1198377
F-Y79AA1000774//ESTs//2.9e-59:296:98//Hs.150536:W20067
F-Y79AA1000782//EST//0.97:78:69//Hs.147351:A1208468
F-Y79AA1000784//Homo sapiens RanBP7/importin 7 mRNA, complete cds//1.1e-178:847:97//Hs.5151:AF098799
F-Y79AA1000794//G-rich RNA sequence binding factor 1//0.83:228:61//Hs.79295:U07231
F-Y79AA1000800//Homo sapiens GABA-B receptor mRNA, complete cds//0.12:244:60//Hs.12307:AF056085
F-Y79AA1000802//Homo sapiens actin binding protein MAYVEN mRNA, complete cds//0.87:466:59//Hs.122967:AF059569
F-Y79AA1000805
F-Y79AA1000824//Titin//1.0:437:58//Hs.83049:X90568
F-Y79AA1000827//Fatty acid synthase (3' region) [human, breast and HepG2 cells, mRNA Partial, 2237 nt]//0.0048:630:57//Hs.83190:U29344
F-Y79AA1000833//TUBULIN ALPHA-4 CHAIN//6.9e-107:603:90//Hs.75318:X06956
F-Y79AA1000850//ESTs, Weakly similar to T22C1.7 [C.elegans]//6.0e-77:368:99//Hs.85660:AA398644
F-Y79AA1000962//Homo sapiens orphan nuclear hormone receptor B073 mRNA, 3' end//0.14:499:58//Hs.37288:D16815
F-Y79AA1000966//ESTs//0.80:52:86//Hs.6671:A1341699
F-Y79AA1000968//ESTs, Moderately similar to initiation factor eIF-2B gamma subunit [R.norvegicus]//6.9e-69:310:94//Hs.76822:A1359536
F-Y79AA1000969//LYMPHOTOXIN-BETA RECEPTOR PRECURSOR//1.0:150:64//Hs.1116:L04270
F-Y79AA1000976//Arachidonate 15-lipoxygenase//0.87:174:66//Hs.73809:M23892
F-Y79AA1000985//Human plectin (PLEC1) mRNA, complete cds//0.091:385:58//Hs.79706:U53204
F-Y79AA1001023
F-Y79AA1001041//Human myt1 homolog (hMYH) gene, complete cds//0.99:37:100//Hs.78489:U63329
F-Y79AA1001048//Acyl-Coenzyme A dehydrogenase, very long chain//8.7e-30:772:60//Hs.82208:L46590
F-Y79AA1001061//ESTs//6.3e-41:303:84//Hs.55855:AA621381
F-Y79AA1001068//EST//3.0e-23:165:90//Hs.157607:A1357511
F-Y79AA1001077//ESTs//4.9e-40:237:94//Hs.11197:AA309047
F-Y79AA1001078
F-Y79AA1001105//Homo sapiens homeodomain protein (OG12) mRNA, complete cds//6.5e-11:247:66//Hs.55967:AF022654
F-Y79AA1001145//ESTs//1.3e-20:234:75//Hs.55855:AA621381
F-Y79AA1001167//Homo sapiens mRNA for KIAA0750 protein, complete cds//1.0:155:63//Hs.5444:AB018293
F-Y79AA1001177//Human hSIAM2 mRNA, complete cds//6.5e-09:299:65//Hs.20191:U76248
F-Y79AA1001185//ESTs//1.7e-56:318:93//Hs.102991:AA639646
F-Y79AA1001211//ESTs//9.1e-108:503:99//Hs.100605:AA305965
F-Y79AA1001216//Peroxisome receptor 1//0.00028:458:57//Hs.158084:Z48054
F-Y79AA1001228//Fragile X mental retardation 2//0.040:207:64//Hs.54472:U48436
F-Y79AA1001233//ESTRAD10L 17 BETA-DEHYDROGENASE 1//6.5e-25:731:60//Hs.85279:U34879
F-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110113307 (RZPD Berlin))//4.0e-135:441:97//Hs.23170:AJ005892
F-Y79AA1001281//ESTs//2.7e-21:157:88//Hs.163825:A1393240
F-Y79AA1001299//Human Inil mRNA, complete cds//2.2e-116:323:93//Hs.155626:U04847
F-Y79AA1001312//ESTs//3.7e-95:448:99//Hs.104469:W38395
F-Y79AA1001323//ESTs//8.9e-50:340:86//Hs.144198:A1017555
F-Y79AA1001384
F-Y79AA1001391//Human Hoxb-13 mRNA, complete cds//8.6e-42:505:70//Hs.66731:U81599
F-Y79AA1001394//ESTs, Weakly similar to F5483.3 [C.elegans]//1.5e-90:424:96//Hs.154221:H23167
F-Y79AA1001402//ESTs//1.0:245:62//Hs.134695:A1088489
F-Y79AA1001493//SRY (sex determining region Y)-box 4//0.38:311:61//Hs.83484:X70683
F-Y79AA1001511//ESTs//9.9e-105:487:99//Hs.153581:AA630465
F-Y79AA1001533//ESTs, Highly similar to RETROVIRUS-RELATED POL POLYPROTEIN [Homo sapiens]//0.95:256:63//Hs.29974:A1360447
F-Y79AA1001541//EST//0.96:202:61//Hs.99141:AA447744
F-Y79AA1001548//ESTs//2.6e-25:166:90//Hs.164036:AA845659
F-Y79AA1001555//ESTs//1.6e-35:191:97//Hs.52885:H29851
F-Y79AA1001581//Cyclin-dependent kinase inhibitor 1C (p57, Kip2)//2.5e-05:272:64//Hs.106070:U22398
F-Y79AA1001585//ESTs//1.1e-84:473:93//Hs.42547:AA210783
F-Y79AA1001594//ESTs//1.7e-08:169:71//Hs.97366:AA393109
F-Y79AA1001603//ESTs//4.6e-07:429:59//Hs.160422:A1363426
F-Y79AA1001613//Homo sapiens mRNA for KIAA0683 protein, complete cds//0.00078:520:57//Hs.12334:AB014583
F-Y79AA1001647//ESTs, Weakly similar to ZK1058.5 [C.elegans]//9.4e-79:421:94//Hs.107039:W27244
F-Y79AA1001665//VON WILLEBRAND FACTOR PRECURSOR//1.0:386:60//Hs.110802:X04385
F-Y79AA1001679//Guanine nucleotide binding protein (G protein), beta polypeptide 1//0.88:243:61//Hs.3620:X04526
F-Y79AA1001692//Insulin-like growth factor binding protein 2//1.9e-06:426:59//Hs.162:X16302
F-Y79AA1001696//ESTs//2.3e-44:249:94//Hs.163665:AA250877
F-Y79AA1001705//Homo sapiens interleukin-1 receptor-associated kinase (IRAK) mRNA, complete cds//0.19:609:58//Hs.77297:L76191
F-Y79AA1001711//ESTs//5.2e-29:224:83//Hs.100461:A1018620
F-Y79AA1001781//Homo sapiens KIAA0443 mRNA, complete cds//0.49:183:66//Hs.113082:AB007903
F-Y79AA1001805//ESTs//1.1e-62:315:98//Hs.16141:W56079
F-Y79AA1001827//ESTs, Weakly similar to Similar to S.cerevisiae YD9335.03c protein [H.sapiens]//2.9e-62:313:98//Hs.15709:W81213
F-Y79AA1001846//ESTs//9.4e-16:146:82//Hs.140588:H60533
F-Y79AA1001848//ESTs, Weakly similar to KIAA0390 [H.sapiens]//1.6e-18:142:90//Hs.103349:A1141124
F-Y79AA1001866//Homo sapiens mRNA for zinc finger protein 10//5.1e-09:215:67//Hs.104115:X52332
F-Y79AA1001874//Homo sapiens Jagged 2 mRNA, complete cds//5.4e-06:412:62//Hs.106387:AF029778
F-Y79AA1001875//ESTs//6.8e-09:198:67//Hs.138036:A1343173
F-Y79AA1001923//Homo sapiens growth-arrest-specific protein (gas) mRNA, complete cds//0.98:430:58//Hs.78501:L13720
F-Y79AA1001963//ESTs//8.1e-131:642:97//Hs.54971:A1424382
F-Y79AA1002027//ESTs//0.00042:58:91//Hs.5375:AA620611
F-Y79AA1002083//ESTs//2.5e-51:285:95//Hs.117205:W88943
F-Y79AA1002089//ESTs, Weakly similar to putative p150 [H.sapiens]//8.3e-53:348:88//Hs.18122:A1338045
F-Y79AA1002093
F-Y79AA1002103//ESTs//1.5e-15:223:71//Hs.97427:AA411865
F-Y79AA1002115
F-Y79AA1002125//ESTs//6.5e-41:206:99//Hs.159257:N40395
F-Y79AA1002139//ESTs, Weakly similar to B0035.14 [C.elegans]//1.2e-24:165:90//Hs.6473:AA853955
F-Y79AA1002204//Homo sapiens mRNA for KIAA0638 protein, partial cds//9.5e-05:393:62//Hs.77864:AB014538
F-Y79AA1002208//ESTs//2.7e-13:211:69//Hs.112469:AA598515
F-Y79AA1002209//ESTs, Weakly similar to TYROSYL-TRNA SYNTHETASE [Bacillus caldotes]//2.3e-113:568:96//Hs.111637:AA305890
F-Y79AA1002210//ESTs, Weakly similar to D2045.8 [C.elegans]//8.6e-33:338:73//Hs.26662:U55984
F-Y79AA1002211//ESTs//2.6e-15:121:75//Hs.159584:AA524477
F-Y79AA1002220//EST//0.010:360:60//Hs.136341:AA482508
F-Y79AA1002229//Human mRNA for KIAA0086 gene, complete cds//0.0041:203:63//Hs.1560:O42045

【0897】

【表596】

F-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//4.1e-176:821:98//Hs.100729:AB014592
 F-Y79AA1002246//Human involucrin mRNA//5.6e-05:525:59//Hs.157091:M13903
 F-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.2e-160:748:98//Hs.96731:AB014555
 F-Y79AA1002298//ESTs//2.5e-05:115:77//Hs.87164:T84489
 F-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//2.1e-130:522:97//Hs.30898:AB014534
 F-Y79AA1002311//ESTs//4.9e-19:126:94//Hs.58595:AA830999
 F-Y79AA1002351//Human high conductance inward rectifier potassium channel alpha subunit mRNA, complete cds//0.028:587:58//Hs.2363:L36059
 F-Y79AA1002361//ESTs//8.7e-29:149:100//Hs.156074:AA824377
 F-Y79AA1002399
 F-Y79AA1002407//ESTs//1.5e-25:183:89//Hs.110031:T52569
 F-Y79AA1002416//CTP synthetase//9.1e-51:489:72//Hs.84112:X52142
 F-Y79AA1002431
 F-Y79AA1002433//EST//0.0037:94:71//Hs.136780:AA772318
 F-Y79AA1002472//Homo sapiens DNA from chromosome 19, BAC 33152//1.1e-37:263:69//Hs.55452:AC003973
 F-Y79AA1002482//ESTs//1.4e-49:313:80//Hs.132590:A1160765
 F-Y79AA1002487//Insulin-like growth factor binding protein 2//0.43:249:61//Hs.162:X16302

【0898】

3'末端クローン配列に対するHuman Unigene相同性検索結果データ

各データは、

クローン配列名、

トップヒットデータのTitle、

P値:比較配列の長さ (base):相同性(%)、

トップヒットデータのAccession No.の順に//で区切って記載した。

なお、同一クローンで5'末端配列に対応する3'末端配列が決定されていないものは空欄とした。相同性のスコアのP値が1より大であった場合はデータは示さない。

【0899】

【表597】

R-HENBA1000005//ESTs. Highly similar to HYPOTHETICAL 31.6 KD PROT
EIN F54F2.9 IN CHROMOSOME III [Caenorhabditis elegans]//5.6e-93:50
1:93//Hs.13015:AA628434
R-HENBA1000030//Human POU domain protein (Brn-3b) mRNA, complete c
ds//0.83:314:61//Hs.266:U06233
R-HENBA1000042//Archain//1.4e-45:282:89//Hs.33642:X81198
R-HENBA1000046//Human mRNA for KIAA0118 gene, partial cds//8.3e-5
2:528:72//Hs.154326:D42087
R-HENBA1000050//EST//0.043:155:63//Hs.149031:A1243340
R-HENBA1000076//ESTs//3.1e-77:394:97//Hs.111742:R39329
R-HENBA1000111//ESTs//1.7e-33:228:85//Hs.146811:AA410788
R-HENBA1000129//ESTs. Weakly similar to contains similarity to hel
icases [C. elegans]//4.4e-90:502:90//Hs.55918:AA151667
R-HENBA1000141//Homo sapiens mRNA for KIAA0797 protein, partial cd
s//2.1e-100:514:94//Hs.27197:AB018340
R-HENBA1000150//Homo sapiens mRNA for KIAA0640 protein, partial cd
s//3.1e-45:435:77//Hs.153026:AB014540
R-HENBA1000156//ESTs. Moderately similar to The KIAA0138 gene prod
uct is novel. [H.sapiens]//7.7e-92:428:100//Hs.126925:AA931237
R-HENBA1000158
R-HENBA1000168//ESTs. Weakly similar to F13B12.1 [C.elegans]//1.3
e-05:58:91//Hs.5570:A1378863
R-HENBA1000180//ESTs//7.7e-90:461:95//Hs.159200:N50545
R-HENBA1000185//ESTs//1.3e-72:371:96//Hs.134506:AA308366
R-HENBA1000193//ESTs//4.2e-103:481:99//Hs.143251:AA769827
R-HENBA1000201//Human Init mRNA, complete cds//3.0e-25:137:99//Hs.
155626:U04847
R-HENBA1000213//ESTs//5.4e-85:465:94//Hs.23412:AA133311
R-HENBA1000216//ESTs//3.0e-37:311:79//Hs.137875:AA993532
R-HENBA1000227//EST//2.2e-100:498:96//Hs.161570:W80404
R-HENBA1000231//Homo sapiens KIAA0414 mRNA, partial cds//2.7e-34:2
87:70//Hs.127649:AB007874
R-HENBA1000243//Homo sapiens mRNA for KIAA0475 protein, complete c
ds//1.3e-23:276:75//Hs.5737:AB007944
R-HENBA1000244//ESTs//2.3e-88:455:96//Hs.8929:AA719019
R-HENBA1000251//ESTs//0.9e-41:56//Hs.120277:A1243808
R-HENBA1000264//ESTs//3.7e-97:487:96//Hs.29258:W37424
R-HENBA1000280//ESTs. Moderately similar to ovarian-specific prote
in [R.norvegicus]//4.9e-14:208:73//Hs.93332:AA811920
R-HENBA1000282//ESTs//2.5e-38:216:94//Hs.120757:R92485
R-HENBA1000288//ESTs//2.6e-43:289:86//Hs.151365:AA643962
R-HENBA1000290//ESTs//5.1e-110:543:96//Hs.139068:AA516409
R-HENBA1000302//Homo sapiens mRNA for KIAA0527 protein, partial cd
s//1.0:122:67//Hs.129748:AB011099
R-HENBA1000303//ESTs//7.4e-76:386:97//Hs.22276:AA191323
R-HENBA1000304//Human Ca2+-dependent activator protein for secreti
on mRNA, complete cds//8.8e-30:160:98//Hs.151301:U36448
R-HENBA1000307//ESTs. Highly similar to 8A-2V protein [M.musculus]
//1.1e-103:489:99//Hs.108881:A018024
R-HENBA1000333//ESTs//9.3e-99:472:98//Hs.163512:AA903238
R-HENBA1000338//EST//5.1e-49:278:92//Hs.150815:A1302560
R-HENBA1000351//Human high-affinity copper uptake protein (hCTR1)
mRNA, complete cds//1.1e-42:270:88//Hs.73614:U83460
R-HENBA1000355//ESTs//1.0e-105:531:96//Hs.61762:A1422243
R-HENBA1000357//Human kpn1 repeat mna (cdna clone pcd-kpni-4), 3'
end//9.4e-89:432:87//Hs.139107:X00629
R-HENBA1000366//ESTs//1.1e-99:524:95//Hs.11785:T65857
R-HENBA1000369//ESTs//6.5e-70:355:96//Hs.124847:AA843938
R-HENBA1000376//Human mRNA for KIAA0205 gene, complete cds//3.6e-4
4:388:77//Hs.3610:D86960
R-HENBA1000387//Human high-affinity copper uptake protein (hCTR1)
mRNA, complete cds//5.5e-47:337:83//Hs.73614:U83460
R-HENBA1000390//Oxytocin receptor//2.4e-16:428:62//Hs.2820:X64878
R-HENBA1000392//ESTs//3.9e-105:531:96//Hs.130661:A1340248
R-HENBA1000396//ESTs. Weakly similar to line-1 protein ORF2 [H.sap
iens]//1.1e-44:447:75//Hs.42849:N31920
R-HENBA1000411//ESTs. Weakly similar to ankyrin 3, long form [H.sap
iens]//6.1e-92:373:99//Hs.48675:A1005282
R-HENBA1000418//ESTs//3.1e-66:315:100//Hs.94133:A1270700
R-HENBA1000422//ESTs//1.6e-99:464:99//Hs.33024:AA002140
R-HENBA1000428//Homo sapiens mRNA for oligophrenin 1//4.9e-85:535:
87//Hs.158122:AJ001189
R-HENBA1000434//ESTs//3.7e-53:266:99//Hs.22782:Z38143
R-HENBA1000442//ESTs//0.93:322:57//Hs.144763:A1218014
R-HENBA1000456//ESTs//4.1e-48:277:93//Hs.6937:AA524349
R-HENBA1000459//ESTs//0.010:184:63//Hs.128797:A1246316
R-HENBA1000460
R-HENBA1000464//EST//0.082:87:70//Hs.147977:A1262370
R-HENBA1000469//Small inducible cytokine A5 (RANTES)//1.4e-65:494:
81//Hs.155464:AF088219

R-HENBA1000488//ESTs. Weakly similar to The KIAA0132 gene product
is related to Drosophila melanogaster ring canal protein. [H.sapie
ns]//1.1e-31:181:94//Hs.61454:AA312449
R-HENBA1000490//ESTs//6.4e-17:132:86//Hs.32855:N25528
R-HENBA1000491//ESTs//2.2e-22:171:85//Hs.8035:AA195087
R-HENBA1000504//ESTs//0.016:282:58//Hs.130778:A1077571
R-HENBA1000505//EST//6.1e-15:116:87//Hs.162783:AA627318
R-HENBA1000508//ESTs//1.1e-28:244:81//Hs.132722:AA618531
R-HENBA1000518//EST//0.60:141:60//Hs.97831:AA400885
R-HENBA1000519//ESTs//2.8e-64:334:96//Hs.97885:AA402414
R-HENBA1000520//ESTs//6.9e-104:503:97//Hs.18370:AA947280
R-HENBA1000523//Cleavage stimulation factor, 3' pre-RNA, subunit
3, 77kd//4.0e-55:203:92//Hs.155510:U15782
R-HENBA1000531//ESTs. Weakly similar to HEAT SHOCK 70 KD PROTEIN I
[H.sapiens]//1.3e-117:550:99//Hs.99722:A1422277
R-HENBA1000540//ESTs//4.7e-72:350:98//Hs.109755:AA180809
R-HENBA1000545//Homo sapiens clone 23892 mRNA sequence//3.7e-68:54
9:80//Hs.91916:AF035317
R-HENBA1000555//ESTs//2.3e-66:342:97//Hs.71916:AA219699
R-HENBA1000557//EST//1.5e-49:297:90//Hs.149580:A1281881
R-HENBA1000561//ESTs. Moderately similar to zinc finger protein [C.
norvegicus]//1.8e-108:550:96//Hs.26799:W74481
R-HENBA1000563//Adenosine kinase//0.16:367:58//Hs.94382:U50196
R-HENBA1000568//ESTs//5.1e-42:321:82//Hs.141024:HO7128
R-HENBA1000569
R-HENBA1000575//ESTs//3.8e-45:352:80//Hs.146811:AA410788
R-HENBA1000588//ESTs//0.18:122:67//Hs.140507:AA761944
R-HENBA1000591//Homo sapiens mRNA for E1B-55kDa-associated protein
//3.9e-113:591:94//Hs.155218:AJ007509
R-HENBA1000592//TYROSINE-PROTEIN KINASE ITK/TSK//0.024:309:61//Hs.
89519:L10717
R-HENBA1000594//ESTs//8.6e-07:172:68//Hs.160289:A1168041
R-HENBA1000604//Human telomerase-associated protein TP-I mRNA, com
plete cds//1.5e-19:129:93//Hs.158334:U86136
R-HENBA1000608//ESTs//2.2e-95:506:94//Hs.6103:AA496424
R-HENBA1000622//ESTs//3.8e-10:440:61//Hs.137538:AA769438
R-HENBA1000636//ESTs. Weakly similar to 50S RIBOSOMAL PROTEIN L20
[C.coli]//1.4e-86:422:97//Hs.26252:AA643235
R-HENBA1000637//Homo sapiens mRNA for KIAA0690 protein, partial cd
s//3.7e-99:443:97//Hs.60103:AB014590
R-HENBA1000655//Human mRNA for KIAA0392 gene, partial cds//1.3e-5
0:426:79//Hs.40100:AB002390
R-HENBA1000657//ESTs//3.0e-74:419:93//Hs.109477:AA477929
R-HENBA1000662//EST//1.1e-90:425:99//Hs.122144:AA780136
R-HENBA1000673//ESTs//1.2e-101:473:99//Hs.138215:A1123922
R-HENBA1000682//ESTs. Weakly similar to putative p150 [H.sapiens]/
//3.5e-114:553:97//Hs.111730:AA604403
R-HENBA1000686//ESTs. Weakly similar to C27F2.7 gene product [C.el
egans]//6.8e-18:137:86//Hs.7049:A1141736
R-HENBA1000702//Human mRNA for tryptophan hydroxylase (EC 1.14.16.
4)//7.4e-52:345:84//Hs.144563:AF057280
R-HENBA1000705//EST//0.21:139:63//Hs.132687:A1033672
R-HENBA1000719//ESTs//8.4e-90:484:94//Hs.29005:AA477213
R-HENBA1000722//ESTs. Weakly similar to similar to enoyl-CoA hydra
tase/isomerases [C.elegans]//7.2e-113:572:95//Hs.28644:A1018612
R-HENBA1000726//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//2.8
e-40:449:75//Hs.74478:U33931
R-HENBA1000727//ESTs//0.0047:267:60//Hs.133095:AA927777
R-HENBA1000747//EST//3.9e-20:160:85//Hs.99048:AA446110
R-HENBA1000749//Small inducible cytokine A5 (RANTES)//4.7e-37:286:
82//Hs.155464:AF088219
R-HENBA1000752//EST//0.041:39:94//Hs.127772:AA961131
R-HENBA1000769//Homo sapiens mRNA for chemokine LEC precursor, com
plete cds//1.6e-32:309:75//Hs.10458:AF088219
R-HENBA1000773//EST//7.5e-05:201:63//Hs.122887:AA767612
R-HENBA1000774//Kangai 1 (suppression of tumorigenicity 6, prostat
e: CD82 antigen (R2 leukocyte antigen, antigen detected by monoclo
nal and antibody 1A4))//1.3e-48:284:90//Hs.103458:X53795
R-HENBA1000791//Human mRNA for KIAA0118 gene, partial cds//1.2e-4
5:291:87//Hs.154326:D42087
R-HENBA1000817//ESTs//8.3e-95:445:99//Hs.107357:AA983939
R-HENBA1000822//ESTs//1.1e-107:522:97//Hs.92832:AA631027
R-HENBA1000827//Homo sapiens Ser/Arg-related nuclear matrix protei
n (SRM160) mRNA, complete cds//2.2e-44:228:98//Hs.18192:AF048977
R-HENBA1000843//Homo sapiens LIM protein mRNA, complete cds//5.6e-
46:410:77//Hs.154103:AF061258
R-HENBA1000851
R-HENBA1000852//Aldehyde dehydrogenase 10 (fatty aldehyde dehydrog
enase)//3.7e-33:284:80//Hs.159608:U46689.
R-HENBA1000867//EST//2.0e-17:211:74//Hs.145670:A1265794

【0900】

【表598】

R-HEMBA1000869//ESTs//3.1e-16:237.71//Hs.116518:AA653202	R-HEMBA1001294//ESTs//1.0:140:65//Hs.149638:AI298324
R-HEMBA1000870//ESTs//1.6e-43:222.98//Hs.69564:AA203608	R-HEMBA1001299//Small inducible cytokine A5 (RANTES)//1.1e-45:307:84//Hs.155464:AF088219
R-HEMBA1000872//ESTs//1.9e-93:453.98//Hs.152622:AA594951	R-HEMBA1001302//Homo sapiens mRNA for APC 2 protein, complete cds//0.53:89:68//Hs.20912:AB012162
R-HEMBA1000876//Small inducible cytokine A5 (RANTES)//3.0e-41:329:79//Hs.155464:AF088219	R-HEMBA1001303//EST//0.00053:271:60//Hs.156148:AI333214
R-HEMBA1000908//ESTs//1.6e-51:291.92//Hs.12247:AI203154	R-HEMBA1001310//ESTs//1.4e-91:486.93//Hs.86228:AA206019
R-HEMBA1000910//EST//0.98:139:64//Hs.132687:AI033672	R-HEMBA1001319//ESTs//0.051:228:61//Hs.99404:AA953977
R-HEMBA1000918//EST//9.6e-30:152.84//Hs.162136:AA526508	R-HEMBA1001323//ESTs//6.2e-83:401.98//Hs.47343:AI282950
R-HEMBA1000919	R-HEMBA1001326//ESTs, Weakly similar to HYPOTHETICAL 55.1 KD PROTEIN IN IN FABI-PES4 INTERGENIC REGION [S.cerevisiae]//1.3e-77:458.92//Hs.9398:N41838
R-HEMBA1000934//ESTs//4.1e-38:254.89//Hs.87784:AA460597	R-HEMBA1001327//ESTs//0.60:251:58//Hs.117162:AA701259
R-HEMBA1000942//ESTs//3.5e-20:172.69//Hs.160065:AI018619	R-HEMBA1001330//Homo sapiens PYRIN (MEFY) mRNA, complete cds//1.1e-46:249:78//Hs.113283:AF018080
R-HEMBA1000943//Homo sapiens mRNA for KIAA0748 protein, complete cds//1.3e-44:281:78//Hs.33187:AB018291	R-HEMBA1001351//ESTs//0.13:230:57//Hs.138510:R94816
R-HEMBA1000946//ESTs//1.6e-68:352.96//Hs.21331:H93074	R-HEMBA1001361//ESTs//3.5e-107:570.94//Hs.7727:AA142837
R-HEMBA1000960//Homo sapiens tapasin (NCS-17) mRNA, complete cds//4.0e-61:347.81//Hs.5247:AF029750	R-HEMBA1001375//ESTs//1.1e-96:454.99//Hs.59584:AA587334
R-HEMBA1000966//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//6.8e-51:362.84//Hs.159187:AB007977	R-HEMBA1001377//ESTs//8.5e-91:459.95//Hs.61859:AA628550
R-HEMBA1000971//ESTs//2.8e-41:246.91//Hs.104287:AI363498	R-HEMBA1001383//ESTs//0.077:381.58//Hs.163093:AA745458
R-HEMBA1000972//Homo sapiens mRNA for XPR2 protein//7.3e-44:341.81//Hs.44766:AJ007590	R-HEMBA1001387//ESTs//2.0e-85:405.99//Hs.152127:AI246482
R-HEMBA1000974//ESTs//1.4e-32:166.100//Hs.149274:AI018170	R-HEMBA1001388//ESTs//1.5e-83:395.99//Hs.105191:AA133439
R-HEMBA1000975//Oxytocin receptor//2.7e-46:563.73//Hs.2820:X64878	R-HEMBA1001391//ESTs//7.7e-90:455.96//Hs.120905:R22204
R-HEMBA1000985//ESTs//4.4e-05:125.69//Hs.147434:AI214464	R-HEMBA1001398//Thromboxane A2 receptor//4.0e-46:279.89//Hs.89887:D38081
R-HEMBA1000986//ESTs//7.8e-44:266.84//Hs.163784:N54902	R-HEMBA1001405//ESTs//1.2e-98:485.97//Hs.73287:W16714
R-HEMBA1000991//EST//1.4e-42:162.86//Hs.149580:AI201881	R-HEMBA1001407//ESTs//2.2e-76:365.99//Hs.110128:AA584364
R-HEMBA1001007	R-HEMBA1001411//ESTs//1.2e-102:476.100//Hs.143162:AI380343
R-HEMBA1001008//ESTs//2.3e-82:463.92//Hs.10339:AA058764	R-HEMBA1001413//ESTs//3.7e-66:321.98//Hs.152472:AA041199
R-HEMBA1001009//ESTs, Weakly similar to non-lens beta gamma-crystallin like protein [H.sapiens]//2.6e-58:280.100//Hs.128738:AA970836	R-HEMBA1001415
R-HEMBA1001017//Homo sapiens mRNA for KIAA0468 protein, complete cds//3.3e-115:587.95//Hs.158287:AB007937	R-HEMBA1001432//Putative mismatch repair/binding protein HSMH3//7.9e-42:183.82//Hs.42674:U61981
R-HEMBA1001019//Cell division cycle 2, G1 to S and G2 to M//1.1e-24:140.95//Hs.58393:X05360	R-HEMBA1001433//ESTs//1.4e-34:240.77//Hs.95611:U51704
R-HEMBA1001020//ESTs//0.52:86.72//Hs.69683:AA115292	R-HEMBA1001435//ESTs//5.6e-23:292.70//Hs.116315:AA629263
R-HEMBA1001022//ESTs//3.4e-18:102.100//Hs.63243:AI123912	R-HEMBA1001442//ESTs//0.76:414.58//Hs.156189:AI419982
R-HEMBA1001024//ESTs//1.9e-07:262.61//Hs.124399:AA832336	R-HEMBA1001446//ESTs//2.2e-95:447.99//Hs.154091:AA767546
R-HEMBA1001026//ESTs//0.0017:142.67//Hs.144109:AI345543	R-HEMBA1001450//ESTs//1.0e-93:491.94//Hs.16130:AA195077
R-HEMBA1001043//Ankyrin G//0.23:244.60//Hs.75893:U13616	R-HEMBA1001454//Human Line-1 repeat mRNA with 2 open reading frame s//1.7e-47:304.88//Hs.23094:M19503
R-HEMBA1001051//Homo sapiens mRNA for KIAA0621 protein, partial cds//6.4e-21:186.79//Hs.132942:AB014521	R-HEMBA1001455//ESTs//7.1e-103:482.99//Hs.97407:AI417220
R-HEMBA1001052//ESTs//5.4e-107:497.99//Hs.121773:AI357886	R-HEMBA1001463
R-HEMBA1001060//ESTs//1.1e-31:298.80//Hs.74821:AA044813	R-HEMBA1001476//Human mRNA for KIAA0186 gene, complete cds//2.0e-25:409.66//Hs.36232:D00008
R-HEMBA1001071//Alpha-1 type 3 collagen//9.1e-34:179.98//Hs.119571:X14420	R-HEMBA1001478
R-HEMBA1001077//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//2.7e-21:417.64//Hs.127338:AB007961	R-HEMBA1001497
R-HEMBA1001080	R-HEMBA1001510//ESTs//3.3e-44:381.78//Hs.139882:AA864426
R-HEMBA1001085//ESTs//1.9e-47:385.79//Hs.146811:AA410788	R-HEMBA1001515//Human Line-1 repeat mRNA with 2 open reading frame s//5.9e-79:528.84//Hs.23094:M19503
R-HEMBA1001088//ESTs//8.7e-102:548.93//Hs.127273:AA522674	R-HEMBA1001517//ESTs//5.8e-32:272.81//Hs.119512:AA487269
R-HEMBA1001094	R-HEMBA1001522//ESTs//1.7e-84:364.95//Hs.117858:AA702493
R-HEMBA1001099//ESTs//0.24:41.97//Hs.18612:T99245	R-HEMBA1001526//ESTs//1.8e-93:527.93//Hs.10624:N64723
R-HEMBA1001109//Small inducible cytokine A5 (RANTES)//2.4e-45:396.80//Hs.155464:AF088219	R-HEMBA1001533//ESTs//1.9e-42:211.100//Hs.55830:AA580270
R-HEMBA1001121//ESTs//1.7e-15:216.71//Hs.141605:H92974	R-HEMBA1001557//ESTs//4.2e-83:413.97//Hs.47546:AA181348
R-HEMBA1001122//ESTs//2.0e-90:474.94//Hs.107884:AA131320	R-HEMBA1001566//Small inducible cytokine A5 (RANTES)//3.4e-50:304.88//Hs.155464:AF088219
R-HEMBA1001123//B-CELL GROWTH FACTOR PRECURSOR//2.7e-45:319.84//Hs.99879:M15530	R-HEMBA1001569//POU domain, class 3, transcription factor 4//2.3e-06:259.62//Hs.2229:X82324
R-HEMBA1001133//ESTs//1.2e-92:443.99//Hs.99626:AA632341	R-HEMBA1001570//Homo sapiens pendrin (PDS) mRNA, complete cds//3.5e-47:456.77//Hs.159275:AF030880
R-HEMBA1001137//ESTs//2.0e-86:426.97//Hs.157103:W60265	R-HEMBA1001579//ESTs//0.11:299.60//Hs.106090:AA457030
R-HEMBA1001140//Small inducible cytokine A5 (RANTES)//2.9e-45:323.83//Hs.155464:AF088219	R-HEMBA1001581//ESTs//0.016:350.61//Hs.124664:AI015652
R-HEMBA1001172//ESTs, Moderately similar to !!!! ALU SUBFAMILY J W ARNING ENTRY !!!! [H.sapiens]//1.1e-39:309.82//Hs.96337:AA225358	R-HEMBA1001585//Human mRNA for KIAA0331 gene, complete cds//0.30:251:63//Hs.146395:AB002329
R-HEMBA1001174//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.21:238.60//Hs.127338:AB007961	R-HEMBA1001589
R-HEMBA1001197//ESTs//0.010:388.61//Hs.14881:R91896	R-HEMBA1001595//ESTs, Weakly similar to SEPTIN 2 [D.melanogaster]//6.9e-71:431.88//Hs.26625:W25874
R-HEMBA1001208//ESTs, Highly similar to Similar to S.cerevisiae hypothetical protein 5 [H.sapiens]//0.27:305.62//Hs.100238:U69194	R-HEMBA1001608//Human kpni repeat mRNA (cdna clone pcd-kpni-8), 3' end//1.3e-73:533.82//Hs.103948:K00627
R-HEMBA1001226//Homo sapiens PYRIN (MEFY) mRNA, complete cds//5.0e-54:333.81//Hs.113283:AF018080	R-HEMBA1001620//ESTs, Highly similar to MYO-INOSITOL-1-PHOSPHATE SYNTHASE [Arabidopsis thaliana]//4.5e-93:537.90//Hs.20218:AA628530
R-HEMBA1001235//EST//2.3e-07:42.92//Hs.141620:N63316	R-HEMBA1001635//Homo sapiens antigen NY-CO-16 mRNA, complete cds//0.054:362.60//Hs.132206:AF039694
R-HEMBA1001247//ESTs, Weakly similar to WWP2 [H.sapiens]//2.9e-20:160.87//Hs.103102:W55932	R-HEMBA1001636//ESTs//4.9e-53:267.97//Hs.47459:AA700158
R-HEMBA1001257//ESTs//3.3e-112:544.97//Hs.128749:AA79728	R-HEMBA1001640//ESTs//2.9e-27:299.72//Hs.65236:AA927623
R-HEMBA1001265//ESTs//8.7e-116:564.98//Hs.155150:AI061435	R-HEMBA1001651//ESTs, Weakly similar to Mi-2 protein [H.sapiens]//1.2e-86:442.95//Hs.63888:AA203398
R-HEMBA1001281//ESTs, Weakly similar to Lpa8p [S.cerevisiae]//2.4e-35:239.87//Hs.103919:AA159181	R-HEMBA1001655//ESTs//1.5e-101:516.95//Hs.86541:AA214554
R-HEMBA1001286//ESTs//1.4e-97:507.95//Hs.26244:AI352674	R-HEMBA1001658
R-HEMBA1001289//ESTs//8.2e-44:122.96//Hs.76267:AA877534	R-HEMBA1001661//Homo sapiens protocadherin 68 (PCH68) mRNA, complete cds//1.3e-16:427.61//Hs.106511:AF029343

【0901】

【表599】

R-HEMBA1001672//Homo sapiens methyl-CpG binding protein MBD3 (MBD3) mRNA, complete cds//1.4e-93:493:92//Hs.107254:AC005943	7//Hs.11050:AL031178
R-HEMBA1001675	R-HEMBA1001979//EST//0.039:167:63//Hs.129451:AA993932
R-HEMBA1001678//Homo sapiens voltage dependent anion channel prote in mRNA, complete cds//4.2e-103:534:94//Hs.7381:AF038962	R-HEMBA1001987//ESTs//3.1e-44:320:83//Hs.136839:H93717
R-HEMBA1001681//ESTs//6.0e-49:292:92//Hs.65588:AA523424	R-HEMBA1001991//Human mRNA for KIAA0355 gene, complete cds//9.5e-47:303:88//Hs.153014:AB002353
R-HEMBA1001702//ESTs//9.0e-98:478:97//Hs.28661:AA805916	R-HEMBA1002003//Homo sapiens mRNA for protein phosphatase 2C (bet a)//1.6e-91:448:97//Hs.5687:AJ005801
R-HEMBA1001709//Homo sapiens mRNA for KIAA0698 protein, complete c ds//6.3e-98:483:96//Hs.31720:AB014598	R-HEMBA1002008//ESTs//9.2e-47:297:87//Hs.142314:AA347930
R-HEMBA1001711//ESTs//5.8e-83:398:98//Hs.34804:AA514960	R-HEMBA1002018//ESTs//9.4e-21:118:97//Hs.7871:AI041837
R-HEMBA1001712//ESTs//0.028:202:63//Hs.105790:AA528095	R-HEMBA1002022//Human mRNA for KIAA0075 gene, partial cds//0.25:196:63//Hs.1189:D38550
R-HEMBA1001714//ESTs, Highly similar to ATPASE INHIBITOR, MITOCHO NDRIAL PRECURSOR [Rattus norvegicus]//1.8e-46:236:98//Hs.132948:AA 194452	R-HEMBA1002035//ESTs//7.7e-101:475:99//Hs.8858:AI131538
R-HEMBA1001718//Small inducible cytokine A5 (RANTES)//8.6e-43:166:88//Hs.155464:AF088219	R-HEMBA1002039//H. sapiens mRNA for phosphoinositide 3-kinase//0.68:256:64//Hs.101238:Y11312
R-HEMBA1001723//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPE ATS CONTAINING PROTEIN IN SISI-MRPL2 INTERGENIC REGION [Saccharomy ces cerevisiae]//7.1e-88:431:96//Hs.29203:AI344105	R-HEMBA1002049//Homo sapiens mRNA for KIAA0563 protein, complete c ds//2.4e-51:254:85//Hs.15731:AB011135
R-HEMBA1001731//EST//0.25:100:68//Hs.149171:AI245712	R-HEMBA1002084//EST//0.31:219:60//Hs.162396:AA527264
R-HEMBA1001734//Human mRNA for KIAA0355 gene, complete cds//2.6e-39:366:77//Hs.153014:AB002353	R-HEMBA1002092//EST//6.4e-72:342:99//Hs.148533:AI200996
R-HEMBA1001744	R-HEMBA1002100//EST//5.6e-38:258:85//Hs.103094:W52354
R-HEMBA1001745//ESTs//6.6e-05:244:62//Hs.157663:AI358623	R-HEMBA1002102//Thiopyridine S-methyltransferase//1.4e-46:403:79//H s.51124:AF019369
R-HEMBA1001746//EST//4.9e-65:409:88//Hs.124673:AA858162	R-HEMBA1002113//Prostaglandin I2 (prostacyclin) synthase //1.4e-76:280:90//Hs.61333:DB3402
R-HEMBA1001761//ESTs//1.9e-44:315:84//Hs.159510:AA297145	R-HEMBA1002119//Homo sapiens ORF12P pseudogene, complete sequence //1.4e-87:362:94//Hs.103443:AF065854
R-HEMBA1001781//ESTs//3.0e-98:462:99//Hs.60059:AI057306	R-HEMBA1002125//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//1.7e-16:94:100//Hs.107747:AI357868
R-HEMBA1001784//EST//1.0e-12:250:68//Hs.152366:AA486721	R-HEMBA1002139//H. sapiens mRNA for nebulin//0.0019:68:88//Hs.83870:X83957
R-HEMBA1001791//EST//1.4e-47:292:89//Hs.163333:AA879053	R-HEMBA1002144//ESTs//3.1e-30:259:72//Hs.141575:AA211734
R-HEMBA1001800//ESTs//8.4e-37:314:79//Hs.105151:AA970243	R-HEMBA1002150//ESTs//7.1e-105:543:95//Hs.32275:AA595199
R-HEMBA1001803//ESTs//4.5e-99:465:99//Hs.135159:AI095823	R-HEMBA1002151//ESTs//2.2e-35:178:100//Hs.77703:W19642
R-HEMBA1001804//Zinc finger protein 148 (pH2-52)//0.78:232:57//Hs.112180:AF039019	R-HEMBA1002153//EST//4.5e-49:458:77//Hs.141708:W44337
R-HEMBA1001808//Homo sapiens mRNA, chromosome 1 specific transcrip t KIAA0500//9.0e-114:548:98//Hs.118164:AB007969	R-HEMBA1002160//Homo sapiens nephrocytin (NPH1) mRNA, partial cd s//1.4e-36:400:75//Hs.75474:AF023674
R-HEMBA1001809//EST//3.8e-63:292:89//Hs.158591:AI369334	R-HEMBA1002161//Homo sapiens EVI5 homolog mRNA, complete cds//1.9e-33:294:77//Hs.26929:AF008915
R-HEMBA1001815//Calcium modulating ligand//1.1e-47:299:87//Hs.13572:AF068179	R-HEMBA1002162//ESTs//1.0e-47:317:85//Hs.48919:W64043
R-HEMBA1001819//ZINC FINGER PROTEIN HF.12//1.2e-16:259:69//Hs.155470:X07290	R-HEMBA1002166//Thromboxane A2 receptor//6.8e-46:296:81//Hs.89887:D38081
R-HEMBA1001820//ESTs//2.6e-86:404:100//Hs.112881:AA620707	R-HEMBA1002177//EST//2.6e-42:215:99//Hs.116880:AA662457
R-HEMBA1001822//EST//2.2e-101:480:99//Hs.159940:AA971578	R-HEMBA1002185//Homo sapiens class-I MHC-restricted T cell associa ted molecule (CRTAM) mRNA, complete cds//6.0e-42:419:73//Hs.159523:AF001622
R-HEMBA1001824//ESTs, Weakly similar to MATRIN 3 [H.sapiens]//6.2e-27:147:97//Hs.23476:AA401210	R-HEMBA1002189//Homo sapiens mRNA for KIAA0792 protein, complete c ds//1.4e-29:244:72//Hs.119387:AB007958
R-HEMBA1001835//EST//0.79:216:64//Hs.47437:N52250	R-HEMBA1002191//ESTs//2.6e-31:275:66//Hs.133852:AI076357
R-HEMBA1001844//ESTs//4.7e-62:319:95//Hs.55200:N98513	R-HEMBA1002199//Human Line-1 repeat mRNA with 2 open reading frame s//4.3e-84:557:84//Hs.23094:W19503
R-HEMBA1001847//ESTs//2.3e-102:522:95//Hs.20879:AA845446	R-HEMBA1002204//EST//0.00057:113:71//Hs.144868:AI202342
R-HEMBA1001861//Homo sapiens mRNA for KIAA0617 protein, complete c ds//1.1e-109:553:96//Hs.78946:AB014517	R-HEMBA1002212//ESTs//1.5e-48:277:93//Hs.104741:AI393315
R-HEMBA1001864//ESTs//7.4e-94:449:99//Hs.132776:AI142853	R-HEMBA1002215//ESTs//1.1e-23:158:90//Hs.152529:AA897151
R-HEMBA1001866//Myelin oligodendrocyte glycoprotein (alternative p roducts)//1.9e-37:357:76//Hs.53217:Z48051	R-HEMBA1002226//Homo sapiens mRNA for KIAA0706 protein, complete c ds//5.1e-21:230:75//Hs.139648:AB014606
R-HEMBA1001869//ESTs, Weakly similar to trithorax homolog HTX, ver sion 2 [H.sapiens]//2.3e-32:193:94//Hs.9489:R84329	R-HEMBA1002229//Homo sapiens growth suppressor related (DOC-1R) mR NA, complete cds//1.5e-47:238:98//Hs.25664:AF089814
R-HEMBA1001888//H.sapiens mRNA for urea transporter//2.0e-47:425:78//Hs.66710:X96969	R-HEMBA1002237//ESTs//6.9e-35:357:76//Hs.116518:AA653202
R-HEMBA1001896//ESTs//3.5e-56:274:99//Hs.129018:H03128	R-HEMBA1002253//EST//6.0e-19:125:81//Hs.140596:AA829426
R-HEMBA1001910	R-HEMBA1002257
R-HEMBA1001912//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARI NG ENTRY !!!! [H.sapiens]//1.5e-73:347:100//Hs.30991:AA994438	R-HEMBA1002267//ESTs, Weakly similar to HYPOTHETICAL 27.8 KD PROTE IN IN VMA7-RPS31A INTERGENIC REGION [S.cerevisiae]//1.3e-31:201:91//Hs.114673:W72675
R-HEMBA1001913//ESTs, Highly similar to GCN20 PROTEIN [Saccharomy ces cerevisiae]//5.1e-57:320:91//Hs.91251:U66685	R-HEMBA1002270//ESTs//4.6e-100:483:97//Hs.34940:AI264314
R-HEMBA1001915//ESTs//4.9e-88:459:95//Hs.122810:AI273706	R-HEMBA1002321//ESTs//2.3e-85:403:99//Hs.120388:AA723595
R-HEMBA1001918//ESTs//1.2e-106:505:99//Hs.98518:AI027125	R-HEMBA1002328//ESTs//1.3e-90:423:100//Hs.117936:AI280818
R-HEMBA1001921//Homo sapiens germinal center kinase related protei n kinase mRNA, complete cds//5.5e-107:534:96//Hs.154934:AF000145	R-HEMBA1002337//ESTs//8.7e-24:147:93//Hs.9893:AA007679
R-HEMBA1001939//ESTs, Moderately similar to !!!! ALU SUBFAMILY J W ARNING ENTRY !!!! [H.sapiens]//2.9e-99:482:98//Hs.96849:AA879470	R-HEMBA1002341//Homo sapiens mRNA for KIAA0771 protein, partial cd s//7.8e-130:642:96//Hs.6162:AB018314
R-HEMBA1001940//Human mRNA for KIAA0392 gene, partial cds//5.6e-45:336:82//Hs.40100:AB002390	R-HEMBA1002348//ESTs//5.0e-71:387:93//Hs.30494:H04822
R-HEMBA1001942//EST//2.6e-84:397:99//Hs.145444:AI203668	R-HEMBA1002349//ESTs//9.7e-88:420:98//Hs.132972:AA543094
R-HEMBA1001945//ESTs//1.4e-92:437:99//Hs.144565:AI192452	R-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCA P-E) mRNA, complete cds//3.9e-123:661:93//Hs.119023:AF092563
R-HEMBA1001950//ESTs//3.9e-43:280:88//Hs.84429:N28866	R-HEMBA1002381//ESTs//1.3e-73:352:99//Hs.56121:AA781435
R-HEMBA1001960//ESTs//0.040:243:62//Hs.29567:AA640421	R-HEMBA1002389//EST//2.3e-05:132:69//Hs.37558:H58237
R-HEMBA1001962//ESTs//0.0071:113:69//Hs.49792:N70048	R-HEMBA1002417//Homo sapiens chromosome 19, cosmid R28784//3.9e-63:358:91//Hs.25527:AC005954
R-HEMBA1001964//ESTs//3.0e-38:239:87//Hs.158126:W26825	R-HEMBA1002419//ESTs, Weakly similar to APK1 antigen [H.sapiens]//5.6e-87:429:96//Hs.13209:AI417849
R-HEMBA1001967//Human DNA sequence from clone 341E18 on chromosome 6p11.2-12.3. Contains a Serine/Threonine Protein Kinase gene (pre sumptive isolog of a Rat gene) and a novel alternatively spliced g ene. Contains a putative CpG island, ESTs and GSSs//1.8e-106:517:9	R-HEMBA1002430//ESTs//0.10:388:57//Hs.119238:AA476267
	R-HEMBA1002439//Human mRNA for KIAA0080 gene, partial cds//2.0e-2

【0902】

【表600】

2:181:80//Hs.74554:D38522	R-HEMBA1002876//ESTs//0.72:202:62//Hs.144816:A1220827
R-HEMBA1002458//ESTs//1.8e-88:448:95//Hs.97914:AA769069	R-HEMBA1002886//EST//3.2e-85:401:99//Hs.96580:AA405670
R-HEMBA1002460//Catalase//0.67:314:60//Hs.76359:X04085	R-HEMBA1002896//Homo sapiens SH3-containing adaptor molecule-1 mRNA, complete cds//1.2e-107:541:95//Hs.33787:AF037261
R-HEMBA1002462//EST//0.032:44:88//Hs.161536:N80395	R-HEMBA1002921//Human mRNA for KIAA0189 gene, complete cds//0.84:103:71//Hs.95140:D80011
R-HEMBA1002475//ESTs. Weakly similar to F08G12.1 [C.elegans]//5.4e-95:488:95//Hs.108115:AA582193	R-HEMBA1002924//ESTs//3.5e-86:423:98//Hs.27513:N34820
R-HEMBA1002477//Homo sapiens KIAA0395 mRNA, partial cds//2.5e-37:281:80//Hs.43681:AL022394	R-HEMBA1002934//Human mRNA for KIAA0118 gene, partial cds//2.1e-50:308:88//Hs.154326:D42087
R-HEMBA1002486//Small inducible cytokine A5 (RANTES)//1.1e-49:311:88//Hs.155464:AF088219	R-HEMBA1002935//ESTs//1.0e-73:384:95//Hs.118193:N74481
R-HEMBA1002495//ESTs//1.2e-94:457:98//Hs.42140:A1188995	R-HEMBA1002937//ESTs//0.052:167:65//Hs.145504:A1254165
R-HEMBA1002498//ESTs//1.7e-35:240:78//Hs.119871:AA705133	R-HEMBA1002939//ESTs//1.6e-94:467:97//Hs.9893:AA007679
R-HEMBA1002503//ESTs//2.3e-14:64:85//Hs.140190:AA701449	R-HEMBA1002944//ESTs//2.7e-17:176:80//Hs.143768:AA229732
R-HEMBA1002508//ESTs//0.00057:160:62//Hs.149661:AA872990	R-HEMBA1002951//ESTs//3.7e-119:565:98//Hs.16218:A1190892
R-HEMBA1002513//Homo sapiens mRNA for histone deacetylase-like protein (JM21)//2.3e-113:456:92//Hs.6764:AJ011972	R-HEMBA1002954//EST//0.076:285:58//Hs.98706:AA431085
R-HEMBA1002515//EST//1.0:153:63//Hs.118045:N51715	R-HEMBA1002968//Thiopurine S-methyltransferase//1.9e-46:314:85//Hs.51124:AF019369
R-HEMBA1002538//Homo sapiens mRNA for KIAA0454 protein, partial cds//5.1e-106:564:93//Hs.129928:AB007923	R-HEMBA1002970//EST//0.00050:164:64//Hs.129630:A1000405
R-HEMBA1002547//ESTs//1.0e-101:539:93//Hs.93872:AA524700	R-HEMBA1002971//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.3e-30:162:99//Hs.5734:AB014579
R-HEMBA1002547//EST//8.7e-27:151:96//Hs.132145:A1041804	R-HEMBA1002973//Small inducible cytokine A5 (RANTES)//5.7e-42:318:81//Hs.155464:AF088219
R-HEMBA1002552//EST//5.9e-49:335:85//Hs.149580:A1281881	R-HEMBA1002997//ESTs//3.2e-18:102:100//Hs.146255:AA197064
R-HEMBA1002555//ESTs//1.1e-77:461:91//Hs.38750:N30012	R-HEMBA1002999//ESTs. Moderately similar to lamina associated polypeptide 1C [R.norvegicus]//1.9e-113:560:96//Hs.125749:A1377682
R-HEMBA1002558//Homo sapiens 4F55 mRNA, complete cds//1.3e-42:264:89//Hs.32567:AF073519	R-HEMBA1003021//Homo sapiens PYRIN (NEFV) mRNA, complete cds//3.3e-42:290:85//Hs.113283:AF018080
R-HEMBA1002561//Small inducible cytokine A5 (RANTES)//6.4e-40:196:78//Hs.155464:AF088219	R-HEMBA1003033//ESTs//2.8e-77:417:94//Hs.138860:W47480
R-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds//1.4e-120:587:97//Hs.151411:AF075587	R-HEMBA1003034//ESTs//3.7e-42:429:74//Hs.132818:A1038577
R-HEMBA1002583//ESTs//7.1e-79:410:95//Hs.21599:AA478904	R-HEMBA1003035//ESTs//0.025:156:64//Hs.8473:T40827
R-HEMBA1002590//EST//3.3e-54:278:97//Hs.138637:N20838	R-HEMBA1003037//ESTs//0.69:381:57//Hs.47312:A1240366
R-HEMBA1002592//ESTs//2.6e-44:500:74//Hs.110934:N26055	R-HEMBA1003041//ESTs. Highly similar to PUTATIVE SERINE/THREONINE-PROTEIN KINASE C41C.4 IN CHROMOSOME II PRECURSOR [Caenorhabditis elegans]//5.6e-34:280:79//Hs.114905:AA088442
R-HEMBA1002621	R-HEMBA1003046//Homo sapiens mitochondrial processing peptidase beta-subunit mRNA, complete cds//1.3e-119:578:97//Hs.44097:AF054182
R-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds//2.2e-77:380:97//Hs.91338:AB018351	R-HEMBA1003064//ESTs//7.8e-85:419:96//Hs.87020:AA706627
R-HEMBA1002628//ESTs//0.0020:167:66//Hs.140605:AA830881	R-HEMBA1003067//Von Hippel-Lindau syndrome//2.0e-30:299:75//Hs.78160:AF010238
R-HEMBA1002629//ESTs//0.00014:50:100//Hs.119132:AA398715	R-HEMBA1003071//ESTs//2.3e-74:360:98//Hs.17270:AA701903
R-HEMBA1002645//EST//2.1e-37:285:82//Hs.141728:W73041	R-HEMBA1003077//ESTs. Weakly similar to KIAA0405 [H.sapiens]//1.1e-90:434:99//Hs.14146:W92235
R-HEMBA1002651//EST//2.2e-23:374:69//Hs.139357:AA420970	R-HEMBA1003078//ESTs//5.9e-16:156:77//Hs.142684:AA902402
R-HEMBA1002659//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.5e-53:406:81//Hs.108966:U48696	R-HEMBA1003079//ESTs//0.16:341:58//Hs.95923:A1075249
R-HEMBA1002661//Homo sapiens mRNA for KIAA0764 protein, complete cds//1.1e-41:296:84//Hs.6232:AB018307	R-HEMBA1003083//Small inducible cytokine A5 (RANTES)//1.9e-39:284:83//Hs.155464:AF088219
R-HEMBA1002666//EST//4.4e-09:79:88//Hs.72015:AA151945	R-HEMBA1003086//EST//1.0e-48:372:82//Hs.161917:AA483223
R-HEMBA1002678//EST. Moderately similar to !!!! ALU SUBFAMILY J WARMING ENTRY !!!! [H.sapiens]//7.6e-104:560:92//Hs.161748:T64896	R-HEMBA1003096//ESTs. Weakly similar to Mouse 19.5 mRNA, complete cds [M.musculus]//4.2e-100:531:94//Hs.104800:AA709155
R-HEMBA1002679//EST//0.15:136:69//Hs.129570:AA995396	R-HEMBA1003098//ESTs//4.2e-107:537:96//Hs.107213:AA121624
R-HEMBA1002688//T-CELL SURFACE PROTEIN TACTILE PRECURSOR//0.16:247:62//Hs.142023:M88282	R-HEMBA1003117//ESTs//2.4e-67:331:97//Hs.157158:A1150058
R-HEMBA1002696//ESTs//3.5e-94:529:92//Hs.16725:AA196477	R-HEMBA1003129//Human nucleolar fibrillar center protein (ASE-1) mRNA, complete cds//2.1e-13:109:88//Hs.118717:U86751
R-HEMBA1002712//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.0e-46:302:86//Hs.15519:AB018315	R-HEMBA1003133//ESTs//1.1e-34:180:98//Hs.159387:A1370845
R-HEMBA1002716//ESTs//1.3e-109:555:96//Hs.9812:AA147884	R-HEMBA1003136//ESTs. Weakly similar to MANNOSE-1-PHOSPHATE GUANYL TRANSFERASE [Saccharomyces cerevisiae]//9.2e-114:577:95//Hs.27059:A1088615
R-HEMBA1002728//Homo sapiens mRNA for KIAA0621 protein, partial cds//3.8e-37:287:81//Hs.132942:AB014521	R-HEMBA1003142//Small inducible cytokine A5 (RANTES)//1.1e-45:285:88//Hs.155464:AF088219
R-HEMBA1002730//ESTs//1.2e-95:488:95//Hs.22030:AA521168	R-HEMBA1003148//Homo sapiens mRNA for dachshund protein//3.6e-118:586:96//Hs.63931:AJ005670
R-HEMBA1002742//ESTs//1.0e-91:437:99//Hs.139987:AA652163	R-HEMBA1003166//ESTs//1.6e-96:479:96//Hs.119940:AA705933
R-HEMBA1002746//ESTs//4.4e-97:468:98//Hs.129903:AA576526	R-HEMBA1003175//ESTs//2.7e-74:407:92//Hs.139167:AA715389
R-HEMBA1002748//ESTs//5.0e-98:475:98//Hs.125461:A1375792	R-HEMBA1003197//ESTs//1.6e-68:384:94//Hs.120969:W92000
R-HEMBA1002750//ESTs//1.6e-42:223:97//Hs.40460:N36090	R-HEMBA1003199//Sjogren syndrome antigen B (autoantigen La)//0.19:328:57//Hs.83715:X69804
R-HEMBA1002768//Homo sapiens mRNA for KIAA0554 protein, partial cds//4.0e-106:545:95//Hs.74750:AB011126	R-HEMBA1003202//Homo sapiens mRNA for KIAA0640 protein, partial cds//1.3e-40:290:83//Hs.153026:AB014540
R-HEMBA1002770//EST//0.34:294:59//Hs.43091:N22127	R-HEMBA1003204//ESTs//1.1e-34:215:91//Hs.108090:AA424943
R-HEMBA1002777//ESTs//3.0e-85:316:98//Hs.17537:C06491	R-HEMBA1003212//ESTs//1.9e-81:441:93//Hs.28471:W20265
R-HEMBA1002779//Human mRNA for KIAA0013 gene, complete cds//0.25:342:58//Hs.48824:D87717	R-HEMBA1003220//ESTs. Weakly similar to MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S28 PRECURSOR [S.cerevisiae]//1.6e-40:232:93//Hs.107707:N32817
R-HEMBA1002780//Homo sapiens DEC-205 mRNA, complete cds//4.2e-46:449:75//Hs.153563:AF011333	R-HEMBA1003222//ESTs. Weakly similar to weak similarity to HSP90 [C.elegans]//1.1e-42:310:85//Hs.23294:W27666
R-HEMBA1002794//ESTs//1.2e-115:559:97//Hs.79741:A1279709	R-HEMBA1003229//ESTs//4.8e-18:133:90//Hs.61763:AA035305
R-HEMBA1002801//EST//0.00049:287:60//Hs.126466:AA913320	R-HEMBA1003235//ESTs//7.7e-35:201:78//Hs.163979:AA828834
R-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds//1.4e-116:559:97//Hs.28307:AF071185	R-HEMBA1003250//Homo sapiens p21-activated kinase 3 (PAK3) mRNA, complete cds//7.4e-05:534:58//Hs.152663:AF068864
R-HEMBA1002816//Human plectin (PLEC1) mRNA, complete cds//0.28:281:62//Hs.79706:U53204	R-HEMBA1003257//EST//1.4e-95:473:97//Hs.32443:H28929
R-HEMBA1002826//EST//6.7e-25:134:99//Hs.134683:A1092013	
R-HEMBA1002833//ESTs. Highly similar to ribosome-binding protein p34 [R.norvegicus]//4.3e-25:137:98//Hs.5337:AA243757	
R-HEMBA1002850//ESTs//0.010:323:57//Hs.18282:W67514	
R-HEMBA1002863//EST//1.1e-67:359:94//Hs.124699:W27830	

【0903】

【表601】

R-HEMBA1003273//Small inducible cytokine A5 (RANTES)//2.6e-38:253:86//Hs.155464:AF088219	R-HEMBA1003680//Human DNA-binding protein (HRC1) mRNA, complete cds//0.86:315:61//Hs.72925:M91083
R-HEMBA1003276//ESTs//7.6e-55:269:99//Hs.23817:AA526392	R-HEMBA1003684//ESTs, Highly similar to ZINC FINGER PROTEIN 7 [Homo sapiens]//1.1e-101:528:95//Hs.22934:AA581379
R-HEMBA1003278//ESTs//2.6e-45:301:71//Hs.51652:AI084785	R-HEMBA1003690//ESTs//0.0021:119:69//Hs.98641:AA429916
R-HEMBA1003281	R-HEMBA1003692//Human cytochrome P450-11B (h11B3) mRNA, complete cds//2.0e-43:360:80//Hs.110194:M29873
R-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds//9.7e-117:551:99//Hs.12836:AB011109	R-HEMBA1003711//ESTs//1.0e-70:375:94//Hs.150407:AI279054
R-HEMBA1003296//ESTs//4.8e-17:210:72//Hs.44451:AA203266	R-HEMBA1003714//VASOACTIVE INTESTINAL POLYPEPTIDE RECEPTOR 1 PRECURSOR//0.94:367:62//Hs.1139:X77777
R-HEMBA1003304//ESTs//2.8e-98:468:98//Hs.120849:AI148353	R-HEMBA1003715//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.1e-77:299:85//Hs.113283:AF018080
R-HEMBA1003309//ESTs//1.8e-97:455:99//Hs.11571:AA713504	R-HEMBA1003720//Homo sapiens TWIK-related acid-sensitive K ⁺ channel 1 (TASK) mRNA, complete cds//1.2e-33:377:74//Hs.24040:AF006823
R-HEMBA1003314//Homo sapiens mRNA for leucine zipper bearing kinase, complete cds//8.9e-113:545:97//Hs.124224:AB001872	R-HEMBA1003725//ESTs//3.8e-103:481:99//Hs.122518:AA778847
R-HEMBA1003322//ESTs//4.9e-79:419:95//Hs.138760:N66869	R-HEMBA1003729//ESTs//2.5e-51:277:95//Hs.26270:AA258839
R-HEMBA1003327//Homo sapiens clone 23622 mRNA sequence//1.4e-16:177:78//Hs.151608:AF052119	R-HEMBA1003733//ESTs//1.9e-69:350:96//Hs.139278:AA702592
R-HEMBA1003328//H. sapiens mRNA for MACH-alpha-2 protein//2.1e-43:269:88//Hs.19949:X98173	R-HEMBA1003742//ESTs, Moderately similar to T13H5.2 [C.elegans]//4.6e-70:348:96//Hs.11282:AI147040
R-HEMBA1003330//Homo sapiens poly(A) binding protein II (PABP2) gene, complete cds//0.66:64:76//Hs.117176:AF026029	R-HEMBA1003758//ESTs//1.7e-52:306:85//Hs.138852:AA284247
R-HEMBA1003348//ESTs//1.4e-35:185:78//Hs.117879:H77357	R-HEMBA1003760//ESTs//7.4e-76:420:93//Hs.26501:H05089
R-HEMBA1003369//ESTs, Weakly similar to F59C6.9 [C.elegans]//3.2e-113:553:97//Hs.65539:AI148540	R-HEMBA1003773//ESTs, Highly similar to SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT [Mus musculus]//1.9e-77:364:100//Hs.12152:AA156214
R-HEMBA1003370//ESTs//2.0e-46:319:86//Hs.37573:H59651	R-HEMBA1003783//ESTs, Weakly similar to COIH6.7 [C.elegans]//2.1e-101:558:93//Hs.18171:AA524327
R-HEMBA1003373//ESTs//1.6e-31:136:81//Hs.114849:AI139588	R-HEMBA1003784//EST//0.83:127:62//Hs.144002:F01600
R-HEMBA1003376//ESTs//3.0e-47:383:80//Hs.138852:AA284247	R-HEMBA1003799//EST//9.7e-30:362:71//Hs.156577:AA860236
R-HEMBA1003380//ESTs, Moderately similar to !!!! ALU SUBFAMILY J W ARNING ENTRY !!!! [H. sapiens]//1.8e-11:261:65//Hs.87578:AI125363	R-HEMBA1003803//ESTs, Weakly similar to Y53C12A.3 [C.elegans]//2.8e-16:93:100//Hs.107747:AI357868
R-HEMBA1003384//EST//0.00013:82:75//Hs.141237:H57847	R-HEMBA1003804//Interleukin 15//0.13:227:62//Hs.111867:AB007295
R-HEMBA1003395//ESTs//5.2e-78:379:98//Hs.162208:AA536127	R-HEMBA1003805//ESTs//0.029:199:65//Hs.91582:T25344
R-HEMBA1003402//ESTs//8.6e-14:108:89//Hs.55424:AA774204	R-HEMBA1003807//EST//2.4e-13:137:81//Hs.145645:AI264163
R-HEMBA1003408//ESTs//1.7e-24:188:85//Hs.70266:Z78309	R-HEMBA1003836//Small inducible cytokine A5 (RANTES)//3.2e-39:284:83//Hs.155464:AF088219
R-HEMBA1003417//ESTs//4.2e-74:396:94//Hs.55220:O11563	R-HEMBA1003838//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 [Paramecium tetraurelia]//6.5e-71:357:96//Hs.107573:AA524333
R-HEMBA1003418//ESTs//3.1e-107:545:95//Hs.3494:AI421013	R-HEMBA1003856//ESTs//8.2e-20:266:71//Hs.48312:N68161
R-HEMBA1003433//Homo sapiens nibrin (NBS) mRNA, complete cds//3.2e-115:544:98//Hs.25812:AF058696	R-HEMBA1003864//ESTs//1.6e-99:528:93//Hs.26890:AA449033
R-HEMBA1003461//ESTs//2.8e-62:304:99//Hs.148747:AI225121	R-HEMBA1003866//POLYPOSIS LOCUS PROTEIN 1//0.30:146:64//Hs.74648:M73547
R-HEMBA1003463//ESTs//2.3e-112:549:97//Hs.104627:AA855516	R-HEMBA1003879//EST, Weakly similar to DNA-REPAIR PROTEIN COMPLEMENTING XP-A CELLS [Homo sapiens]//2.1e-59:295:98//Hs.161661:AA166911
R-HEMBA1003480//Homo sapiens PYRIN (MEFV) mRNA, complete cds//7.7e-76:529:84//Hs.113283:AF018080	R-HEMBA1003880//Homo sapiens clone 24760 mRNA sequence//3.8e-34:286:79//Hs.61408:AF070621
R-HEMBA1003528//ESTs//2.1e-59:312:96//Hs.22505:R41688	R-HEMBA1003885//ESTs//4.6e-50:293:90//Hs.142314:AA347930
R-HEMBA1003531//ESTs//2.2e-17:116:93//Hs.140217:AA702760	R-HEMBA1003893//Calcium modulating ligand//2.1e-43:294:86//Hs.13572:AF068179
R-HEMBA1003538//Complement component C1r//4.7e-25:333:68//Hs.1279:MI4058	R-HEMBA1003902//ESTs//1.8e-43:300:85//Hs.146811:AA410788
R-HEMBA1003545//ESTs//8.7e-89:432:98//Hs.99497:AA776817	R-HEMBA1003908//ESTs//3.5e-91:477:94//Hs.6638:AA536187
R-HEMBA1003548//EST//0.0091:274:60//Hs.148336:AA911673	R-HEMBA1003926//ESTs//7.9e-44:294:87//Hs.164036:AA845659
R-HEMBA1003555//ESTs, Weakly similar to NUCLEOTIDE-BINDING PROTEIN 1 [H. sapiens]//2.8e-93:495:93//Hs.91619:AA552351	R-HEMBA1003937//Homo sapiens mRNA for KIAA0585 protein, partial cds//3.5e-48:276:81//Hs.72660:AB011157
R-HEMBA1003556//ESTs//7.1e-44:406:77//Hs.141575:AA211734	R-HEMBA1003939
R-HEMBA1003560//ESTs//4.0e-34:182:97//Hs.14811:AA434522	R-HEMBA1003942//ESTs//1.6e-81:428:94//Hs.50418:AA524669
R-HEMBA1003568//ESTs//2.0e-101:486:98//Hs.118570:AI342058	R-HEMBA1003950//ESTs//8.1e-54:283:95//Hs.145528:AI261545
R-HEMBA1003569//ESTs, Moderately similar to metastasis-associated gene [H. sapiens]//4.0e-63:343:93//Hs.58598:AA625440	R-HEMBA1003953//ESTs//3.8e-30:194:89//Hs.99681:AA504591
R-HEMBA1003571//Homo sapiens clone 23632 mRNA sequence//3.7e-47:338:84//Hs.46918:AF052099	R-HEMBA1003958//ESTs//4.0e-45:394:77//Hs.141602:N63562
R-HEMBA1003579//EST//0.00057:239:60//Hs.162828:AA643892	R-HEMBA1003959//ESTs//5.2e-28:197:86//Hs.9951:W56253
R-HEMBA1003581//ESTs//2.6e-10:118:79//Hs.44856:N37065	R-HEMBA1003976//ESTs//2.0e-29:232:84//Hs.133947:AI074525
R-HEMBA1003591//ESTs//2.4e-96:460:98//Hs.128741:AI244212	R-HEMBA1003978//ESTs//3.2e-115:549:98//Hs.76798:AI050882
R-HEMBA1003595//Human mRNA for KIAA0118 gene, partial cds//1.7e-48:421:78//Hs.154326:D42087	R-HEMBA1003985//ESTs, Weakly similar to !!!! ALU SUBFAMILY J W ARNING ENTRY !!!! [H. sapiens]//2.2e-91:448:97//Hs.117834:AA766771
R-HEMBA1003597//EST//1.6e-38:313:80//Hs.160911:AI371042	R-HEMBA1003987//ESTs//8.1e-36:193:88//Hs.151844:N92756
R-HEMBA1003598//ESTs//0.0085:273:61//Hs.145333:AI251374	R-HEMBA1003989//Human mRNA for KIAA0241 gene, partial cds//3.6e-43:360:81//Hs.150275:D87682
R-HEMBA1003615	R-HEMBA1004000//EST//5.5e-62:308:97//Hs.50438:N74105
R-HEMBA1003617//ESTs//1.0e-111:574:95//Hs.4552:W68167	R-HEMBA1004011//ESTs//8.6e-85:431:96//Hs.36185:R99899
R-HEMBA1003621//EST//1.7e-31:288:78//Hs.140909:R49387	R-HEMBA1004012//ESTs//1.3e-40:309:83//Hs.140329:AA714011
R-HEMBA1003622//EST//1.1e-46:468:75//Hs.139093:AA166888	R-HEMBA1004015//ESTs//5.1e-97:453:99//Hs.111446:AI333774
R-HEMBA1003630//ESTs//1.4e-21:411:69//Hs.128729:AA973021	R-HEMBA1004024//ESTs//5.2e-19:159:79//Hs.138856:H47461
R-HEMBA1003637//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB W ARNING ENTRY !!!! [H. sapiens]//9.3e-24:189:84//Hs.142208:AA209438	R-HEMBA1004038//ESTs//1.3e-41:346:79//Hs.146173:AA906191
R-HEMBA1003640//ISLET AMYLOID POLYPEPTIDE PRECURSOR//2.5e-42:332:81//Hs.51048:X68830	R-HEMBA1004042//ESTs//0.0012:201:69//Hs.24248:AA528253
R-HEMBA1003645//ESTs//2.4e-77:423:94//Hs.99539:R59010	R-HEMBA1004045//ESTs, Weakly similar to putative p150 [H. sapiens]//1.5e-22:365:70//Hs.99692:AA811804
R-HEMBA1003646//ESTs//2.6e-98:549:91//Hs.96427:AA151783	R-HEMBA1004048//ESTs//9.5e-104:497:98//Hs.77735:AI125469
R-HEMBA1003656//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//5.6e-44:245:77//Hs.67619:AB007957	R-HEMBA1004049//HEAT SHOCK 70 KD PROTEIN 1//6.3e-31:176:96//Hs.8997:MI1717
R-HEMBA1003662//Human TBX2 (TBX2) mRNA, complete cds//2.6e-17:144:84//Hs.32931:U28049	
R-HEMBA1003667//Farnesyltransferase, CAAX box, beta//1.3e-22:170:88//Hs.117596:L00635	
R-HEMBA1003679//ESTs, Weakly similar to trithorax homolog HTX, version 2 [H. sapiens]//4.1e-87:434:97//Hs.9489:R84329	

【0904】

【表602】

R-HENBA1004055//ESTs//1.7e-115:577:96//Hs.59503:W63754	R-HENBA1004433//Human Line-1 repeat mRNA with 2 open reading frame s//2.9e-32:463:68//Hs.23094:M19503
R-HENBA1004056//Homo sapiens PYRIN (MEFY) mRNA, complete cds//5.2e-78:577:82//Hs.113283:AF018080	R-HENBA1004460//ESTs//2.0e-104:574:93//Hs.46848:AA195829
R-HENBA1004074//EST//1.0:152:61//Hs.149093:A1243988	R-HENBA1004461//ESTs//2.9e-102:503:98//Hs.16370:AA017033
R-HENBA1004086//ESTs//4.0e-53:266:98//Hs.34658:N98652	R-HENBA1004479//ELK1, member of ETS oncogene family//1.1e-45:310:75//Hs.116549:AL009172
R-HENBA1004097//ESTs//4.4e-46:279:91//Hs.110533:H16251	R-HENBA1004482//ESTs//9.1e-05:322:62//Hs.34489:AA759306
R-HENBA1004131//Human mRNA for KIAA0128 gene, partial cds//3.0e-43:534:69//Hs.90998:O50918	R-HENBA1004502//ESTs//6.9e-112:566:96//Hs.93985:N50034
R-HENBA1004132//ESTs//4.6e-47:316:86//Hs.141602:N63562	R-HENBA1004506//EST//5.3e-59:456:80//Hs.72412:AA160941
R-HENBA1004133	R-HENBA1004507
R-HENBA1004138//EST//1.7e-08:211:64//Hs.129189:AA988736	R-HENBA1004509//ESTs, Moderately similar to HYPOTHETICAL 52.2 KD PROTEIN IN MPRI-GCM20 INTERGENIC REGION [Saccharomyces cerevisiae]//2.9e-82:262:99//Hs.12820:AA004271
R-HENBA1004143//ESTs//4.0e-25:137:97//Hs.21307:AA203320	R-HENBA1004534//ESTs, Highly similar to ENDOTHELIAL ACTIN-BINDING PROTEIN [Homo sapiens]//1.1e-43:281:89//Hs.58414:AA196947
R-HENBA1004146//Small inducible cytokine A5 (RANTES)//4.1e-27:191:86//Hs.155464:AF088219	R-HENBA1004538//EST//3.3e-15:270:71//Hs.136667:AA707972
R-HENBA1004150//GRANULOCYTOGENESIS//0.99:357:59//Hs.79381:M81637	R-HENBA1004554
R-HENBA1004164//Human mRNA for KIAA0118 gene, partial cds//9.5e-47:313:84//Hs.154326:D42087	R-HENBA1004560//ESTs//8.2e-25:179:88//Hs.96560:W22924
R-HENBA1004168//Homo sapiens geminin mRNA, complete cds//7.7e-112:563:95//Hs.59988:AF067855	R-HENBA1004573//ESTs, Moderately similar to ALR [H.sapiens]//1.0:305:60//Hs.30272:AA134913
R-HENBA1004199	R-HENBA1004577//ESTs//7.9e-50:319:89//Hs.22660:AA582243
R-HENBA1004200//EST//3.1e-89:441:97//Hs.141173:R97701	R-HENBA1004586//ESTs//2.6e-73:384:96//Hs.9582:R39769
R-HENBA1004202//ESTs, Weakly similar to GTP-BINDING PROTEIN YPTM1 [Zea mays]//1.7e-107:552:94//Hs.10092:A1189282	R-HENBA1004596//ESTs//6.0e-22:190:82//Hs.42530:NA1661
R-HENBA1004203//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.5e-96:275:98//Hs.15832:AB014518	R-HENBA1004610//ESTs//1.2e-91:438:98//Hs.47823:AA780767
R-HENBA1004207//Leptin receptor//1.1e-117:573:97//Hs.54515:U50748	R-HENBA1004617//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//4.6e-52:327:85//Hs.159897:AB007970
R-HENBA1004225//EST//9.7e-34:186:95//Hs.137567:R20617	R-HENBA1004629//ESTs//2.3e-19:215:76//Hs.111995:A1375915
R-HENBA1004227//ESTs, Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]//4.0e-16:117:91//Hs.92033:AA255832	R-HENBA1004631//ESTs//3.6e-99:470:98//Hs.49303:AA810785
R-HENBA1004238//Human mRNA for KIAA0355 gene, complete cds//3.0e-46:338:83//Hs.153014:AB002353	R-HENBA1004632//ESTs//1.0:128:66//Hs.159182:AA831152
R-HENBA1004241//ESTs//1.3e-10:93:87//Hs.137511:AA456389	R-HENBA1004637//ESTs, Highly similar to HYPOTHETICAL 83.6 KD PROT EIN ROS3.2 IN CHROMOSOME III [Caenorhabditis elegans]//4.8e-111:532:98//Hs.12263:AA282393
R-HENBA1004246//Homo sapiens LIM protein mRNA, complete cds//2.7e-43:511:72//Hs.154103:AF061258	R-HENBA1004638//ESTs//1.2e-66:341:95//Hs.122687:A1278454
R-HENBA1004248//ESTs, Highly similar to INSULIN-INDUCED GROWTH RESPONSE PROTEIN CL-6 [Rattus norvegicus]//2.1e-61:221:86//Hs.7089:W37284	R-HENBA1004666//ESTs//2.1e-65:333:96//Hs.98873:AA625442
R-HENBA1004264//ESTs//1.5e-80:425:95//Hs.107206:AA234962	R-HENBA1004669//ESTs//0.00039:116:74//Hs.138725:N76348
R-HENBA1004267//ESTs, Moderately similar to !!! ALU SUBFAMILY SP WARNING ENTRY !!! [H.sapiens]//1.4e-89:465:95//Hs.113660:D20018	R-HENBA1004670//ESTs//1.7e-16:116:89//Hs.56825:A1057560
R-HENBA1004272//ESTs//4.5e-111:577:94//Hs.115696:N57931	R-HENBA1004672//EST//6.7e-76:315:97//Hs.20821:R19368
R-HENBA1004275//Homo sapiens clone 617 unknown mRNA, complete sequence//1.4e-111:553:96//Hs.93677:AF091081	R-HENBA1004693//ESTs//6.4e-68:327:99//Hs.159066:A1093252
R-HENBA1004276//ESTs, Highly similar to BETA-ADAPTIN [Homo sapiens; Rattus norvegicus; Bos taurus]//4.4e-92:559:89//Hs.28298:AA203228	R-HENBA1004697//ESTs//9.3e-98:467:98//Hs.62637:AA043562
R-HENBA1004286//Homo sapiens TGF beta receptor associated protein-1 mRNA, complete cds//6.2e-108:538:97//Hs.101766:AF022795	R-HENBA1004705//EST//0.0034:271:58//Hs.112503:AA599042
R-HENBA1004289//Sulfolipase, dehydroepiandrosterone (DHEA) -p referring//1.7e-34:223:75//Hs.81884:U13061	R-HENBA1004709//EST//1.3e-55:392:85//Hs.149580:A1281881
R-HENBA1004295//ESTs, Weakly similar to weakly similar to ANK repeat region of Fowlpox virus BamHI-ori7 protein [C.elegans]//3.6e-93:496:94//Hs.14337:AA534961	R-HENBA1004711//Small inducible cytokine A5 (RANTES)//1.9e-47:449:76//Hs.155464:AF088219
R-HENBA1004306//ESTs//3.4e-26:363:68//Hs.70279:AA757426	R-HENBA1004725//EST//1.8e-71:424:88//Hs.155712:A1309235
R-HENBA1004312//ESTs//4.8e-64:351:94//Hs.138611:H82679	R-HENBA1004730//Homo sapiens clone 23892 mRNA sequence//2.1e-44:467:73//Hs.91916:AF035317
R-HENBA1004321//Zinc finger protein 44 (KIX 7)//2.6e-37:415:64//Hs.51199:X16281	R-HENBA1004733//EST//0.99:84:65//Hs.161372:A1423151
R-HENBA1004323//ESTs//2.1e-40:280:70//Hs.153300:AA928904	R-HENBA1004734//ESTs//1.8e-82:421:96//Hs.21275:N73275
R-HENBA1004327//ESTs//3.8e-72:343:99//Hs.151708:AA554714	R-HENBA1004736//Ataxia telangiectasia mutated (includes complementation groups A, C and D)//9.5e-39:296:82//Hs.51187:U82828
R-HENBA1004330//ESTs//4.0e-52:270:97//Hs.24654:AA456561	R-HENBA1004748//ESTs//1.7e-43:166:86//Hs.37573:H59651
R-HENBA1004334//ESTs//1.6e-46:234:98//Hs.47159:A1310231	R-HENBA1004751//ESTs//8.0e-23:155:88//Hs.149464:A1279428
R-HENBA1004335//ESTs//1.9e-25:250:76//Hs.155880:AA703336	R-HENBA1004752//Thromboxane A2 receptor//2.7e-45:281:89//Hs.89887:D38081
R-HENBA1004341//ESTs//3.7e-101:480:98//Hs.69321:AA633240	R-HENBA1004753//40S RIBOSOMAL PROTEIN S20//8.3e-67:475:84//Hs.8102:L06498
R-HENBA1004353//Homo sapiens mRNA for c-myc binding protein, complete cds//1.3e-75:444:90//Hs.80686:D89667	R-HENBA1004756//ESTs//2.0e-81:384:99//Hs.129545:N68679
R-HENBA1004354//Human mRNA for KIAA0355 gene, complete cds//5.9e-39:286:83//Hs.153014:AB002353	R-HENBA1004758//EST//2.0e-43:367:80//Hs.133006:A1049504
R-HENBA1004356//SINGLE-STRANDED DNA-BINDING PROTEIN MSSP-1//1.3e-107:576:93//Hs.55458:X77494	R-HENBA1004763//ESTs//2.0e-108:567:94//Hs.3757:W87380
R-HENBA1004366//ESTs//2.3e-94:524:91//Hs.111496:AA652869	R-HENBA1004768//ESTs, Weakly similar to RETROVIRUS-RELATED POL YPROTEIN [Mus musculus]//1.4e-47:379:81//Hs.141273:H66705
R-HENBA1004372//EST//0.27:198:60//Hs.162665:AA605057	R-HENBA1004770//ESTs//0.0014:246:61//Hs.124857:AA687092
R-HENBA1004389//ESTs//4.1e-102:490:98//Hs.153708:AA687264	R-HENBA1004771//ESTs//1.1e-12:323:63//Hs.124146:AA699633
R-HENBA1004394//ESTs//1.5e-94:471:96//Hs.151647:AA002084	R-HENBA1004776//ESTs//2.5e-112:567:95//Hs.12680:W74476
R-HENBA1004396//Small inducible cytokine A5 (RANTES)//6.2e-41:285:83//Hs.155464:AF088219	R-HENBA1004778//ESTs//1.4e-33:272:75//Hs.141123:AA848167
R-HENBA1004405//ESTs//2.0e-44:329:83//Hs.136839:H93717	R-HENBA1004795
R-HENBA1004408//ESTs, Weakly similar to homologous to mouse Rsu-1 [H.sapiens]//6.1e-89:420:99//Hs.88365:AA648933	R-HENBA1004803//ESTs//1.0e-48:319:86//Hs.139231:W87732
R-HENBA1004429//ESTs, Weakly similar to homeotic protein protein z-hx-1 [M.musculus]//3.0e-112:552:96//Hs.12940:A1123518	R-HENBA1004806
	R-HENBA1004807//ESTs//6.2e-77:362:100//Hs.140945:AA47676
	R-HENBA1004816//EST//4.3e-18:246:72//Hs.150552:A1053784
	R-HENBA1004820//Human arginine-rich nuclear protein mRNA, complete cds//5.0e-14:141:85//Hs.80510:W74002
	R-HENBA1004847
	R-HENBA1004850//ESTs//1.2e-83:395:99//Hs.30925:AA577120
	R-HENBA1004863//ESTs//7.5e-21:204:79//Hs.35036:H95267
	R-HENBA1004864
	R-HENBA1004865//EST//6.7e-18:191:75//Hs.129944:AA429362
	R-HENBA1004880//EST//4.4e-70:346:98//Hs.145094:AA452409
	R-HENBA1004889//ESTs//4.8e-117:496:97//Hs.15641:W63676
	R-HENBA1004900//ESTs//1.2e-15:283:68//Hs.157606:A1357470

【0905】

【表603】

R-HEMBA1004909//ESTs//7.3e-44:366.79//Hs.140329:AA714011	/Hs.83733:X15606
R-HEMBA1004918//Human mRNA for KIAA0392 gene, partial cds//4.6e-5	R-HEMBA1005353//ESTs//1.7e-81:406.96//Hs.155374:A1341467
0:313.89//Hs.40100:AB002390	R-HEMBA1005359//Homo sapiens neuronal thread protein AD7c-NTP mRNA
R-HEMBA1004923//ESTs//0.013:162.64//Hs.143655:A1128388	A, complete cds//4.7e-46:294.81//Hs.129735:AF010144
R-HEMBA1004929//EST//2.3e-48:250.97//Hs.131589:A1025053	R-HEMBA1005367//Alcohol dehydrogenase 2 (class I), beta polypeptid
R-HEMBA1004930//Cytochrome P450, subfamily I (aromatic compound-in	e//1.0:210.62//Hs.4.X03350
ducible), polypeptide 2//1.2e-70:547.80//Hs.1361:M55053	R-HEMBA1005372//ESTs//5.2e-95:451.99//Hs.135219:A1091653
R-HEMBA1004933//ESTs, Weakly similar to R06C7.6 [C.elegans]//5.3e-	R-HEMBA1005374//ESTs//1.5e-107:502.99//Hs.118208:AA947305
110:530.98//Hs.18029:A1422883	R-HEMBA1005389//Fc fragment of IgA, receptor for//1.0e-39:311.80//
R-HEMBA1004934//ESTs//1.3e-103:522.96//Hs.40415:AA037215	Hs.54486:X54150
R-HEMBA1004944//ESTs//6.0e-21:97.84//Hs.141973:M21434	R-HEMBA1005394//ESTs, Weakly similar to coded for by C. elegans cD
R-HEMBA1004954//ESTs//7.9e-112:596.93//Hs.6225:W61007	NA yk30b3.5 [C.elegans]//4.0e-88:489.92//Hs.43864:AA131568
R-HEMBA1004956//ESTs//3.1e-58:280.100//Hs.120750:AA741074	R-HEMBA1005403//EST//0.0011:78.75//Hs.127061:AA863278
R-HEMBA1004960//ESTs//6.9e-89:476.93//Hs.163738:AA601040	R-HEMBA1005408//ESTs//3.2e-29:395.71//Hs.117532:AA676725
R-HEMBA1004972//ESTs//3.0e-72:381.95//Hs.55014:AA934035	R-HEMBA1005410//ESTs//1.5e-18:271.70//Hs.144604:A1052059
R-HEMBA1004973//ESTs//2.7e-91:441.98//Hs.28144:A1292065	R-HEMBA1005411//ESTs//1.1e-35:335.77//Hs.141181:R98757
R-HEMBA1004977//ESTs//2.0e-95:446.99//Hs.29690:A1168404	R-HEMBA1005423//Homo sapiens cyclin-dependent kinase inhibitor (CD
R-HEMBA1004978//Homo sapiens natural killer cell group 2-F (NKG2-F)	KN2C) mRNA, complete cds//1.8e-118:453.99//Hs.4854:AF041248
mRNA, complete cds//0.43:187.67//Hs.129734:A1001683	R-HEMBA1005426//Chromosome 1 specific transcript KIAA0491//0.25:26
R-HEMBA1004980//Human mRNA for KIAA0331 gene, complete cds//6.4e-5	4:61//Hs.136309:AB007960
3:305.91//Hs.146395:AB002329	R-HEMBA1005443//Homo sapiens (clone s153) mRNA fragment//1.7e-47:3
R-HEMBA1004983//ESTs//0.16:482.57//Hs.131929:A1021894	05:87//Hs.6445:L40391
R-HEMBA1004995	R-HEMBA1005447//ESTs//5.7e-83:529.86//Hs.114253:AA745961
R-HEMBA1005008//EST, Weakly similar to mariner transposase [H.sapi	R-HEMBA1005468//ESTs//7.3e-23:249.73//Hs.61199:AA024494
ens]//6.9e-51:482.78//Hs.141601:M63520	R-HEMBA1005469//Human mRNA for KIAA0355 gene, complete cds//4.5e-4
R-HEMBA1005009//ESTs, Highly similar to ACTIN 1 [Naegleria fowler	5:320.85//Hs.153014:AB002353
i]//3.8e-109:551.96//Hs.103180:A1365212	R-HEMBA1005472//Human knpi repeat mRNA (cdna clone pcd-knpi-8), 3'
R-HEMBA1005019//Homo sapiens mRNA for KIAA0648 protein, partial cd	end//8.4e-73:464.87//Hs.103948:X00627
s//2.0e-105:542.94//Hs.31921:AB014548	R-HEMBA1005475//ESTs//0.32:192.59//Hs.62694:AA100445
R-HEMBA1005029//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTA	R-HEMBA1005497
SE HOMOLOG [Homo sapiens]//7.4e-95:491.94//Hs.16085:A1261382	R-HEMBA1005500//ESTs//2.2e-43:307.85//Hs.146811:AA410788
R-HEMBA1005035//Human mRNA for KIAA0033 gene, partial cds//2.3e-6	R-HEMBA1005506//75 kDa infertility-related sperm protein [human, t
4:312.85//Hs.22271:D26067	estis, mRNA Partial, 2427 nt]//0.11:295.60//Hs.62608:S58544
R-HEMBA1005039//ESTs, Weakly similar to zinc finger protein [H.sap	R-HEMBA1005508//ESTs//2.8e-55:319.93//Hs.50150:N90870
iens]//2.6e-48:443.78//Hs.139019:M99348	R-HEMBA1005511//ESTs, Weakly similar to similar to mouse MMR1 [C.e
R-HEMBA1005047//ESTs, Highly similar to RAS-RELATED PROTEIN RAB-5	legans]//2.6e-82:387.99//Hs.67466:A1219740
A [Canis familiaris]//1.2e-87:542.87//Hs.16258:A1376436	R-HEMBA1005517//ESTs//4.6e-77:469.90//Hs.126787:AA203322
R-HEMBA1005050//ESTs//6.3e-46:311.86//Hs.159510:AA297145	R-HEMBA1005518//ESTs//1.5e-108:561.94//Hs.123167:AA601045
R-HEMBA1005062//ESTs//1.1e-14:216.58//Hs.129935:AA994451	R-HEMBA1005520//Putative mismatch repair/binding protein hMSH3//7.
R-HEMBA1005066//Human clone 23574 mRNA sequence//2.2e-24:303.73//H	5e-44:179.84//Hs.42674:U61981
s.79385:U90905	R-HEMBA1005526//ESTs//8.7e-46:308.86//Hs.146811:AA410788
R-HEMBA1005075//EST//0.65:214.62//Hs.133991:A1075789	R-HEMBA1005528//ESTs, Highly similar to POP2 PROTEIN [Saccharomyc
R-HEMBA1005079//Human BENE mRNA, partial cds//1.9e-44:304.83//Hs.8	es cerevisiae]//8.6e-115:578.95//Hs.17035:A1080471
5889:U17077	R-HEMBA1005530//ESTs//1.5e-110:551.96//Hs.107294:W72350
R-HEMBA1005083//ESTs//2.6e-74:356.98//Hs.132272:A139358	R-HEMBA1005548//ESTs//1.7e-100:510.96//Hs.9115:N90926
R-HEMBA1005101//Homo sapiens SYT interacting protein SIP mRNA, com	R-HEMBA1005552//Interleukin 10//2.4e-38:306.80//Hs.2180:M57627
plete cds//1.7e-111:545.96//Hs.11170:AF080561	R-HEMBA1005558//ESTs, Weakly similar to unknown [S.cerevisiae]//5.
R-HEMBA1005113//ESTs//1.1e-101:512.95//Hs.7972:A1052739	3e-77:439.91//Hs.22897:R43193
R-HEMBA1005123//Ley 1-L//3.6e-58:519.77//Hs.37062:AC005952	R-HEMBA1005568//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARN1
R-HEMBA1005133//H.sapiens mRNA for MACH-alpha-2 protein//8.3e-46:3	NG ENTRY !!!! [H.sapiens]//3.4e-31:182.76//Hs.133526:N21103
09:85//Hs.19949:X98173	R-HEMBA1005570//ESTs//3.3e-67:411.88//Hs.142245:AA489709
R-HEMBA1005149//Homo sapiens mRNA, chromosome 1 specific transcrip	R-HEMBA1005576//EST//0.91:52.73//Hs.149518:A1280497
t KIAA0488//4.7e-36:394.75//Hs.67619:AB007957	R-HEMBA1005577
R-HEMBA1005152//Homo sapiens antigen NY-CO-16 mRNA, complete cds//	R-HEMBA1005581//Homo sapiens mRNA for MEGF5, partial cds//3.1e-28:
3.6e-32:362.77//Hs.132206:AF039694	561.64//Hs.57929:AB011538
R-HEMBA1005159//EST//7.4e-47:252.94//Hs.134930:A1093397	R-HEMBA1005582//ESTs//6.0e-73:371.97//Hs.103758:C06392
R-HEMBA1005185//ESTs//5.2e-48:305.89//Hs.14920:AA910914	R-HEMBA1005583//ESTs//8.3e-79:413.95//Hs.62348:AA419539
R-HEMBA1005201//ESTs//4.7e-58:293.97//Hs.23752:C05766	R-HEMBA1005588//Human c-yes-1 mRNA//2.6e-52:403.83//Hs.75680:M1599
R-HEMBA1005202//ESTs//1.0:169.59//Hs.153423:A1198239	0
R-HEMBA1005219//Homo sapiens putative tumor suppressor protein (12	R-HEMBA1005593//ESTs//3.3e-30:139.80//Hs.142273:W37905
3F2) mRNA, complete cds//0.84:191.61//Hs.26931:AF061836	R-HEMBA1005595//ESTs//1.1e-97:454.100//Hs.27497:A1274820
R-HEMBA1005223//ESTs//0.75:90.70//Hs.127446:AA167284	R-HEMBA1005606//EST//1.0e-12:313.64//Hs.162402:AA573125
R-HEMBA1005232//EST//0.056:162.67//Hs.65649:F13687	R-HEMBA1005609//ESTs//0.49:278.58//Hs.76235:W56390
R-HEMBA1005241//ESTs//3.6e-113:564.96//Hs.12770:W84331	R-HEMBA1005616//EST//1.3e-98:470.99//Hs.122230:AA781422
R-HEMBA1005244//ESTs//6.4e-22:118.100//Hs.21396:AA114834	R-HEMBA1005621//ESTs, Weakly similar to MITOTIC MAD2 PROTEIN [S.ce
R-HEMBA1005251//ESTs//8.5e-36:213.92//Hs.161554:AA393896	revisiae]//2.8e-95:539.92//Hs.19400:AA662845
R-HEMBA1005252//Homo sapiens mRNA for KIAA0585 protein, partial cd	R-HEMBA1005627//Human mRNAs for adipogenesis inhibitory factor//5.5
s//6.1e-49:277.93//Hs.72660:AB011157	e-38:317.78//Hs.1721:X58377
R-HEMBA1005274//ESTs//3.7e-65:322.98//Hs.105166:AA668862	R-HEMBA1005631//Human mRNA for KIAA0393 gene, complete cds//2.3e-1
R-HEMBA1005275//ESTs//2.1e-29:298.73//Hs.33393:R83391	1:279.65//Hs.15245:AF041081
R-HEMBA1005293//ESTs//3.5e-93:448.98//Hs.12066:A1208611	R-HEMBA1005632//EST//1.5e-10:181.70//Hs.120259:AA731522
R-HEMBA1005296//ESTs//4.3e-33:168.100//Hs.13916:A1025750	R-HEMBA1005634//Homo sapiens mRNA for chemokine LEC precursor, com
R-HEMBA1005304//Small inducible cytokine A5 (RANTES)//2.8e-50:315:	plete cds//1.4e-25:234.80//Hs.10458:AF088219
82//Hs.155464:AF088219	R-HEMBA1005666//ESTs//2.3e-103:534.95//Hs.14512:AA205973
R-HEMBA1005311//Homo sapiens 4F5S mRNA, complete cds//1.3e-44:318:	R-HEMBA1005670//ESTs//2.6e-39:166.81//Hs.139414:A1279477
83//Hs.32567:AF073519	R-HEMBA1005679//Esterase D/formylglutathione hydrolase//1.3e-50:32
R-HEMBA1005314//ESTs//3.0e-103:491.98//Hs.41606:A1095046	2:88//Hs.82193:M13450
R-HEMBA1005315//EST//1.9e-29:370.72//Hs.161483:N59169	R-HEMBA1005680//Homo sapiens LIM protein mRNA, complete cds//3.3e-
R-HEMBA1005318//ESTs//3.9e-110:535.97//Hs.26771:AA126472	43:343.81//Hs.154103:AF061258
R-HEMBA1005331//Interleukin adhesion molecule 2//7.6e-39:256.87/	R-HEMBA1005685//Human homeodomain protein (Prox 1) mRNA, complete

【0906】

【表604】

cds//D.0050:235:64//Hs.159437:U44060	A-BINDING PROTEIN NAB2 [S.cerevisiae]//1.6e-66:377:91//Hs.108674:W25821
R-HEMBA1005699//Human putative EPH-related PTK receptor ligand LER K-8 (Eplg8) mRNA, complete cds//1.7e-47:376:84//Hs.26988:U66406	R-HEMBA1006284//ESTs//3.7e-110:544:96//Hs.55296:A1084735
R-HEMBA1005705//ESTs//3.0e-53:259:99//Hs.55314:AA772055	R-HEMBA1006291//ESTs//2.2e-91:457:96//Hs.114611:N37019
R-HEMBA1005717//EST//2.5e-59:287:99//Hs.146870:A1159943	R-HEMBA1006293//ESTs//5.4e-78:370:99//Hs.155111:A1202037
R-HEMBA1005732//Homo sapiens mRNA for cartilage-associated protein (CASP)//1.2e-45:398:79//Hs.155481:AJ006470	R-HEMBA1006309//ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN//3.7e-40:167:86//Hs.74478:U33931
R-HEMBA1005737//ESTs//2.5e-57:416:83//Hs.23245:AA053815	R-HEMBA1006310//ESTs, Weakly similar to reverse transcriptase [M. musculus]//5.6e-76:417:94//Hs.111754:A1204587
R-HEMBA1005746//EST//0.098:125:68//Hs.136945:AA765672	R-HEMBA1006328//Small inducible cytokine A5 (RANTES)//2.8e-60:397:78//Hs.155464:AF088219
R-HEMBA1005755//EST//2.2e-22:180:84//Hs.141488:N47096	R-HEMBA1006334//Human occludin mRNA, complete cds//0.72:369:59//Hs.93518:U49184
R-HEMBA1005765//Human peptide transporter (HPEPT1) mRNA, complete cds//3.9e-47:404:80//Hs.2217:U21936	R-HEMBA1006344//Human plectin (PLEC1) mRNA, complete cds//0.016:217:64//Hs.79705:U53204
R-HEMBA1005780//ESTs//1.3e-106:512:97//Hs.11901:AA173974	R-HEMBA1006347//ESTs, Highly similar to HYPOTHETICAL 97.6 KD PROT EIN IN SHP1-SEC17 INTERGENIC REGION [Saccharomyces cerevisiae]//3.6e-119:582:97//Hs.42343:A1417075
R-HEMBA1005813//Homo sapiens mRNA for chemokine LEC precursor, complete cds//2.0e-33:195:84//Hs.10458:AF088219	R-HEMBA1006349//ESTs//5.2e-57:305:94//Hs.6338:AA411382
R-HEMBA1005815//ESTs//7.6e-19:290:71//Hs.112218:A1038601	R-HEMBA1006359//ESTs//8.2e-90:426:99//Hs.100873:AA678008
R-HEMBA1005822//ESTs//5.4e-49:246:98//Hs.34804:AA514960	R-HEMBA1006364//ESTs//2.2e-98:582:91//Hs.23837:AA541787
R-HEMBA1005829//ESTs//2.7e-72:344:99//Hs.54548:A1039201	R-HEMBA1006377//EST//0.0097:145:62//Hs.133027:A1049830
R-HEMBA1005834//ESTs//1.6e-44:317:82//Hs.157029:A1080618	R-HEMBA1006380//Homo sapiens mRNA for KIAA0594 protein, partial cds//1.0e-41:349:79//Hs.154872:AB011166
R-HEMBA1005852//ESTs//1.6e-102:544:93//Hs.9911:AA098911	R-HEMBA1006381//ESTs//5.1e-46:320:85//Hs.37573:HS9651
R-HEMBA1005853//ESTs//1.8e-78:398:95//Hs.140248:AA757917	R-HEMBA1006398//Human Line-1 repeat mRNA with 2 open reading frame s//9.0e-87:582:84//Hs.23094:W19503
R-HEMBA1005884//EST//2.6e-18:275:67//Hs.139357:AA420970	R-HEMBA1006416//ESTs//1.5e-17:251:73//Hs.33950:A1218923
R-HEMBA1005891//ESTs//2.1e-89:427:98//Hs.67317:A1022252	R-HEMBA1006419//EST//8.5e-65:353:94//Hs.141309:H72778
R-HEMBA1005894	R-HEMBA1006421//Oxytocin receptor//1.2e-12:249:68//Hs.2820:X64878
R-HEMBA1005909//ESTs//2.6e-91:436:99//Hs.147492:A1215686	R-HEMBA1006424//ESTs, Weakly similar to pot. ORF II [H.sapiens]//6.3e-13:263:66//Hs.43127:AA258004
R-HEMBA1005911//ESTs//1.1e-85:446:95//Hs.134494:A1076363	R-HEMBA1006426//ESTs//6.5e-84:401:99//Hs.37303:C16964
R-HEMBA1005921//ESTs//1.4e-84:428:95//Hs.127993:AA970632	R-HEMBA1006438//EST//0.87:266:57//Hs.99456:AA457380
R-HEMBA1005931//Homo sapiens mRNA for KIAA0526 protein, complete cds//9.5e-45:446:75//Hs.59403:AB011098	R-HEMBA1006445//ESTs//2.0e-81:414:96//Hs.58153:W72033
R-HEMBA1005934//ESTs//0.20:142:65//Hs.97079:AA370867	R-HEMBA1006446//Homo sapiens mRNA for cadherin-6, complete cds//1.6e-05:487:58//Hs.32963:D31784
R-HEMBA1005962//ESTs//1.8e-87:409:100//Hs.161292:A1199418	R-HEMBA1006461//ESTs//5.1e-78:393:97//Hs.142677:R95895
R-HEMBA1005963	R-HEMBA1006467//ESTs, Weakly similar to putative p150 [H.sapiens]//3.0e-17:342:63//Hs.111730:AA604403
R-HEMBA1005990//Homo sapiens l-1 receptor candidate protein mRNA, complete cds//2.2e-113:580:95//Hs.26285:AF082516	R-HEMBA1006471//ESTs//3.8e-66:370:92//Hs.14063:T77441
R-HEMBA1005991//Human antisecretory factor-1 mRNA, complete cds//2.0e-45:551:70//Hs.148495:AF050199	R-HEMBA1006474
R-HEMBA1005999//ESTs//7.5e-24:201:69//Hs.157029:A1080618	R-HEMBA1006483//Human G protein-coupled receptor (STRL22) mRNA, complete cds//4.2e-40:365:78//Hs.46468:U45984
R-HEMBA1006002//ESTs//3.1e-112:573:95//Hs.61233:A1379875	R-HEMBA1006485//H.sapiens mRNA for aminopeptidase//2.5e-92:517:91//Hs.132243:Y07701
R-HEMBA1006005//EST//1.0:105:63//Hs.145273:A1249436	R-HEMBA1006486//EST//7.0e-47:240:76//Hs.161917:AA483223
R-HEMBA1006031//Homo sapiens mRNA for KIAA0725 protein, partial cds//2.4e-28:444:67//Hs.26450:AB018268	R-HEMBA1006489//ESTs//2.1e-93:440:99//Hs.125264:AA873350
R-HEMBA1006035//ESTs//4.5e-94:465:97//Hs.44625:N49951	R-HEMBA1006492//ESTs//0.0034:52:90//Hs.163219:AA810720
R-HEMBA1006036//ESTs//6.1e-90:420:100//Hs.126771:AA916508	R-HEMBA1006494//EST//1.8e-06:192:67//Hs.141401:H93387
R-HEMBA1006042//EST//1.5e-88:424:98//Hs.132551:AA948490	R-HEMBA1006497//ESTs//6.2e-45:232:97//Hs.118015:N33117
R-HEMBA1006067	R-HEMBA1006502//Complement component 5 receptor 1 (C5a ligand)//8.7e-16:135:72//Hs.2161:M62505
R-HEMBA1006081//ESTs//7.8e-68:356:95//Hs.27410:N25612	R-HEMBA1006507//Homo sapiens mRNA for KIAA0666 protein, partial cds//3.9e-117:570:96//Hs.153858:AB014566
R-HEMBA1006090//ESTs//5.1e-66:320:99//Hs.99551:AA461517	R-HEMBA1006521//ESTs//9.9e-99:496:96//Hs.64906:AA677300
R-HEMBA1006091//ESTs//2.0e-84:441:94//Hs.9658:AA506313	R-HEMBA1006530//ESTs//0.18:260:60//Hs.24970:A1057628
R-HEMBA1006100//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//3.4e-43:328:82//Hs.73614:U83460	R-HEMBA1006535//GS1 PROTEIN//0.52:267:62//Hs.78991:M86934
R-HEMBA1006108//ESTs//1.5e-44:228:98//Hs.26368:AA789297	R-HEMBA1006540//EST//0.016:143:66//Hs.148189:AA897331
R-HEMBA1006121//ESTs//1.6e-116:547:99//Hs.34151:A1279293	R-HEMBA1006546//Homo sapiens mRNA for KIAA0582 protein, partial cds//2.2e-48:287:91//Hs.79507:AB011154
R-HEMBA1006124//EST//1.6e-20:286:64//Hs.148457:A1198931	R-HEMBA1006559//ESTs, Moderately similar to neurodegeneration-associated protein 1 [R.norvegicus]//1.8e-109:547:96//Hs.21122:AA191594
R-HEMBA1006130//ESTs//8.8e-47:231:99//Hs.16470:AA121635	R-HEMBA1006562//EST//1.1e-13:327:63//Hs.149641:A1283064
R-HEMBA1006138//Homo sapiens mRNA for KIAA0792 protein, complete cds//8.7e-27:296:73//Hs.119387:AB007958	R-HEMBA1006566//ESTs//2.6e-59:311:97//Hs.146014:R51876
R-HEMBA1006142//ESTs//1.5e-27:255:70//Hs.139507:T77542	R-HEMBA1006569//ESTs//4.7e-89:458:96//Hs.42861:W74725
R-HEMBA1006155//ESTs//4.9e-64:353:94//Hs.84560:R41212	R-HEMBA1006579//ESTs//2.9e-19:110:99//Hs.126191:AA873876
R-HEMBA1006158//Deoxyuridine triphosphatase//0.99:162:62//Hs.82113:U31930	R-HEMBA1006583//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//9.5e-29:276:76//Hs.144563:AF057280
R-HEMBA1006173//ESTs//7.5e-85:462:92//Hs.79092:H29627	R-HEMBA1006595//ESTs//1.3e-96:487:96//Hs.43228:N67390
R-HEMBA1006182//ESTs//5.5e-29:218:72//Hs.141466:H96906	R-HEMBA1006597//Small inducible cytokine A5 (RANTES)//9.8e-44:291:85//Hs.155464:AF088219
R-HEMBA1006198//ESTs//2.1e-34:282:82//Hs.142068:AA176125	R-HEMBA1006612
R-HEMBA1006235//Homo sapiens clone 24422 mRNA sequence//6.9e-112:545:97//Hs.109268:AF070557	R-HEMBA1006617//ESTs//1.2e-25:225:80//Hs.138852:AA284247
R-HEMBA1006248//ESTs, Highly similar to ZINC FINGER PROTEIN MFG1 [Mus musculus]//3.3e-114:581:95//Hs.23617:AA928683	R-HEMBA1006624//ESTs//1.9e-93:454:98//Hs.72531:AA773630
R-HEMBA1006252//Human mRNA for KIAA0080 gene, partial cds//7.0e-48:284:76//Hs.74554:D38522	R-HEMBA1006631//Human mRNA for KIAA0033 gene, partial cds//7.5e-60:286:90//Hs.22271:D26067
R-HEMBA1006253//Homo sapiens 45kDa splicing factor mRNA, complete cds//5.7e-30:179:91//Hs.15836:AF083384	R-HEMBA1006635//ESTs, Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//2.7e-91:426:100//Hs.139469:A129988
R-HEMBA1006259//Homo sapiens KIAA0421 mRNA, partial cds//1.5e-45:326:84//Hs.41742:AB007881	
R-HEMBA1006268//ESTs, Highly similar to c-Jun leucine zipper inter active [M.musculus]//1.2e-97:529:93//Hs.10552:AA524401	
R-HEMBA1006272//ESTs, Moderately similar to RETROVIRUS-RELATED PRO TEASE [H.sapiens]//2.7e-88:484:92//Hs.104129:AA923278	
R-HEMBA1006278//H.sapiens PAP mRNA//5.2e-56:585:71//Hs.49007:X76770	
R-HEMBA1006283//ESTs, Weakly similar to NUCLEAR POLYADENYLATED RN	

【0907】

【表605】

9	R-HEMBA1006639//ESTs, Highly similar to POLYADENYLATE-BINDING PROTEIN [Homo sapiens]//3.4e-37:186:100//Hs.109818:AA411185	R-HEMBA1007194//ESTs//9.0e-68:336:98//Hs.49760:AA741051
	R-HEMBA1006643//ESTs//1.8e-35:189:97//Hs.139640:AA846777	R-HEMBA1007203//Homo sapiens mRNA for KIAA0214 protein, complete cds//1.7e-62:332:95//Hs.3363:086987
	R-HEMBA1006648//Homo sapiens integrin-linked kinase (ILK) mRNA, complete cds//8.1e-108:567:94//Hs.6196:U40282	R-HEMBA1007205//Human c-yes-1 mRNA//4.5e-49:390:80//Hs.75680:M15990
	R-HEMBA1006652//ESTs//7.6e-100:536:93//Hs.142613:AA129427	R-HEMBA1007224//Homo sapiens mRNA for KIAA0797 protein, partial cds//7.4e-98:471:97//Hs.27197:AB018340
	R-HEMBA1006653//ESTs//2.0e-33:181:87//Hs.153599:AI282511	R-HEMBA1007251//ESTs//1.6e-78:377:99//Hs.98912:AA436864
	R-HEMBA1006665//EST//1.2e-13:141:72//Hs.145596:AI263102	R-HEMBA1007256//ESTs//3.5e-20:127:79//Hs.137352:AA024934
	R-HEMBA1006674//ESTs//3.3e-32:212:83//Hs.95115:AA206594	R-HEMBA1007267//Homo sapiens KIAA0395 mRNA, partial cds//8.8e-48:343:83//Hs.43681:AL022394
	R-HEMBA1006676//ESTs//2.6e-95:510:93//Hs.39140:AI041842	R-HEMBA1007273//ESTs//1.0e-98:472:98//Hs.122610:AA807062
	R-HEMBA1006682//EST//1.4e-05:277:62//Hs.145762:AI269435	R-HEMBA1007279//ESTs//3.3e-107:558:94//Hs.126480:AI221207
	R-HEMBA1006695//Homo sapiens apoptotic protease activating factor 1 (Apop-1) mRNA, complete cds//1.9e-32:261:79//Hs.77579:AF013263	R-HEMBA1007281//EST//0.074:244:63//Hs.29304:R73543
	R-HEMBA1006696//ESTs//4.5e-95:448:99//Hs.155694:AI032695	R-HEMBA1007288//EST//9.4e-43:344:81//Hs.162112:AA524804
	R-HEMBA1006708//ESTs, Weakly similar to Miller-Dieker lissencephaly gene [H. sapiens]//1.1e-92:483:94//Hs.6525:AI205313	R-HEMBA1007300//ESTs//0.096:371:57//Hs.102680:N52990
	R-HEMBA1006709//ESTs//3.4e-25:207:80//Hs.88617:AA872062	R-HEMBA1007301
	R-HEMBA1006717	R-HEMBA1007319//ESTs//7.7e-113:570:96//Hs.29263:AI337917
	R-HEMBA1006737//EST//5.9e-30:317:75//Hs.140568:AA826002	R-HEMBA1007320//ESTs, Moderately similar to hypothetical protein 2 [H. sapiens]//5.5e-15:311:64//Hs.142764:AA205569
	R-HEMBA1006744//Interleukin 10//3.7e-41:419:74//Hs.2180:M57627	R-HEMBA1007322//Human knp1 repeat mRNA (cdna clone pcd-knp1-4), 3' end//5.7e-49:383:83//Hs.139107:K00629
	R-HEMBA1006754//ESTs//1.2e-46:276:83//Hs.141254:AI334099	R-HEMBA1007327//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.9e-42:371:79//Hs.154069:U06452
	R-HEMBA1006758//ESTs//0.00043:48:100//Hs.157265:AA489646	R-HEMBA1007341//EST//3.0e-17:291:68//Hs.150788:AI301848
	R-HEMBA1006767//EST//0.094:120:65//Hs.159873:R92763	R-HEMBA1007342//EST//2.7e-11:263:67//Hs.145259:AI218684
	R-HEMBA1006779//EST//9.3e-45:298:85//Hs.149580:AI281881	R-HEMBA1007347//Homo sapiens DEC-205 mRNA, complete cds//9.7e-47:368:82//Hs.153563:AF011333
	R-HEMBA1006780//ESTs//1.6e-46:423:77//Hs.141602:N63562	R-HEMBA1000005//ESTs, Weakly similar to putative p150 [H. sapiens]//3.3e-44:341:71//Hs.111730:AA604403
	R-HEMBA1006789//ESTs//7.6e-55:245:95//Hs.6459:AI092936	R-HEMBA1000008//Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds//3.2e-40:292:83//Hs.129708:AF064090
	R-HEMBA1006795//ESTs//8.6e-47:315:78//Hs.140491:W52705	R-HEMBA1000018//H. sapiens mRNA for urea transporter//5.0e-49:311:87//Hs.66710:X96969
	R-HEMBA1006796//ESTs//0.26:175:65//Hs.103280:AI334978	R-HEMBA1000024//ESTs//7.5e-21:234:76//Hs.157049:AI345418
	R-HEMBA1006807//Homo sapiens DEC-205 mRNA, complete cds//5.7e-47:461:75//Hs.153563:AF011333	R-HEMBA1000025//ESTs//2.2e-36:371:78//Hs.56562:AA056332
	R-HEMBA1006821//ESTs//3.5e-12:222:68//Hs.150439:AI016305	R-HEMBA1000030//ESTs//3.2e-76:373:97//Hs.140190:AA701449
	R-HEMBA1006824//Homo sapiens mRNA, clone: RES4-16//6.7e-51:298:90//Hs.121493:D25272	R-HEMBA1000036//ESTs, Highly similar to HYPOTHETICAL 43.2 KD PROTEIN C34E10.1 IN CHROMOSOME III [Caenorhabditis elegans]//6.0e-92:477:95//Hs.4877:AA418465
	R-HEMBA1006832//ESTs//0.0050:108:70//Hs.12853:T65556	R-HEMBA1000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds//2.5e-92:467:97//Hs.20815:AF084928
	R-HEMBA1006849//Human mRNA for KIAA0118 gene, partial cds//2.1e-49:367:83//Hs.154326:D42087	R-HEMBA1000039//ESTs//1.8e-43:361:71//Hs.108206:N64702
	R-HEMBA1006865//ESTs//0.85:112:63//Hs.116430:AA644665	R-HEMBA1000044//EST//7.6e-70:367:95//Hs.140860:R42954
	R-HEMBA1006877//Homo sapiens mRNA for KIAA0772 protein, complete cds//1.8e-67:611:74//Hs.15519:AB018315	R-HEMBA1000048//EST//1.5e-45:262:91//Hs.157627:AI357802
	R-HEMBA1006885//ESTs//2.4e-66:347:96//Hs.100624:N95453	R-HEMBA1000050//ESTs//0.039:91:74//Hs.163189:AA236903
	R-HEMBA1006900//ESTs//2.7e-91:466:96//Hs.32984:R89739	R-HEMBA1000054//ESTs//3.0e-104:550:94//Hs.152395:AA533107
	R-HEMBA1006921//ESTs//2.2e-33:170:100//Hs.152277:AA593117	R-HEMBA1000055//ESTs, Moderately similar to UBIQUITIN-CYTOCHROME C REDUCTASE COMPLEX SUBUNIT VI REQUIRING PROTEIN [H. sapiens]//1.1e-72:350:99//Hs.116490:AA659584
	R-HEMBA1006926//ESTs, Weakly similar to ZK1053.6 [C. elegans]//2.9e-28:213:84//Hs.9096:AA029400	R-HEMBA1000059//ESTs//1.7e-10:200:70//Hs.163954:N57939
	R-HEMBA1006929//ESTs//4.0e-13:210:66//Hs.100895:AA479308	R-HEMBA1000083//Homo sapiens mRNA for GCP170, complete cds//6.0e-41:337:80//Hs.4953:D63997
	R-HEMBA1006936//ESTs//3.9e-05:60:93//Hs.8737:W22712	R-HEMBA1000089//Human mRNA for KIAA0355 gene, complete cds//3.5e-39:487:70//Hs.153014:AB002353
	R-HEMBA1006938//EST//0.0021:244:62//Hs.144237:W52382	R-HEMBA1000099//ESTs//5.7e-37:353:75//Hs.22910:W18193
	R-HEMBA1006941//Homo sapiens mRNA for putative thioredoxin-like protein//6.5e-77:371:98//Hs.42644:AJ010841	R-HEMBA1000103//Homo sapiens mRNA for KIAA0640 protein, partial cds//6.5e-18:298:69//Hs.153026:ABD14540
	R-HEMBA1006949//ESTs//1.2e-67:335:98//Hs.25780:R51321	R-HEMBA1000113//EST//8.2e-94:437:100//Hs.136893:AA805239
	R-HEMBA1006973//ESTs//0.029:242:61//Hs.146074:N34457	R-HEMBA1000119//Homo sapiens ASMTL gene//1.2e-84:428:95//Hs.6315:Y15521
	R-HEMBA1006976//EST//0.70:206:61//Hs.147092:AI189827	R-HEMBA1000136//ESTs//0.043:262:59//Hs.61304:AA025692
	R-HEMBA1006993//Human mRNA for KIAA0327 protein, complete cds//2.6e-47:368:80//Hs.149323:AB002325	R-HEMBA1000141//ESTs//5.0e-38:254:79//Hs.141658:N77915
	R-HEMBA1006996//ESTs//0.027:326:58//Hs.105008:AA451679	R-HEMBA1000144//ESTs//9.6e-05:235:60//Hs.61700:AA033951
	R-HEMBA1007002//ESTs//0.13:116:66//Hs.26928:Z41440	R-HEMBA1000173//EST//9.6e-44:258:76//Hs.161917:AA483223
	R-HEMBA1007017//ESTs//4.3e-47:208:87//Hs.155243:N70293	R-HEMBA1000175//ESTs//4.8e-98:475:97//Hs.149740:AI199558
	R-HEMBA1007018//ESTs, Moderately similar to LIC-2 [R. norvegicus]//2.8e-112:558:96//Hs.107905:AI248363	R-HEMBA1000198//ESTs//1.0:123:62//Hs.116602:AA665965
	R-HEMBA1007045	R-HEMBA1000215//Human mRNA for KIAA0355 gene, complete cds//2.2e-46:302:86//Hs.153014:AB002353
	R-HEMBA1007051//ESTs//2.5e-39:321:80//Hs.146811:AA410788	R-HEMBA1000217//ESTs//2.2e-105:496:99//Hs.65973:AI339364
	R-HEMBA1007052//EST//3.4e-41:377:74//Hs.44634:N34839	R-HEMBA1000218//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//1.1e-48:292:79//Hs.133089:AF064019
	R-HEMBA1007062//ESTs//1.2e-92:439:99//Hs.162882:AA807140	R-HEMBA1000226//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN B0495.8 IN CHROMOSOME II [C. elegans]//5.1e-73:449:89//Hs.16803:AA843214
	R-HEMBA1007066//ESTs//0.85:204:61//Hs.22795:AI208272	R-HEMBA1000240//ESTs//1.1e-109:536:97//Hs.13528:AA523106
	R-HEMBA1007073//ESTs//6.6e-52:362:85//Hs.30821:AI096866	R-HEMBA1000244//Small inducible cytokine A5 (RANTES)//9.5e-42:323:83//Hs.155464:AF088219
	R-HEMBA1007078//EST, Moderately similar to !!! ALU SUBFAMILY SQ W ARNING ENTRY !!!! [H. sapiens]//7.2e-40:163:83//Hs.152369:AA504818	R-HEMBA1000250//EST//8.8e-12:284:64//Hs.145960:AI276783
	R-HEMBA1007085//ESTs//8.1e-103:519:96//Hs.90638:AI348087	R-HEMBA1000258//EST//4.5e-14:315:66//Hs.162551:AA584782
	R-HEMBA1007087//ESTs//3.1e-51:354:86//Hs.6449:W95025	
	R-HEMBA1007112//EST//0.090:328:59//Hs.136623:AA633597	
	R-HEMBA1007113//Homo sapiens mRNA, clone: RES4-16//1.1e-47:427:76//Hs.121493:D25272	
	R-HEMBA1007129//ESTs//6.1e-13:314:65//Hs.137538:AA769438	
	R-HEMBA1007147	
	R-HEMBA1007149//ESTs//9.7e-103:540:94//Hs.127240:AA149818	
	R-HEMBA1007151//ESTs//8.2e-102:505:96//Hs.24948:AA977674	
	R-HEMBA1007174//Homo sapiens epsilon 2b mRNA, complete cds//1.6e-104:529:94//Hs.22396:AF062085	
	R-HEMBA1007178//ESTs//2.2e-57:366:90//Hs.21648:AI302954	

【0908】

【表606】

R-HEM8B1000264	4.0e-76:399:95//Hs.124106:AA948100
R-HEM8B1000266//ESTs, Weakly similar to similar to the beta transducin family [C.elegans]//2.7e-102:556:93//Hs.16079:AA083522	R-HEM8B1000652//ESTs//1.5e-14:271:64//Hs.163954:N57939
R-HEM8B1000272//ESTs//4.3e-91:480:94//Hs.107467:H11385	R-HEM8B1000665//ESTs//4.2e-12:109:87//Hs.41407:W94988
R-HEM8B1000274//Homo sapiens mRNA for KIAA0557 protein, partial cds//7.9e-24:198:72//Hs.101414:AB011129	R-HEM8B1000671//ESTs//2.8e-68:439:87//Hs.140491:W52705
R-HEM8B1000284//ESTs//4.8e-64:389:91//Hs.118043:N50458	R-HEM8B1000673//EST//0.58:46:82//Hs.142286:AA338293
R-HEM8B1000307//Human mRNA for KIAA0355 gene, complete cds//3.6e-43:288:87//Hs.153014:AB002353	R-HEM8B1000684//ESTs//8.5e-20:307:72//Hs.122825:AA765454
R-HEM8B1000312//ESTs//6.0e-23:272:73//Hs.121354:AA758601	R-HEM8B1000705//Small inducible cytokine A5 (RANTES)//4.6e-24:165:78//Hs.155464:AF088219
R-HEM8B1000317//ESTs//7.5e-90:424:99//Hs.150042:A1298034	R-HEM8B1000706//EST//1.2e-10:211:65//Hs.105524:AA521412
R-HEM8B1000318//Small inducible cytokine A5 (RANTES)//3.3e-41:318:80//Hs.155464:AF088219	R-HEM8B1000709//ESTs, Weakly similar to putative p150 [H.sapiens]//3.9e-50:245:99//Hs.111730:AA604403
R-HEM8B1000335//ESTs//3.7e-15:324:65//Hs.85077:AA968576	R-HEM8B1000725//Human mRNA for KIAA0308 gene, partial cds//0.11:350:59//Hs.10351:AB002306
R-HEM8B1000336//ESTs//6.4e-76:402:95//Hs.17207:H92480	R-HEM8B1000726//EST//5.3e-49:303:88//Hs.149580:A1281881
R-HEM8B1000337//EST//2.1e-80:391:97//Hs.118990:A1378084	R-HEM8B1000738//Homo sapiens mRNA, clone:RES4-16//2.5e-49:302:89//Hs.121493:D25272
R-HEM8B1000338//Small inducible cytokine A5 (RANTES)//4.0e-39:274:85//Hs.155464:AF088219	R-HEM8B1000749//ESTs//1.6e-49:331:86//Hs.152788:AA630925
R-HEM8B1000339//EST//5.8e-41:336:79//Hs.151873:AA205736	R-HEM8B1000763//ESTs//9.7e-104:474:95//Hs.77480:AA100522
R-HEM8B1000341//EST//3.8e-19:310:68//Hs.37573:H59651	R-HEM8B1000770//EST//1.0e-75:359:99//Hs.136564:AA642445
R-HEM8B1000343//EST//1.1e-77:396:95//Hs.162664:AA605020	R-HEM8B1000781//ESTs//5.3e-66:317:99//Hs.28827:A1125541
R-HEM8B1000354//Human mRNA for KIAA0186 gene, complete cds//1.7e-15:293:65//Hs.36232:D80008	R-HEM8B1000789//ESTs//5.9e-83:394:99//Hs.120842:AA435771
R-HEM8B1000369//ESTs//1.6e-21:234:73//Hs.111583:AA63590	R-HEM8B1000790//PLATELET GLYCOPROTEIN V PRECURSOR//1.3e-37:193:75//Hs.73734:Z23091
R-HEM8B1000374//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.3e-56:335:77//Hs.92381:AB007956	R-HEM8B1000794//ESTs//7.1e-98:490:96//Hs.105743:AA532718
R-HEM8B1000376//H.sapiens mRNA for urea transporter//2.7e-50:525:74//Hs.66710:X96969	R-HEM8B1000807//ESTs//2.6e-22:145:92//Hs.53913:AA908961
R-HEM8B1000391//ESTs//6.6e-50:316:88//Hs.142259:AA288840	R-HEM8B1000810//Small inducible cytokine A5 (RANTES)//1.8e-34:206:79//Hs.155464:AF088219
R-HEM8B1000399//Homo sapiens mRNA for cell cycle checkpoint protein//3.8e-109:531:97//Hs.16184:AJ001642	R-HEM8B1000821//ESTs//2.4e-90:425:99//Hs.118659:A1052447
R-HEM8B1000402//H.sapiens mRNA for MACH-alpha-2 protein//2.7e-35:369:72//Hs.19949:X98173	R-HEM8B1000822//ESTs//1.7e-45:288:89//Hs.24130:R27124
R-HEM8B1000404//ESTs//0.088:298:59//Hs.61607:AA032026	R-HEM8B1000826//Small inducible cytokine A5 (RANTES)//2.9e-51:245:82//Hs.155464:AF088219
R-HEM8B1000420//EST//2.2e-78:376:98//Hs.160787:A1336591	R-HEM8B1000827//EST//2.8e-40:295:84//Hs.149580:A1281881
R-HEM8B1000434//Human mRNA for KIAA0118 gene, partial cds//3.9e-50:302:89//Hs.154326:D42087	R-HEM8B1000831//ESTs//4.0e-59:291:98//Hs.62675:AA044176
R-HEM8B1000438//ESTs, Weakly similar to !!! ALU CLASS B WARNING ENTRY !!! [H.sapiens]//0.30:214:63//Hs.142209:AA873303	R-HEM8B1000835//ESTs//7.3e-21:124:82//Hs.102671:N52545
R-HEM8B1000441//Human c-yes-1 mRNA//2.2e-46:280:90//Hs.75680:M15990	R-HEM8B1000840//ATPase, Na+/K+ transporting, beta 2 polypeptide//1.3e-43:163:84//Hs.78854:AF007876
R-HEM8B1000449//ESTs//7.8e-59:332:92//Hs.87013:AA130221	R-HEM8B1000848//Homo sapiens mRNA for KIAA0565 protein, complete cds//9.5e-41:367:78//Hs.129740:AB011137
R-HEM8B1000455//EST//4.8e-14:421:65//Hs.68832:AA088438	R-HEM8B1000852//EST//1.2e-09:188:70//Hs.127869:AA968599
R-HEM8B1000472//ESTs//1.1e-104:505:98//Hs.132824:A1033396	R-HEM8B1000870//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase)//1.0e-41:483:73//Hs.2379:U23942
R-HEM8B1000480//Human mRNA for KIAA0392 gene, partial cds//2.5e-49:295:90//Hs.40100:AB002390	R-HEM8B1000876//EST//0.0022:211:63//Hs.125552:AA884141
R-HEM8B1000487//EST//0.78:18:150:82//Hs.142068:AA176125	R-HEM8B1000883//ESTs//1.4e-65:343:95//Hs.98269:H27247
R-HEM8B1000490//Small inducible cytokine A5 (RANTES)//4.0e-39:320:80//Hs.155464:AF088219	R-HEM8B1000887//ESTs//4.0e-22:212:79//Hs.138965:A1004740
R-HEM8B1000491//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.7e-50:312:76//Hs.113283:AF018080	R-HEM8B1000888//EST//8.2e-07:196:64//Hs.118276:W15258
R-HEM8B1000493//ESTs//7.1e-18:150:82//Hs.142068:AA176125	R-HEM8B1000890//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.1e-46:327:83//Hs.51048:X68830
R-HEM8B1000510//EST//1.4e-45:139:97//Hs.152260:AA489703	R-HEM8B1000893//EST//4.7e-34:242:85//Hs.149580:A1281881
R-HEM8B1000518//Human mRNA for KIAA0118 gene, partial cds//4.8e-50:415:78//Hs.154326:D42087	R-HEM8B1000908//EST//0.95:27:100//Hs.142568:AA285066
R-HEM8B1000523//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.7e-57:497:78//Hs.113283:AF018080	R-HEM8B1000910//ESTs//1.9e-36:318:78//Hs.141140:AA715983
R-HEM8B1000530//ESTs//2.7e-73:425:90//Hs.141254:A1334099	R-HEM8B1000913//Human mRNA for KIAA0327 protein, complete cds//2.5e-33:367:73//Hs.149323:AB002325
R-HEM8B1000550//EST//2.9e-11:113:79//Hs.161503:N68662	R-HEM8B1000915//ESTs//0.00018:188:61//Hs.144847:A1222742
R-HEM8B1000554//Human huntingtin interacting protein (HIP1) mRNA, complete cds//8.2e-13:92:81//Hs.97206:AF052288	R-HEM8B1000917//Homo sapiens KIAA0414 mRNA, partial cds//3.7e-41:228:84//Hs.127649:AB007874
R-HEM8B1000556//ESTs//1.1e-94:529:92//Hs.33476:N36986	R-HEM8B1000921//ESTs//2.2e-62:307:98//Hs.97044:AA365784
R-HEM8B1000564//ESTs//1.3e-19:128:91//Hs.142058:N34258	R-HEM8B1000947//ESTs, Weakly similar to F26E4.13 [C.elegans]//3.3e-60:350:91//Hs.49163:AA532881
R-HEM8B1000573//ESTs//1.6e-86:494:90//Hs.120979:A1160709	R-HEM8B1000959//Human Line-1 repeat mRNA with 2 open reading frames//8.1e-84:546:86//Hs.23094:M19503
R-HEM8B1000575//ESTs//1.6e-45:232:74//Hs.141019:AA287618	R-HEM8B1000973//ESTs//6.8e-95:445:99//Hs.105859:A1419354
R-HEM8B1000586//ESTs//5.1e-42:281:83//Hs.138852:AA284247	R-HEM8B1000975//ESTs//1.2e-39:197:100//Hs.26176:A1032007
R-HEM8B1000589//ESTs//1.0e-10:184:71//Hs.142677:R95895	R-HEM8B1000981//EST//7.7e-58:284:98//Hs.60179:AA007242
R-HEM8B1000591//ESTs//3.2e-40:406:75//Hs.138787:H73704	R-HEM8B1000985//ESTs//1.2e-103:524:95//Hs.43102:AA131369
R-HEM8B1000592//ESTs//1.8e-97:455:99//Hs.94229:W65391	R-HEM8B1000991//EST//0.99:58:72//Hs.100246:T23625
R-HEM8B1000598//Human antisecretory factor-1 mRNA, complete cds//1.8e-46:305:85//Hs.148495:AF050199	R-HEM8B1000996//Homo sapiens LIM protein mRNA, complete cds//1.3e-41:482:70//Hs.154103:AF061258
R-HEM8B1000623//ESTs//8.3e-47:277:92//Hs.6045:W67125	R-HEM8B1001004//ESTs//5.7e-70:362:95//Hs.6434:W27112
R-HEM8B1000630//ESTs//5.1e-106:538:96//Hs.13422:A1082249	R-HEM8B1001008//ESTs, Weakly similar to hypothetical L1 protein [H.sapiens]//2.3e-25:339:71//Hs.129992:H58762
R-HEM8B1000631//ESTs//5.1e-100:508:96//Hs.110379:N58152	R-HEM8B1001011//ESTs//4.0e-53:325:92//Hs.33268:A1191214
R-HEM8B1000632//ESTs//6.2e-44:371:80//Hs.132722:AA618531	R-HEM8B1001014//ESTs//1.3e-46:323:83//Hs.163980:AA715814
R-HEM8B1000637//Human mRNA for KIAA0800 gene, partial cds//6.4e-49:254:86//Hs.74554:D38522	R-HEM8B1001020//Homo sapiens PYRIN (MEFV) mRNA, complete cds//3.0e-46:305:76//Hs.113283:AF018080
R-HEM8B1000638//EST//2.2e-38:371:76//Hs.162236:AA551582	R-HEM8B1001024//ESTs//8.5e-47:374:80//Hs.141602:N63562
R-HEM8B1000643//ESTs//0.0049:191:62//Hs.55445:W31963	R-HEM8B1001037//ESTs//2.6e-47:282:91//Hs.155384:Z78385
R-HEM8B1000649//ESTs, Moderately similar to hTAF1168 [H.sapiens]//	R-HEM8B1001047//EST//6.2e-33:232:74//Hs.160146:A1049975
	R-HEM8B1001051//EST//3.7e-79:385:98//Hs.95290:AA046107

【0909】

【表607】

R-HEM81001056//Homo sapiens mRNA for KIAA0618 protein, complete cds//1.1e-87:497:91//Hs.15832:AB014518	0.88:365:58//Hs.389:X76342
R-HEM81001058//Homo sapiens mRNA for KIAA0475 protein, complete cds//2.2e-26:125:81//Hs.5737:AB007944	R-HEM81001424//ESTs//1.3e-88:466:94//Hs.42174:AA194644
R-HEM81001060//ESTs//1.9e-37:541:69//Hs.141534:N64785	R-HEM81001426//ESTs//2.2e-45:337:82//Hs.37573:H59651
R-HEM81001063//ESTs//4.4e-42:269:88//Hs.55855:AA621381	R-HEM81001429//ESTs//3.8e-59:543:76//Hs.158803:AI376846
R-HEM81001068//Homo sapiens liprin-beta2 mRNA, partial cds//9.1e-107:512:97//Hs.12953:AF034803	R-HEM81001436//ESTs//3.7e-69:332:99//Hs.156518:AA724317
R-HEM81001095//Human HsLIM15 mRNA for HsLIM15, complete cds//1.2e-20:233:70//Hs.37181:D64108	R-HEM81001443//ESTs//4.8e-54:270:98//Hs.21898:AI088201
R-HEM81001102//Human mRNA for KIAA0355 gene, complete cds//9.1e-40:299:82//Hs.153014:AB002353	R-HEM81001449//ESTs//3.2e-43:170:84//Hs.150727:AI292236
R-HEM81001105//Homo sapiens PYRIN (MEFV) mRNA, complete cds//4.8e-46:296:87//Hs.113283:AF018080	R-HEM81001454//ESTs//9.1e-46:304:86//Hs.139190:N55515
R-HEM81001114//ESTs//6.2e-44:293:86//Hs.70279:AA757426	R-HEM81001458//ESTs//3.2e-98:478:97//Hs.50144:N67293
R-HEM81001117//ESTs//1.1e-80:471:90//Hs.61935:T75092	R-HEM81001463//Homo sapiens KIAA0421 mRNA, partial cds//4.3e-50:440:78//Hs.41742:AB007881
R-HEM81001119//ESTs//4.0e-38:213:84//Hs.109140:AI289942	R-HEM81001464//ESTs, Weakly similar to K01H12.1 [C.elegans]//0.25:222:61//Hs.13275:AI341468
R-HEM81001126	R-HEM81001482//ESTs, Moderately similar to zinc finger protein [R.norvegicus]//0.8e-53:83//Hs.26799:W74481
R-HEM81001133//Human SS-A/Ro ribonucleoprotein autoantigen 60 kd subunit mRNA, complete cds//1.6e-24:285:73//Hs.554:M25077	R-HEM81001500//EST//1.4e-13:310:67//Hs.162663:AA604515
R-HEM81001137//ESTs//4.6e-10:66:100//Hs.74924:AI332962	R-HEM81001521//Homo sapiens mRNA for KIAA0737 protein, complete cds//2.5e-29:186:92//Hs.17630:AB018280
R-HEM81001142//EST//6.4e-48:315:85//Hs.149580:AI281881	R-HEM81001527//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//4.7e-51:404:81//Hs.141429:AA631915
R-HEM81001151	R-HEM81001531//ESTs//3.3e-13:250:67//Hs.139158:AA226159
R-HEM81001153//ESTs, Moderately similar to !!!! ALU SUBFAMILY J W ARNING ENTRY !!!! [H.sapiens]//1.3e-65:331:96//Hs.154179:AA579197	R-HEM81001535//H.sapiens mRNA for sigma 3B protein//1.9e-39:291:82//Hs.154782:X99459
R-HEM81001169//Oxytocin receptor//1.5e-25:165:73//Hs.2820:X64878	R-HEM81001536//Human mRNA for KIAA0355 gene, complete cds//5.0e-44:318:83//Hs.153014:AB002353
R-HEM81001175//ESTs//3.5e-41:233:93//Hs.129218:AA991162	R-HEM81001537//Homo sapiens KIAA0409 mRNA, partial cds//3.2e-47:318:80//Hs.5158:AB007869
R-HEM81001177	R-HEM81001555//ESTs//2.6e-13:182:71//Hs.112671:AI377274
R-HEM81001182//ESTs//1.9e-86:455:95//Hs.6937:AA524349	R-HEM81001562//ESTs//1.7e-43:316:83//Hs.151365:AA843962
R-HEM81001199	R-HEM81001564//EST//1.3e-35:141:81//Hs.162197:AA535216
R-HEM81001208//ESTs//3.3e-43:216:99//Hs.121806:N71183	R-HEM81001565//Human mRNA for KIAA0331 gene, complete cds//5.1e-18:152:85//Hs.146395:AB002329
R-HEM81001209//ESTs//6.7e-80:409:96//Hs.141185:R99549	R-HEM81001585//ESTs//1.1e-32:190:84//Hs.33354:AA179944
R-HEM81001210//ESTs//2.2e-46:290:88//Hs.103329:D11573	R-HEM81001586//ESTs//4.9e-94:447:99//Hs.124084:AA843219
R-HEM81001218//Kangai 1 (suppression of tumorigenicity 6, prostate; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclonal and antibody 1A4))//3.1e-44:298:87//Hs.103458:X53795	R-HEM81001588//EST//8.3e-27:363:69//Hs.141603:N66015
R-HEM81001221//ESTs//9.4e-75:353:100//Hs.151504:AA550817	R-HEM81001603//ESTs//1.2e-101:482:99//Hs.12403:AI090184
R-HEM81001234//ESTs, Highly similar to 65 KD YES-ASSOCIATED PROTEIN [Gallus gallus]//3.8e-80:400:96//Hs.71873:AA148213	R-HEM81001618//ESTs//5.8e-35:437:70//Hs.136868:AA805044
R-HEM81001242//ESTs//1.6e-63:404:87//Hs.25534:AA149560	R-HEM81001619//EST//1.7e-38:476:70//Hs.139093:AA166888
R-HEM81001249//ESTs//3.8e-34:360:70//Hs.150727:AI292236	R-HEM81001630//Homo sapiens mRNA, clone:RES4-16//5.7e-41:193:90//Hs.121493:D25272
R-HEM81001253//EST//0.0011:84:77//Hs.124579:AA853987	R-HEM81001635//ESTs//9.5e-34:304:82//Hs.140444:AI002082
R-HEM81001254//ESTs//4.5e-95:444:99//Hs.161059:AI431268	R-HEM81001637//ESTs//1.0e-42:443:74//Hs.21978:AA009633
R-HEM81001267//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//1.3e-50:524:73//Hs.159897:AB007970	R-HEM81001641//EST//2.4e-06:67:86//Hs.162398:AA527813
R-HEM81001271//Human mRNA for KIAA0118 gene, partial cds//4.0e-45:323:84//Hs.154326:D42087	R-HEM81001653//ESTs//4.8e-80:381:99//Hs.140502:AA06438
R-HEM81001282//EST//2.9e-78:401:96//Hs.72871:AA169412	R-HEM81001665//ESTs//2.3e-44:372:79//Hs.132818:AI038577
R-HEM81001288//ESTs, Highly similar to HYPOTHETICAL 27.3 KD PROTEIN ZK353.7 IN CHROMOSOME III [Caenorhabditis elegans]//2.6e-104:515:97//Hs.16606:W81021	R-HEM81001668//ESTs//0.73:212:62//Hs.8928:N32572
R-HEM81001289//ESTs//7.8e-45:440:75//Hs.44702:AI148840	R-HEM81001673//Homo sapiens mRNA for KIAA0646 protein, complete cds//5.9e-117:573:97//Hs.24439:AB014546
R-HEM81001294//ESTs//1.9e-100:476:99//Hs.109017:AI057112	R-HEM81001684//ESTs, Moderately similar to Tbc1 [M.musculus]//5.4e-106:523:97//Hs.26939:AA804534
R-HEM81001302	R-HEM81001685//ESTs, Moderately similar to !!!! ALU SUBFAMILY J W ARNING ENTRY !!!! [H.sapiens]//1.9e-43:292:86//Hs.96337:AA225358
R-HEM81001304//ESTs//4.0e-92:431:99//Hs.113750:AI091154	R-HEM81001695//ESTs//3.7e-101:539:94//Hs.78289:R60867
R-HEM81001314//Interleukin 10//6.3e-41:334:79//Hs.2180:M57627	R-HEM81001704//EST//0.96:248:57//Hs.163025:AA703038
R-HEM81001315//Interleukin 10//1.9e-43:285:87//Hs.2180:M57627	R-HEM81001706//ESTs//1.3e-39:308:81//Hs.141318:N71080
R-HEM81001317//Human cytochrome P450-11B (h11B3) mRNA, complete cds//8.4e-45:357:81//Hs.110194:M29873	R-HEM81001707//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.9e-32:277:73//Hs.142764:AA205569
R-HEM81001326//ESTs//0.85:174:62//Hs.133487:AI393754	R-HEM81001717//ESTs//1.6e-34:225:87//Hs.57883:AA218645
R-HEM81001331//ESTs, Weakly similar to DFS70 [H.sapiens]//6.5e-61:313:96//Hs.43071:AA206222	R-HEM81001735//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//8.6e-11:158:71//Hs.141263:H64113
R-HEM81001335//EST//5.2e-80:381:99//Hs.116769:AA630365	R-HEM81001736//ESTs//0.0035:223:60//Hs.21354:AA203403
R-HEM81001337//ESTs//2.7e-84:404:99//Hs.148966:AI242639	R-HEM81001747//EST//9.9e-55:293:81//Hs.112866:AA620488
R-HEM81001339//ESTs//2.1e-97:485:96//Hs.88357:AA262470	R-HEM81001749//ESTs//2.5e-13:95:91//Hs.139888:M25287
R-HEM81001346	R-HEM81001753//ESTs//2.6e-07:141:70//Hs.144604:AI052059
R-HEM81001348//ESTs//1.1e-43:295:85//Hs.163604:R94354	R-HEM81001756//EST//2.6e-06:165:64//Hs.121195:AA757211
R-HEM81001356//EST//6.0e-11:89:88//Hs.152366:AA486721	R-HEM81001760//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//1.3e-24:264:74//Hs.70008:L00352
R-HEM81001364//ESTs, Moderately similar to !!!! ALU SUBFAMILY J W ARNING ENTRY !!!! [H.sapiens]//3.0e-12:129:79//Hs.9792:AA027055	R-HEM81001762//ESTs//2.1e-81:447:93//Hs.152766:AA211369
R-HEM81001366//Human mRNA for KIAA0118 gene, partial cds//1.2e-50:550:72//Hs.154326:D42087	R-HEM81001785//ESTs//0.040:390:58//Hs.116651:AA993405
R-HEM81001367//ESTs//1.2e-19:165:82//Hs.146314:R99617	R-HEM81001797//ESTs//2.1e-90:428:99//Hs.8958:AA169253
R-HEM81001369//Small inducible cytokine A5 (RANTES)//1.9e-25:217:80//Hs.155464:AF088219	R-HEM81001802//Desain//9.9e-95:497:93//Hs.119104:M63391
R-HEM81001380//ESTs//4.0e-08:216:63//Hs.143763:AI174205	R-HEM81001812//ESTs//1.2e-12:91:78//Hs.138852:AA284247
R-HEM81001384//ESTs//6.6e-110:547:96//Hs.6671:AI341699	R-HEM81001816//Human Line-1 repeat mRNA with 2 open reading frames//5.9e-13:143:76//Hs.23094:M19503
R-HEM81001387//ESTs//1.1e-104:497:98//Hs.87654:AA853970	R-HEM81001831//Homo sapiens PAM COOH-terminal interactor protein 1 (PCIP1) mRNA, complete cds//5.5e-106:498:98//Hs.159396:AF056209
R-HEM81001394//ESTs//6.4e-73:428:89//Hs.139922:AA281350	R-HEM81001836//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//9.6e-39:288:73//Hs.67619:AB007957
R-HEM81001410//Alcohol dehydrogenase 7 sigma subunit (class IV)//	R-HEM81001839

【0910】

【表608】

R-HEM81001850//EST//0.020:119:68//Hs.32767:H38125	R-HEM81002280//EST//2.9e-41:247:90//Hs.161917:AA483223
R-HEM81001863//EST//4.5e-17:226:72//Hs.157253:AA357539	R-HEM81002300//ESTs//8.4e-19:229:75//Hs.138463:N72305
R-HEM81001867//ESTs//2.3e-16:254:68//Hs.123664:AA805106	R-HEM81002306//Homo sapiens KIAA0432 mRNA, complete cds//0.0021:138:67//Hs.155174:AB007892
R-HEM81001868//EST//9.8e-30:155:100//Hs.160572:AA888397	R-HEM81002327//EST//0.042:249:61//Hs.121097:AA714637
R-HEM81001869//ESTs//2.8e-42:376:78//Hs.141973:N21434	R-HEM81002329//ESTs//1.7e-94:453:99//Hs.7114:R24312
R-HEM81001872//EST//0.85:156:64//Hs.119501:AA487980	R-HEM81002340//ESTs//5.8e-15:163:77//Hs.26378:H10228
R-HEM81001874//EST//0.64:107:70//Hs.147482:A1215572	R-HEM81002342//Homo sapiens mRNA for putative thioredoxin-like protein//0.85:46:84//Hs.42644:AJ010841
R-HEM81001875//EST//0.079:199:59//Hs.121810:AA775240	R-HEM81002358//ESTs//2.0e-52:319:81//Hs.140255:AA708322
R-HEM81001880//Thromboxane A2 receptor//9.0e-47:297:88//Hs.89887:D38081	R-HEM81002359//ESTs//2.7e-106:517:97//Hs.13534:AI051613
R-HEM81001899//ESTs//6.3e-68:323:100//Hs.121538:AA609310	R-HEM81002364//Human mRNA for KIAA0080 gene, partial cds//5.3e-37:360:65//Hs.74554:D38522
R-HEM81001905//ESTs//4.4e-19:227:73//Hs.146173:AA906191	R-HEM81002371//Catalase//3.3e-22:235:77//Hs.76359:X04085
R-HEM81001906//ESTs//1.6e-90:463:95//Hs.28266:H46725	R-HEM81002381//Homo sapiens (JH8) mRNA, partial cds//1.0e-08:120:78//Hs.142296:AF072467
R-HEM81001908//Homo sapiens EVI5 homolog mRNA, complete cds//3.7e-27:557:64//Hs.26929:AF008915	R-HEM81002383//ESTs//3.5e-108:520:98//Hs.45140:DB0055
R-HEM81001910//EST//6.0e-37:308:78//Hs.162197:AA535216	R-HEM81002387
R-HEM81001911//Homo sapiens tapasin (NGS-17) mRNA, complete cds//8.0e-58:367:79//Hs.5247:AF029750	R-HEM81002415//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARMING ENTRY !!!! [H. sapiens]//2.3e-23:168:77//Hs.133526:N21103
R-HEM81001915//ESTs//3.1e-73:395:93//Hs.17054:A1139897	R-HEM81002425//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//3.2e-57:304:90//Hs.144563:AF057280
R-HEM81001921//Human mRNA for KIAA0392 gene, partial cds//2.7e-50:323:88//Hs.40100:AB002390	R-HEM81002442//ESTs//2.7e-48:289:87//Hs.155243:N70293
R-HEM81001922//H. sapiens mRNA for novel member of serine-arginine domain protein, SRp129//7.4e-38:531:70//Hs.153086:Y11251	R-HEM81002453//Human mRNA for KIAA0355 gene, complete cds//6.2e-45:292:87//Hs.153014:AB002353
R-HEM81001925//Human mRNA for KIAA0327 protein, complete cds//9.5e-19:199:77//Hs.149323:AB002325	R-HEM81002457//Human mRNA for KIAA0118 gene, partial cds//2.7e-46:546:71//Hs.154326:D42087
R-HEM81001930//EST//1.9e-18:136:78//Hs.132635:A1032875	R-HEM81002458//EST//1.8e-72:343:100//Hs.162006:AA508089
R-HEM81001944//EST//0.034:228:57//Hs.93664:N23366	R-HEM81002477//ESTs//1.6e-38:215:93//Hs.18240:AA460083
R-HEM81001945//ESTs//1.8e-83:439:95//Hs.7341:N57875	R-HEM81002489//ESTs//1.2e-101:534:94//Hs.7981:H15176
R-HEM81001947//EST//5.6e-109:533:97//Hs.48855:AA134589	R-HEM81002492//ESTs//5.0e-14:350:62//Hs.99205:AA204969
R-HEM81001950//ESTs//1.5e-107:583:93//Hs.8033:N94998	R-HEM81002495//ESTs//2.1e-19:147:86//Hs.163747:AA174017
R-HEM81001952//ESTs//3.1e-40:283:85//Hs.146811:AA410788	R-HEM81002502//ESTs, Weakly similar to p40 [H. sapiens]//1.2e-68:336:98//Hs.141515:T41142
R-HEM81001953//Human mRNA for KIAA0080 gene, partial cds//6.2e-50:284:83//Hs.74554:D38522	R-HEM81002509//ESTs//2.7e-97:459:99//Hs.127638:A1014615
R-HEM81001957//EST//4.8e-50:382:81//Hs.149580:A1281881	R-HEM81002510//ESTs, Weakly similar to located at OATL1 [H. sapiens]//2.2e-48:265:95//Hs.48827:AA873278
R-HEM81001962//EST//1.5e-20:143:88//Hs.11924:W26972	R-HEM81002520//EST//7.2e-40:198:84//Hs.140493:AA804538
R-HEM81001967//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.3e-61:296:88//Hs.153468:AB011147	R-HEM81002522//Human putative transmembrane receptor IL-1Rrp mRNA, complete cds//0.50:142:69//Hs.159301:U43672
R-HEM81001973//ESTs//1.4e-48:303:88//Hs.132722:AA618531	R-HEM81002531//EST//0.024:147:61//Hs.148305:AA909605
R-HEM81001983//ESTs//2.6e-72:374:95//Hs.141022:H06475	R-HEM81002534//EST//3.1e-22:168:84//Hs.146794:A1149478
R-HEM81001988//ESTs//2.0e-31:204:88//Hs.142531:N91572	R-HEM81002545//ESTs//9.2e-90:421:99//Hs.118317:A1033259
R-HEM81001990//ESTs//9.4e-115:574:96//Hs.44426:AA173223	R-HEM81002550//ESTs, Weakly similar to similar to S. cerevisiae LAG1 [C. elegans]//5.1e-22:210:81//Hs.11896:T68813
R-HEM81001996	R-HEM81002556//ISLET AMYLOID POLYPEPTIDE PRECURSOR//1.9e-45:344:82//Hs.51048:X68830
R-HEM81001997//ESTs//7.6e-78:380:98//Hs.32682:H37798	R-HEM81002579//ESTs//4.6e-47:326:85//Hs.155184:AA573189
R-HEM81002002//Human knpi repeat mRNA (cdna clone pcd-kpni-8), 3' end//3.0e-18:222:71//Hs.103948:K00627	R-HEM81002582//ESTs//0.00036:91:76//Hs.140039:AA047045
R-HEM81002005//EST//2.2e-41:339:80//Hs.160833:A1345334	R-HEM81002590//ESTs//1.0e-37:210:84//Hs.36658:N91138
R-HEM81002009//EST//2.9e-44:245:94//Hs.28788:R66896	R-HEM81002596//Human mRNA for KIAA0118 gene, partial cds//2.2e-46:297:87//Hs.154326:D42087
R-HEM81002015//EST//0.0027:198:63//Hs.160868:A1359052	R-HEM81002600//EST//2.5e-17:147:84//Hs.121918:AA777424
R-HEM81002042//ESTs//1.1e-75:529:84//Hs.106919:AA523900	R-HEM81002601//ESTs//7.8e-68:358:95//Hs.101489:R66923
R-HEM81002043//ESTs//7.9e-40:292:83//Hs.70279:AA757426	R-HEM81002603//EST//1.1e-47:281:90//Hs.149580:A1281881
R-HEM81002044//ESTs//2.1e-92:460:94//Hs.115897:AA156638	R-HEM81002607//ESTs//5.4e-75:379:97//Hs.29438:H42896
R-HEM81002045//Homo sapiens PYRIN (MEFY) mRNA, complete cds//5.6e-75:301:85//Hs.113283:AF018080	R-HEM81002610//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARMING ENTRY !!!! [H. sapiens]//6.2e-07:140:70//Hs.155456:AA707265
R-HEM81002049//ESTs//3.8e-77:409:94//Hs.122624:R82638	R-HEM81002613//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//8.5e-47:278:83//Hs.159187:AB007977
R-HEM81002050//ESTs//8.7e-45:330:82//Hs.44702:A1148840	R-HEM81002614//ESTs//3.4e-81:383:99//Hs.13012:AI094150
R-HEM81002068//ESTs//8.3e-70:333:99//Hs.134807:A1090671	R-HEM81002617//Homo sapiens protease-activated receptor 4 mRNA, complete cds//7.4e-19:151:80//Hs.137574:AF055917
R-HEM81002069//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds//1.5e-75:486:81//Hs.129735:AF010144	R-HEM81002623//ESTs//1.6e-45:288:87//Hs.138852:AA284247
R-HEM81002092//ESTs//6.5e-46:331:83//Hs.22910:W18193	R-HEM81002635//Small inducible cytokine A5 (RANTES)//5.5e-39:278:81//Hs.155464:AF088219
R-HEM81002094//EST//3.6e-45:280:88//Hs.149580:A1281881	R-HEM81002664//EST//8.9e-49:315:87//Hs.149580:A1281881
R-HEM81002115	R-HEM81002677//ESTs//0.65:159:62//Hs.163517:A1419775
R-HEM81002139//ESTs//4.2e-45:318:85//Hs.107657:AA126814	R-HEM81002683//H. sapiens mRNA for delta 4-3-oxosteroid 5 beta-reductase//8.6e-54:543:75//Hs.2638:Z28339
R-HEM81002142//Homo sapiens haemopoietic progenitor homeobox HPX4 2B (HPX42B) mRNA, complete cds//1.4e-45:281:88//Hs.125231:AF068006	R-HEM81002684//ESTs//3.0e-18:148:87//Hs.158270:AA776646
R-HEM81002152//EST//4.3e-39:250:89//Hs.156552:AA833553	R-HEM81002686//ESTs//6.1e-80:419:96//Hs.103002:W02753
R-HEM81002189//H. sapiens mRNA for translin associated protein X//1.4e-47:328:85//Hs.96247:X95073	R-HEM81002692//ESTs//3.3e-58:451:82//Hs.141254:AI334099
R-HEM81002190//ESTs//8.3e-05:122:70//Hs.41974:AF039185	R-HEM81002697//ESTs//6.2e-86:423:98//Hs.129812:AA769487
R-HEM81002193//Human sky mRNA for Sky, complete cds//8.9e-24:398:69//Hs.301:U18934	R-HEM81002699//EST//5.6e-46:322:84//Hs.140231:AI054398
R-HEM81002217//EST//6.6e-50:303:89//Hs.149580:A1281881	R-HEM81002702//ESTs//5.6e-36:412:72//Hs.154993:AA142842
R-HEM81002218//ESTs//2.3e-19:150:86//Hs.136031:W95841	R-HEM81002705//POLYPOSIS LOCUS PROTEIN 1//0.024:412:58//Hs.74648:W73547
R-HEM81002232//ESTs//8.9e-47:445:77//Hs.163971:N27584	R-HEM81002712//ESTs//9.0e-96:451:99//Hs.136806:AA805682
R-HEM81002247//EST//6.6e-09:236:65//Hs.130578:A1004631	R-HEM81000009//ESTs//3.0e-78:392:96//Hs.163947:AA678701
R-HEM81002249//ESTs//5.2e-16:325:64//Hs.156253:A1334807	
R-HEM81002254//Human Line-1 repeat mRNA with 2 open reading frame s//3.8e-99:590:88//Hs.23094:M19503	
R-HEM81002255//Human mRNA for KIAA0365 gene, partial cds//5.6e-45:342:83//Hs.84123:AB002363	
R-HEM81002266//ESTs//4.4e-98:472:98//Hs.65366:A1189112	

【0911】

【表609】

R-MAMMA1000019//Small inducible cytokine A5 (RANTES)//1.5e-47:247:87//Hs.155464:AF088219	R-MAMMA1000372//ESTs//1.0e-46:307:85//Hs.145032:AA343523
R-MAMMA1000020//Zinc finger protein 2 (AI-5)//4.9e-49:384:80//Hs.155533:X60152	R-MAMMA1000385//ESTs//8.2e-97:467:98//Hs.152282:AA412065
R-MAMMA1000025//Homo sapiens KIAA0441 mRNA, complete cds//4.7e-11:154:71//Hs.32511:AB007901	R-MAMMA1000388//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//8.6e-14:106:92//Hs.32170:AB015132
R-MAMMA1000043//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.0e-58:277:84//Hs.93121:AB018304	R-MAMMA1000395//ESTs//1.9e-57:292:96//Hs.11365:AI301060
R-MAMMA1000045//ESTs//1.0e-38:225:92//Hs.142567:AA287165	R-MAMMA1000402//ESTs, Moderately similar to RETROVIRUS-RELATED POLYPROTEIN [Mus musculus]//9.1e-47:316:81//Hs.13698:N38973
R-MAMMA1000055//EST//0.14:91:67//Hs.144061:AA96350	R-MAMMA1000410//Archaeal//1.8e-40:443:74//Hs.33642:X81198
R-MAMMA1000057//Fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, Bombay phenotype included)//3.8e-77:545:83//Hs.6974:7:W35531	R-MAMMA1000413//Homo sapiens mRNA for KIAA0792 protein, complete cds//1.3e-27:304:72//Hs.119387:AB007958
R-MAMMA1000069//ESTs//8.0e-108:546:96//Hs.44856:N37065	R-MAMMA1000414//ESTs//2.9e-27:181:87//Hs.141254:AI334099
R-MAMMA1000084//Homo sapiens clone 23632 mRNA sequence//7.3e-43:31:83//Hs.46918:AF052099	R-MAMMA1000416//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//1.5e-58:282:82//Hs.97203:U83171
R-MAMMA1000085//ESTs, Highly similar to PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C [Schizosaccharomyces pombe]//7.7e-104:546:94//Hs.7779:AA045241	R-MAMMA1000421//Thromboxane A2 receptor//4.9e-48:372:80//Hs.89887:D38081
R-MAMMA1000092//EST, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.2e-22:287:71//Hs.136063:U51713	R-MAMMA1000422//ESTs//0.077:240:62//Hs.123136:AA631067
R-MAMMA1000103//LOW-DENSITY LIPOPROTEIN RECEPTOR PRECURSOR//8.4e-49:334:86//Hs.70008:L00352	R-MAMMA1000423//Human mRNA for KIAA0392 gene, partial cds//1.3e-48:375:81//Hs.40100:AB002390
R-MAMMA1000117//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.1e-08:96:80//Hs.115088:AA230172	R-MAMMA1000424//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.4e-44:418:75//Hs.154069:U06452
R-MAMMA1000129//EST//2.8e-64:310:99//Hs.136394:AA523577	R-MAMMA1000429//ESTs//3.9e-113:565:96//Hs.5076:N53461
R-MAMMA1000133	R-MAMMA1000431//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//8.6e-68:302:85//Hs.97203:U83171
R-MAMMA1000134//ESTs//1.1e-21:152:87//Hs.163747:AA174017	R-MAMMA1000444//Calcium modulating ligand//5.5e-44:344:81//Hs.13572:AF068179
R-MAMMA1000139//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0501//6.3e-40:288:78//Hs.159897:AB007970	R-MAMMA1000446//ESTs//1.0:236:60//Hs.126958:AI147447
R-MAMMA1000143//EST//5.0e-52:314:89//Hs.149580:AI281881	R-MAMMA1000458
R-MAMMA1000155//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.5e-59:562:75//Hs.77579:AF013263	R-MAMMA1000468//ESTs//4.4e-51:271:96//Hs.6839:AA055176
R-MAMMA1000163//ESTs//2.8e-92:457:96//Hs.114413:AA884787	R-MAMMA1000472//ESTs//5.4e-39:146:86//Hs.141581:AA315361
R-MAMMA1000171//Homo sapiens mRNA for putative lipoprotein synthase, partial//2.5e-39:173:83//Hs.53531:AJ224162	R-MAMMA1000478//ESTs//2.3e-74:365:98//Hs.140591:AA828959
R-MAMMA1000173//ESTs, Highly similar to SRC SUBSTRATE P80/85 PROTEIN [Callus gallus]//2.4e-07:63:90//Hs.90367:AI357069	R-MAMMA1000483//ESTs//9.9e-23:235:75//Hs.163592:AA280886
R-MAMMA1000175//EST//0.66:217:58//Hs.146444:AI127611	R-MAMMA1000490//EST//2.1e-80:500:87//Hs.142137:AA213759
R-MAMMA1000183//ESTs//6.7e-30:341:73//Hs.125254:AA872054	R-MAMMA1000500//Small inducible cytokine A5 (RANTES)//4.7e-43:283:86//Hs.155464:AF088219
R-MAMMA1000198//EST//2.8e-45:185:88//Hs.149580:AI281881	R-MAMMA1000501//ESTs//4.2e-37:250:86//Hs.141323:N80390
R-MAMMA1000221//ESTs, Weakly similar to circadian clock protein [Mus musculus]//1.4e-41:272:90//Hs.68398:AA421103	R-MAMMA1000516//Human mRNA for KIAA0392 gene, partial cds//5.1e-46:459:75//Hs.40100:AB002390
R-MAMMA1000227//EST//2.4e-38:388:76//Hs.144175:H70425	R-MAMMA1000522//ESTs//9.5e-16:226:70//Hs.116673:AA669267
R-MAMMA1000241//EST//0.0027:263:61//Hs.37532:H57946	R-MAMMA1000559//ESTs//5.2e-34:244:84//Hs.150727:AI292236
R-MAMMA1000251//Homo sapiens mRNA for KIAA0772 protein, complete cds//5.3e-47:322:86//Hs.15519:AB018315	R-MAMMA1000565//EST//2.7e-38:386:76//Hs.162404:AA573131
R-MAMMA1000254//Homo sapiens tumor necrosis factor superfamily member LIGHT mRNA, complete cds//2.2e-43:315:83//Hs.129708:AF064090	R-MAMMA1000567//EST//0.33:49:79//Hs.147754:AI220561
R-MAMMA1000257//EST//1.6e-62:330:93//Hs.141728:W73041	R-MAMMA1000576//ESTs//4.9e-57:348:89//Hs.108921:N31211
R-MAMMA1000264//Von Hippel-Lindau syndrome//2.3e-31:141:81//Hs.78160:AF010238	R-MAMMA1000583//Homo sapiens KIAA0412 mRNA, partial cds//1.3e-52:73:77//Hs.6200:AB007872
R-MAMMA1000266//ESTs//3.4e-34:150:81//Hs.163980:AA715814	R-MAMMA1000585//ESTs//5.1e-40:337:78//Hs.130815:AA936548
R-MAMMA1000270//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//2.7e-57:304:78//Hs.159187:AB007977	R-MAMMA1000594//Small inducible cytokine A5 (RANTES)//3.0e-45:225:80//Hs.155464:AF088219
R-MAMMA1000277//Thiopurine S-methyltransferase//3.7e-27:380:71//Hs.51124:AF019369	R-MAMMA1000597//ESTs//2.0e-98:461:99//Hs.43212:AA993042
R-MAMMA1000278//ESTs//5.2e-99:504:95//Hs.8494:W72694	R-MAMMA1000605//CD4 receptor (exons 1 and 2) [human, T-lymphocyte, mRNA, 3429 nt]//1.5e-50:500:73//Hs.116007:S79267
R-MAMMA1000279//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//3.1e-58:295:83//Hs.92381:AB007956	R-MAMMA1000612//ESTs, Highly similar to HYPOTHETICAL TRP-ASP REPEATS CONTAINING PROTEIN IN SISI-MRPL2 INTERGENIC REGION [Saccharomyces cerevisiae]//8.6e-108:559:94//Hs.29203:AI344105
R-MAMMA1000284//EST//4.1e-10:151:73//Hs.60742:AA017066	R-MAMMA1000616//EST//0.071:169:60//Hs.144096:AI032180
R-MAMMA1000287	R-MAMMA1000621//ESTs//1.0e-90:477:94//Hs.26073:R96361
R-MAMMA1000302//Homo sapiens KIAA0432 mRNA, complete cds//1.0:50:84//Hs.155174:AB007892	R-MAMMA1000623
R-MAMMA1000307//Human mRNA for KIAA0033 gene, partial cds//1.8e-48:468:76//Hs.22271:D26067	R-MAMMA1000625//ESTs//3.4e-98:556:91//Hs.119482:AI361002
R-MAMMA1000309//ESTs//1.7e-94:491:94//Hs.135106:AI335251	R-MAMMA1000643//EST//4.9e-74:379:96//Hs.137447:AA342203
R-MAMMA1000312//ESTs//8.9e-74:377:96//Hs.133163:AI051434	R-MAMMA1000664//Homo sapiens mRNA for putative lipoprotein synthase, partial//3.2e-43:400:76//Hs.53531:AJ224162
R-MAMMA1000313//EST//8.3e-19:294:62//Hs.127400:AA954491	R-MAMMA1000669//EST//6.9e-53:368:84//Hs.149580:AI281881
R-MAMMA1000331//ESTs, Moderately similar to envelope protein [H.sapiens]//8.6e-54:278:97//Hs.139170:AA662998	R-MAMMA1000670//ESTs, Highly similar to HYPOTHETICAL PROTEIN IN TOMB 3' REGION [Klebsiella pneumoniae]//8.4e-98:464:98//Hs.31431:AI022065
R-MAMMA1000339//EST//6.8e-44:169:89//Hs.149580:AI281881	R-MAMMA1000672//ESTs//2.0e-80:382:99//Hs.106747:AI080476
R-MAMMA1000340//Homo sapiens mRNA for KIAA0625 protein, partial cds//0.82:204:61//Hs.154919:AB014525	R-MAMMA1000684//ESTs//6.2e-72:357:98//Hs.67896:AA865212
R-MAMMA1000348//ESTs//3.3e-34:320:75//Hs.139158:AA226159	R-MAMMA1000696//Human mRNA for KIAA0345 gene, complete cds//3.3e-52:216:75//Hs.98938:AB002343
R-MAMMA1000356//ESTs, Highly similar to URIDYLATE KINASE [Saccharomyces cerevisiae]//0.42:172:61//Hs.11463:AA535912	R-MAMMA1000707//EST//7.0e-11:195:68//Hs.147002:AI184644
R-MAMMA1000360//Human mRNA for KIAA0118 gene, partial cds//3.8e-43:212:82//Hs.154326:D42087	R-MAMMA1000713//Homo sapiens DEC-205 mRNA, complete cds//1.5e-45:485:74//Hs.153563:AF011333
R-MAMMA1000361//ESTs//3.1e-17:188:68//Hs.164036:AA845659	R-MAMMA1000714//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//1.2e-29:158:79//Hs.142764:AA205569
	R-MAMMA1000718//ESTs//3.1e-45:264:88//Hs.152413:AA780515
	R-MAMMA1000720//ESTs//7.4e-44:244:87//Hs.111742:R39329
	R-MAMMA1000723//Homo sapiens mRNA for alpha(1,2)fucosyltransferase, complete cds//5.6e-52:350:82//Hs.46328:D87942
	R-MAMMA1000731//ESTs//1.1e-19:420:66//Hs.35036:H95267
	R-MAMMA1000732//EST//2.9e-20:229:74//Hs.135400:AI056893
	R-MAMMA1000733//ESTs, Weakly similar to HYPOTHETICAL 92.1 KD PROTEIN

【表610】

IN ZK1098.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.2e-35:37 1:74//Hs.141429:AA631915	R-MAMMA1001038//Human mRNA for KIAA0392 gene, partial cds//3.0e-5 0:298:91//Hs.40100:AB002390
R-MAMMA1000734//Homo sapiens SEC63 (SEC63) mRNA, complete cds//2.1 e-58:253:98//Hs.31575:AF100141	R-MAMMA1001041//ESTs//3.6e-86:445:95//Hs.122625:R68650
R-MAMMA1000738//ESTs, Weakly similar to similar to Achlya ambisexualis antheridiol steroid receptor [C.elegans]//2.3e-116:557:98//Hs. s.71472:AA632288	R-MAMMA1001050//EST//2.2e-54:387:85//Hs.149580:A1281881
R-MAMMA1000744//ESTs//0.015:143:67//Hs.135382:A1224205	R-MAMMA1001059//ESTs, Moderately similar to RNA helicase [M.muscul us]//1.7e-13:273:65//Hs.98738:A1015487
R-MAMMA1000746//Human Line-1 repeat mRNA with 2 open reading frame s//2.3e-90:568:86//Hs.23094:M19503	R-MAMMA1001067//ESTs//1.3e-38:324:78//Hs.20190:AA525532
R-MAMMA1000752//Interleukin 10//2.8e-43:339:80//Hs.2180:M57627	R-MAMMA1001073//ESTs//5.2e-106:554:94//Hs.12336:W63748
R-MAMMA1000760//EST//5.0e-44:306:86//Hs.162404:AA573131	R-MAMMA1001074//Human mRNA for KIAA0355 gene, complete cds//1.2e-3 8:544:68//Hs.153014:AB002353
R-MAMMA1000761//EST//5.0e-41:187:85//Hs.162335:AA564256	R-MAMMA1001075//ESTs//2.0e-98:463:99//Hs.18341:M38944
R-MAMMA1000775//Human mRNA for KIAA0355 gene, complete cds//3.0e-4 6:465:76//Hs.153014:AB002353	R-MAMMA1001078//Human Line-1 repeat mRNA with 2 open reading frame s//1.7e-84:556:85//Hs.23094:M19503
R-MAMMA1000776//ESTs//1.9e-43:429:73//Hs.141742:W22204	R-MAMMA1001082//ESTs//2.4e-71:356:97//Hs.152302:T90222
R-MAMMA1000778//ESTs//1.8e-31:445:70//Hs.111723:M57439	R-MAMMA1001091//ESTs//4.7e-83:429:95//Hs.154412:AA310926
R-MAMMA1000782//EST//0.0019:102:68//Hs.120686:AA747150	R-MAMMA1001092//Homo sapiens X-ray repair cross-complementing prot ein 2 (XRCC2) mRNA, complete cds//6.4e-34:262:82//Hs.129727:AF0355 87
R-MAMMA1000798//ESTs//1.4e-13:267:69//Hs.140156:AA704163	R-MAMMA1001105//Human putative RNA binding protein RNPL mRNA, comp lete cds//4.2e-27:232:76//Hs.61840:U28686
R-MAMMA1000802//Clathrin, light polypeptide (Lcb)//1.5e-45:358:76/ Hs.73919:X81637	R-MAMMA1001110//ESTs//1.6e-17:128:87//Hs.161314:A1421576
R-MAMMA1000831//ESTs//1.3e-104:510:97//Hs.17494:AA572675	R-MAMMA1001126//CD4 receptor (exons 1 and 2) [human, T-lymphocyte, mRNA, 3429 nt]//8.8e-53:462:78//Hs.116007:S79267
R-MAMMA1000839//EST//2.9e-51:307:89//Hs.149580:A1281881	R-MAMMA1001133//Homo sapiens tapasin (NCS-17) mRNA, complete cds// 1.8e-59:460:81//Hs.5247:AF029750
R-MAMMA1000841//ESTs//1.3e-34:412:72//Hs.121256:AA757902	R-MAMMA1001139//ESTs//1.3e-62:341:94//Hs.18819:R01029
R-MAMMA1000842//ESTs, Moderately similar to !!! ALU SUBFAMILY J W ARNING ENTRY !!! [H.sapiens]//9.4e-44:363:79//Hs.96337:AA225358	R-MAMMA1001143//ESTs//3.0e-48:383:80//Hs.152340:AA521399
R-MAMMA1000843//ESTs//2.2e-106:525:97//Hs.152016:AA603097	R-MAMMA1001145//Calcium modulating ligand//5.1e-48:403:79//Hs.1357 2:AF068179
R-MAMMA1000845//ESTs//1.6e-66:327:98//Hs.156900:AA468955	R-MAMMA1001154//EST//6.8e-35:313:75//Hs.162404:AA573131
R-MAMMA1000851//ESTs//3.7e-14:115:86//Hs.140590:R76251	R-MAMMA1001161//Homo sapiens tapasin (NCS-17) mRNA, complete cds// 1.1e-58:409:84//Hs.5247:AF029750
R-MAMMA1000855//Human mRNA for KIAA0392 gene, partial cds//5.7e-4 7:281:91//Hs.40100:AB002390	R-MAMMA1001162//ESTs, Highly similar to t-BOP [M.musculus]//2.1e-9 1:430:99//Hs.129982:A1420970
R-MAMMA1000856//EST//1.8e-16:150:79//Hs.136811:AA789212	R-MAMMA1001181//ESTs//5.0e-112:557:96//Hs.118181:W02251
R-MAMMA1000862//EST//3.2e-05:93:73//Hs.161205:A1419311	R-MAMMA1001186//ESTs//3.8e-85:410:99//Hs.163811:W44959
R-MAMMA1000863//ESTs//1.0e-46:446:73//Hs.153432:AA098922	R-MAMMA1001191//ESTs//0.018:57:87//Hs.141253:AA226519
R-MAMMA1000865//Homo sapiens clone 23632 mRNA sequence//3.0e-39:32 4:80//Hs.46918:AF052099	R-MAMMA1001198//ESTs, Weakly similar to involved in signaling by t he epidermal growth factor receptor [M.musculus]//2.6e-80:358:96// Hs.163827:AA074202
R-MAMMA1000867//ESTs//9.8e-16:193:76//Hs.152340:AA521399	R-MAMMA1001202//ESTs//7.0e-43:230:95//Hs.79788:AA527348
R-MAMMA1000875//EST//3.1e-24:301:72//Hs.132635:A1032875	R-MAMMA1001203//Clathrin, light polypeptide (Lcb)//2.8e-65:348:79/ Hs.73919:X81637
R-MAMMA1000876//ESTs//9.9e-48:246:97//Hs.112165:AA621243	R-MAMMA1001206//EST//0.098:84:72//Hs.162941:AA635148
R-MAMMA1000877//ESTs//1.4e-38:324:79//Hs.141024:H07128	R-MAMMA1001215//ESTs//1.3e-43:156:86//Hs.155243:N70293
R-MAMMA1000880//Homo sapiens mRNA for KIAA0594 protein, partial cd s//3.2e-40:542:68//Hs.154872:AB011166	R-MAMMA1001220//ESTs//8.9e-17:276:68//Hs.116518:AA653202
R-MAMMA1000883//ESTs//1.0:207:60//Hs.47199:N51107	R-MAMMA1001222//ESTs//0.49:112:66//Hs.24668:AA897315
R-MAMMA1000897//ESTs//2.6e-78:383:97//Hs.41067:A1310215	R-MAMMA1001243//EST//0.99:143:62//Hs.68522:C20701
R-MAMMA1000905//Human mRNA for KIAA0331 gene, complete cds//9.7e-5 3:307:91//Hs.146395:AB002329	R-MAMMA1001244//ESTs//2.2e-06:79:83//Hs.123163:AA809619
R-MAMMA1000906//ESTs//8.0e-25:206:83//Hs.141825:AA017093	R-MAMMA1001249//ESTs//4.2e-58:343:97//Hs.147139:A1191307
R-MAMMA1000908//ESTs//4.4e-32:176:96//Hs.38559:AA701634	R-MAMMA1001256//ESTs, Moderately similar to hypothetical protein 2 [H.sapiens]//4.7e-31:221:77//Hs.142764:AA205569
R-MAMMA1000914//ESTs//0.032:150:63//Hs.119162:AA399989	R-MAMMA1001259//ESTs//1.3e-43:266:90//Hs.6193:AA045149
R-MAMMA1000921//Human 53K isoform of Type II phosphatidylinositol- 4-phosphate 5-kinase (PIPK) mRNA, complete cds//7.7e-38:269:74//H s.108966:U48596	R-MAMMA1001260//Homo sapiens mRNA for KIAA0661 protein, complete c ds//2.0e-21:226:75//Hs.65238:AB014561
R-MAMMA1000931//ESTs//1.2e-80:457:91//Hs.122319:AA782335	R-MAMMA1001268//H.sapiens HCG II mRNA//2.4e-53:181:85//Hs.146333:X 81001
R-MAMMA1000940//ESTs//3.3e-43:329:87//Hs.35254:A1133727	R-MAMMA1001271//ESTs, Highly similar to PUTATIVE SERINE/THREONIN E-PROTEIN KINASE EMK [Mus musculus]//1.1e-108:546:95//Hs.18999:N30 643
R-MAMMA1000941//ESTs//7.5e-55:306:84//Hs.163936:AA632281	R-MAMMA1001274//Homo sapiens mRNA for KIAA0572 protein, partial cd s//4.4e-32:188:94//Hs.14409:AB011144
R-MAMMA1000942//ESTs//2.5e-83:405:98//Hs.116491:AA650428	R-MAMMA1001280//EST//0.0015:170:62//Hs.116770:AA630371
R-MAMMA1000943//Cytochrome P450, subfamily I (aromatic compound-in ducible), polypeptide 2//9.3e-79:567:80//Hs.1361:M55053	R-MAMMA1001292//ESTs//5.6e-102:481:99//Hs.94810:AA811876
R-MAMMA1000956//EST//5.7e-53:256:100//Hs.162209:AA536178	R-MAMMA1001296//Homo sapiens mRNA for KIAA0563 protein, complete c ds//2.2e-27:348:70//Hs.15731:AB011135
R-MAMMA1000957//Kangai 1 (suppression of tumorigenicity 6, prostat e; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclo nal and antibody 1A4))//7.5e-49:340:85//Hs.103458:X53795	R-MAMMA1001298//ESTs//1.4e-44:375:79//Hs.70279:AA757426
R-MAMMA1000962//Homo sapiens mRNA for KIAA0575 protein, complete c ds//2.0e-48:216:85//Hs.153468:AB011147	R-MAMMA1001305//Human G protein-coupled receptor (STRL22) mRNA, co mplete cds//4.0e-43:300:85//Hs.46468:U45984
R-MAMMA1000968//EST//6.2e-46:302:86//Hs.149580:A1281881	R-MAMMA1001322//Homo sapiens stress-activated protein kinase 4 mRN A, complete cds//8.8e-12:188:70//Hs.55771:AF004709
R-MAMMA1000975//ESTs//1.4e-85:428:96//Hs.141742:W22204	R-MAMMA1001324//ESTs//5.3e-68:297:88//Hs.121228:AA709471
R-MAMMA1000979//Homo sapiens mRNA for KIAA0761 protein, partial cd s//8.0e-39:338:79//Hs.93121:AB018304	R-MAMMA1001330//ESTs//1.6e-57:429:83//Hs.70279:AA757426
R-MAMMA1000987//EST//2.8e-41:249:90//Hs.149580:A1281881	R-MAMMA1001341//Homo sapiens 4F5S mRNA, complete cds//4.8e-27:285: 75//Hs.32567:AF073519
R-MAMMA1000988//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//3.9e-50:445:77//Hs.77579:AF013263	R-MAMMA1001343//ESTs//8.1e-51:273:93//Hs.162208:AA536127
R-MAMMA1001003//Sialophorin (gp115, leukosialin, CD43)//4.1e-51:2 82:82//Hs.80738:X52075	R-MAMMA1001346//ESTs//1.0:122:65//Hs.33028:AA482478
R-MAMMA1001008//ESTs, Weakly similar to renin [H.sapiens]//1.9e-8 2:405:97//Hs.25863:AA630313	R-MAMMA1001383//ESTs//1.4e-45:377:80//Hs.114671:M39322
R-MAMMA1001021//Homo sapiens DEC-205 mRNA, complete cds//3.0e-44:3 09:86//Hs.153563:AF011333	R-MAMMA1001388//EST//7.7e-47:361:80//Hs.162197:AA535216
R-MAMMA1001024//ESTs//6.8e-35:333:78//Hs.107657:AA126814	R-MAMMA1001397//EST//8.7e-48:337:83//Hs.149580:A1281881
R-MAMMA1001030//ESTs//1.6e-110:552:96//Hs.59483:AA524536	
R-MAMMA1001035//ESTs//1.0e-45:273:85//Hs.138856:H47461	

【0913】

【表611】

R-MAMMA1001408//EST//1.2e-38:251:87//Hs.162677:AA604831	R-MAMMA1001815//EST//0.00053:371:59//Hs.133255:A1052659
R-MAMMA1001411//ESTs//4.3e-93:435:99//Hs.105460:AA780275	R-MAMMA1001817//Human mRNA for KIAA0226 gene, complete cds//2.1e-4
R-MAMMA1001419//Homo sapiens translation initiation factor 4e mRNA, complete cds//1.6e-19:117:96//Hs.19122:AF038957	6:325:87//Hs.44106:D86979
R-MAMMA1001420//ESTs//7.3e-96:507:95//Hs.55299:A1335267	R-MAMMA1001818
R-MAMMA1001435//ESTs//5.0e-97:459:99//Hs.144843:A1222168	R-MAMMA1001820//EST//1.9e-49:303:89//Hs.149580:A1281881
R-MAMMA1001442//ESTs//7.1e-28:167:83//Hs.141019:AA287618	R-MAMMA1001824//Homo sapiens 4F5S mRNA, complete cds//4.3e-48:438:
R-MAMMA1001446//Homo sapiens KIAA0432 mRNA, complete cds//6.2e-19:	75//Hs.32567:AF073519
328:67//Hs.155174:AB007892	R-MAMMA1001836//ESTs//3.8e-06:128:71//Hs.143611:M78140
R-MAMMA1001452//EST//5.6e-44:487:75//Hs.161476:M57542	R-MAMMA1001837//Homo sapiens KIAA0395 mRNA, partial cds//3.8e-47:3
R-MAMMA1001465	39:83//Hs.43681:AL022394
R-MAMMA1001476//Homo sapiens yeast permease-like molecule 3 (YSL3) mRNA, complete cds//0.79:182:66//Hs.136529:AF058317	R-MAMMA1001848//ESTs//2.1e-16:125:85//Hs.161662:AA836811
R-MAMMA1001487//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-35:3	R-MAMMA1001851//ESTs//4.5e-48:344:84//Hs.138856:H47461
28:78//Hs.43681:AL022394	R-MAMMA1001854//Small inducible cytokine A5 (RANTES)//2.6e-38:280:
R-MAMMA1001501//ESTs//4.6e-100:472:98//Hs.123660:AA813065	83//Hs.155464:AF088219
R-MAMMA1001502//Human mRNA for KIAA0080 gene, partial cds//5.6e-1	R-MAMMA1001858//ESTs//1.1e-44:331:83//Hs.44702:A1148840
5:220:69//Hs.74554:D38522	R-MAMMA1001864//Homo sapiens mRNA for KIAA0475 protein, complete c
R-MAMMA1001510	ds//7.8e-31:262:77//Hs.5737:AB007944
R-MAMMA1001522//ESTs//3.2e-16:214:75//Hs.152816:AA634242	R-MAMMA1001868//Homo sapiens antigen NY-CO-16 mRNA, complete cds//
R-MAMMA1001547//H. sapiens mRNA for urea transporter//2.3e-45:282:8	9.2e-06:450:58//Hs.132206:AF039694
9//Hs.66710:X96969	R-MAMMA1001874//Human high-affinity copper uptake protein (hCTR1)
R-MAMMA1001551//Human 53K isoform of Type II phosphatidylinositol-	mRNA, complete cds//4.9e-46:332:83//Hs.73614:U83460
4-phosphate 5-kinase (PIPK) mRNA, complete cds//1.9e-56:489:76//H	R-MAMMA1001878//Cytochrome P450, 51 (lanosterol 14-alpha-demethyla
s.108966:U48696	se)//1.2e-46:429:78//Hs.2379:U23942
R-MAMMA1001575//ESTs//4.3e-92:440:98//Hs.162882:AA807140	R-MAMMA1001880//ESTs, Moderately similar to !!!! ALU SUBFAMILY J W
R-MAMMA1001576//ESTs, Highly similar to TUBULIN GAMMA CHAIN [Homo	ARNING ENTRY !!!! [H.sapiens]//7.6e-26:230:79//Hs.106008:AA147606
sapiens]//1.9e-111:549:96//Hs.21635:A1417305	R-MAMMA1001890//ESTs//1.1e-39:338:79//Hs.146811:AA410788
R-MAMMA1001590//ESTs//1.1e-63:324:96//Hs.142217:AA278441	R-MAMMA1001907//Kangai 1 (suppression of tumorigenicity 6, prostat
R-MAMMA1001600//ESTs//5.6e-15:159:78//Hs.138633:H98792	e; CD82 antigen (R2 leukocyte antigen, antigen detected by monoclo
R-MAMMA1001604	nal and antibody 1A4))//6.7e-47:283:89//Hs.103458:X53795
R-MAMMA1001606//ESTs, Weakly similar to finger protein kox1 [H.sap	R-MAMMA1001908//ESTs//0.043:134:65//Hs.145333:A1251374
iens]//1.9e-97:488:96//Hs.143263:A1057616	R-MAMMA1001931//ESTs//1.8e-75:361:99//Hs.148125:AA693801
R-MAMMA1001620//Homo sapiens mRNA, clone:RES4-16//5.4e-43:408:76//	R-MAMMA1001956//Homo sapiens mRNA for KIAA0706 protein, complete c
Hs.121493:D25272	ds//1.4e-18:174:77//Hs.139648:AB014606
R-MAMMA1001627//Homo sapiens mRNA for KIAA0772 protein, complete c	R-MAMMA1001963//ESTs//6.7e-28:206:84//Hs.163254:AA828790
ds//2.0e-49:472:76//Hs.15519:AB018315	R-MAMMA1001969//ESTs, Weakly similar to hypothetical protein [H.sap
R-MAMMA1001630//ESTs, Weakly similar to putative p150 [H.sapiens]//	piens]//6.7e-24:331:71//Hs.140506:AA308018
/6.8e-15:168:73//Hs.115216:AA291074	R-MAMMA1001970//ESTs//8.9e-61:286:84//Hs.141575:AA211734
R-MAMMA1001633//EST//5.1e-14:228:68//Hs.141456:N36377	R-MAMMA1001992//ESTs//4.4e-43:339:82//Hs.155498:W27084
R-MAMMA1001635//ESTs//3.4e-37:368:75//Hs.164033:AA769606	R-MAMMA1002009//Small inducible cytokine A5 (RANTES)//4.6e-24:330:
R-MAMMA1001649	70//Hs.155464:AF088219
R-MAMMA1001663//Homo sapiens neuronal thread protein AD7c-NTP mRNA	R-MAMMA1002011//ESTs//9.5e-72:360:97//Hs.13525:R39054
A, complete cds//1.7e-54:272:81//Hs.129735:AF010144	R-MAMMA1002032//Human melanoma antigen recognized by T-cells (MAR
R-MAMMA1001670//Small inducible cytokine A5 (RANTES)//5.7e-50:304:	T-1) mRNA//3.7e-45:370:80//Hs.154069:U06452
89//Hs.155464:AF088219	R-MAMMA1002033//EST//4.6e-23:264:74//Hs.161917:AA483223
R-MAMMA1001671//EST//1.9e-14:312:65//Hs.137153:R46248	R-MAMMA1002041//ESTs//3.8e-100:465:100//Hs.141361:A1206412
R-MAMMA1001679//H. sapiens mRNA for rho GTP-dissociation inhibitor	R-MAMMA1002042//Homo sapiens 4F5S mRNA, complete cds//1.1e-43:407:
1//0.066:196:62//Hs.159161:X69550	76//Hs.32567:AF073519
R-MAMMA1001683//ESTs//4.9e-94:447:98//Hs.134464:A1151081	R-MAMMA1002047//Homo sapiens mRNA for chemokine LEC precursor, com
R-MAMMA1001686//Homo sapiens mRNA, chromosome 1 specific transcrip	plete cds//1.9e-37:316:74//Hs.10458:AF088219
t KIAA0488//1.0e-17:246:73//Hs.67619:AB007957	R-MAMMA1002056//EST//1.3e-51:310:90//Hs.149580:A1281881
R-MAMMA1001692//Human mRNA for KIAA0063 gene, complete cds//2.1e-4	R-MAMMA1002058//ESTs//5.9e-16:135:84//Hs.95807:AA146979
7:294:89//Hs.3094:D31884	R-MAMMA1002068//ESTs, Weakly similar to HYPOTHETICAL 43.3 KD PROTE
R-MAMMA1001711//ESTs//2.4e-86:439:96//Hs.18498:M52088	IN IN QOXD-VPR INTERGENIC REGION [Bacillus subtilis]//4.0e-45:404:
R-MAMMA1001715//ESTs//1.2e-73:399:93//Hs.124620:A1082338	78//Hs.138596:N38806
R-MAMMA1001730//ESTs//1.1e-85:403:99//Hs.125464:A1084596	R-MAMMA1002078//EST//2.2e-15:207:71//Hs.132635:A1032875
R-MAMMA1001735//ESTs, Highly similar to TUBULIN BETA-5 CHAIN [Gal	R-MAMMA1002082//Homo sapiens mRNA for TSC403 protein, complete cds
lus gallus]//3.7e-110:552:96//Hs.6923:A1161158	//1.7e-42:314:83//Hs.10887:AB013924
R-MAMMA1001740//ESTs//4.6e-45:342:82//Hs.37573:H59651	R-MAMMA1002084//Human mRNA for KIAA0392 gene, partial cds//3.7e-4
R-MAMMA1001743//EST//2.7e-58:412:85//Hs.149742:A1285666	6:308:87//Hs.40100:AB002390
R-MAMMA1001744	R-MAMMA1002093//EST//0.89:213:60//Hs.151201:A1125907
R-MAMMA1001745//EST//5.6e-54:374:84//Hs.137041:AA877817	R-MAMMA1002108//ESTs//1.0e-95:515:93//Hs.29002:H11347
R-MAMMA1001751//EST//3.5e-36:375:73//Hs.139715:M25041	R-MAMMA1002118
R-MAMMA1001754//EST//0.18:144:66//Hs.71957:AA151413	R-MAMMA1002125//Thromboxane A2 receptor//7.2e-43:335:83//Hs.89887:
R-MAMMA1001757//ESTs//1.0e-98:488:96//Hs.45184:C14904	D38081
R-MAMMA1001760//ESTs//8.7e-29:206:86//Hs.143310:A1142276	R-MAMMA1002132//Homo sapiens neuronal thread protein AD7c-NTP mRNA
R-MAMMA1001764//EST//0.00012:434:58//Hs.120051:AA707847	A, complete cds//1.4e-58:396:78//Hs.129735:AF010144
R-MAMMA1001768//Human mRNA for KIAA0327 protein, complete cds//2.3	R-MAMMA1002140//Homo sapiens nephrin (NPHS1) mRNA, complete cds//
e-41:299:85//Hs.149323:AB002325	1.4e-37:422:75//Hs.128834:AF035835
R-MAMMA1001769//EST//1.7e-15:139:81//Hs.162399:AA572825	R-MAMMA1002143//ESTs//0.050:123:69//Hs.8231:AA152276
R-MAMMA1001771//ESTs, Moderately similar to semaphorin B [M.muscul	R-MAMMA1002145//Homo sapiens KIAA0426 mRNA, complete cds//5.0e-21:
us]//7.6e-43:257:91//Hs.7634:AA481246	371:69//Hs.97476:AB007886
R-MAMMA1001783//Human high-affinity copper uptake protein (hCTR1)	R-MAMMA1002153//ESTs//2.0e-31:159:77//Hs.130815:AA936548
mRNA, complete cds//5.6e-42:272:86//Hs.73614:U83460	R-MAMMA1002155//Human Line-1 repeat mRNA with 2 open reading frame
R-MAMMA1001785//ESTs//1.5e-87:431:98//Hs.131065:AA972238	s//8.7e-39:506:69//Hs.23094:M19503
R-MAMMA1001788//EST//0.95:108:62//Hs.145881:A1274644	R-MAMMA1002156//Homo sapiens mRNA for putative lipoic acid synthet
R-MAMMA1001790//ESTs//4.0e-41:340:80//Hs.158045:AA425744	ase, partial//2.9e-44:336:82//Hs.53531:AJ224162
R-MAMMA1001806//EST//1.4e-40:297:84//Hs.141240:H60313	R-MAMMA1002158//ESTs//3.0e-40:313:83//Hs.118273:AA626040
R-MAMMA1001812//EST//2.4e-93:446:98//Hs.129034:AA776892	R-MAMMA1002170//Homo sapiens mRNA for TRAF5, complete cds//7.7e-3
	7:370:77//Hs.29736:AB000509
	R-MAMMA1002174//ESTs//2.5e-16:186:75//Hs.141203:HS2638

【0914】

【表612】

R-MAMMA1002198//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//6.2e-51:318:82//Hs.92381:AB007956	R-MAMMA1002475//ESTs. Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//3.4e-31:263:79//Hs.38687:AA744496
R-MAMMA1002209//ESTs//9.2e-34:111:88//Hs.141575:AA211734	R-MAMMA1002480//ESTs. Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-34:159:79//Hs.133526:N21103
R-MAMMA1002215//ESTs//3.6e-101:530:94//Hs.26780:N50038	R-MAMMA1002485//Homo sapiens stanniocalcin-2 (STC-2) mRNA, complete cds//8.9e-116:560:97//Hs.155223:AF055460
R-MAMMA1002219//Homo sapiens mRNA for KIAA0640 protein, partial cds//5.2e-45:283:88//Hs.153026:AB014540	R-MAMMA1002494//ESTs//3.2e-47:303:88//Hs.155243:N70293
R-MAMMA1002230//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//9.1e-50:330:77//Hs.108966:U48696	R-MAMMA1002498//Human novel homeobox mRNA for a DNA binding protein//0.0043:331:58//Hs.37035:U07664
R-MAMMA1002236	R-MAMMA1002524//ESTs//0.0039:354:61//Hs.125797:AA806277
R-MAMMA1002243	R-MAMMA1002530//Homo sapiens cytosolic phospholipase A2 gamma (cPLA2 gamma) mRNA, complete cds//3.9e-103:529:95//Hs.18858:AF065214
R-MAMMA1002250//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.2e-44:299:87//Hs.113283:AF018080	R-MAMMA1002545//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.5e-50:317:88//Hs.153468:AB011147
R-MAMMA1002267//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//1.6e-54:207:81//Hs.92381:AB007956	R-MAMMA1002554//ESTs//2.3e-85:445:95//Hs.139140:AA218851
R-MAMMA1002268//ESTs//2.9e-94:439:100//Hs.68061:AI042283	R-MAMMA1002556//ESTs. Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.0e-12:280:65//Hs.12725:T65058
R-MAMMA1002269//ESTs//7.4e-05:170:65//Hs.140466:AA766772	R-MAMMA1002566//ESTs//2.3e-88:421:99//Hs.17602:AA705681
R-MAMMA1002282//ESTs//7.8e-09:69:78//Hs.159502:AA225141	R-MAMMA1002571//ESTs//5.1e-97:456:99//Hs.152834:AA595693
R-MAMMA1002292//ESTs//5.3e-64:334:94//Hs.113606:AI138751	R-MAMMA1002573//ESTs//3.1e-38:258:87//Hs.163989:R74433
R-MAMMA1002293//ESTs. Moderately similar to plakophilin 2b [H.sapiens]//1.7e-39:203:81//Hs.154257:AI275982	R-MAMMA1002585//ESTs//7.8e-96:533:91//Hs.26009:H49371
R-MAMMA1002294//EST//8.1e-43:326:82//Hs.149580:AI281881	R-MAMMA1002590//ESTs//0.61:202:62//Hs.161190:AI419258
R-MAMMA1002297//ESTs//6.5e-45:323:83//Hs.155475:AA761454	R-MAMMA1002597//Cytochrome P450, subfamily 11B (phenobarbital-inducible), polypeptide 6//2.9e-21:177:75//Hs.1360:W29874
R-MAMMA1002298//ESTs//1.7e-68:355:96//Hs.52683:H87153	R-MAMMA1002598//ESTs//3.4e-113:544:97//Hs.20263:AA573737
R-MAMMA1002299//ESTs. Highly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//2.3e-58:346:91//Hs.140385:AA773359	R-MAMMA1002603//Thiopurine S-methyltransferase//7.6e-35:225:80//Hs.51124:AF019369
R-MAMMA1002308	R-MAMMA1002612//Cytochrome P450, subfamily 1 (aromatic compound-inducible), polypeptide 2//4.2e-46:424:75//Hs.1361:M55053
R-MAMMA1002310//Human melanoma antigen recognized by T-cells (MART-1) mRNA//2.2e-44:280:87//Hs.154069:U06452	R-MAMMA1002617//ESTs//1.1e-38:229:92//Hs.96987:W27389
R-MAMMA1002311//Human LINE-1 repeat mRNA with 2 open reading frames//2.3e-70:503:81//Hs.23094:M19503	R-MAMMA1002618//Landsteiner-Wiener blood group glycoprotein//1.3e-27:185:73//Hs.108287:L27670
R-MAMMA1002312//EST//1.7e-31:144:80//Hs.135936:N36094	R-MAMMA1002619//ESTs//1.7e-95:480:96//Hs.54873:AA526306
R-MAMMA1002317//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//4.3e-49:457:76//Hs.144563:AF057280	R-MAMMA1002622//Thromboxane A2 receptor//3.2e-46:298:87//Hs.89887:D38081
R-MAMMA1002319//ESTs//3.9e-38:297:70//Hs.140326:AA827183	R-MAMMA1002623//EST//4.3e-49:336:85//Hs.149580:AI281881
R-MAMMA1002322//ESTs//1.1e-46:301:86//Hs.155498:W27084	R-MAMMA1002625//ESTs. Moderately similar to ovarian-specific protein [R.norvegicus]//2.3e-35:308:79//Hs.93332:AA811920
R-MAMMA1002329//EST//2.6e-09:146:72//Hs.132366:AI026658	R-MAMMA1002629//Homo sapiens mRNA for small GTP-binding protein, complete cds//9.7e-57:283:86//Hs.115325:D84488
R-MAMMA1002332//Homo sapiens clone 23892 mRNA sequence//2.6e-45:387:70//Hs.91916:AF035317	R-MAMMA1002636//Human mRNA for KIAA0392 gene, partial cds//1.2e-49:303:89//Hs.40100:AB002390
R-MAMMA1002333//EST//1.8e-09:139:74//Hs.137800:AA886897	R-MAMMA1002637//ESTs//1.3e-55:391:85//Hs.95074:AI144421
R-MAMMA1002339//ESTs//4.2e-47:310:76//Hs.138865:W57618	R-MAMMA1002646//ESTs//7.4e-36:182:80//Hs.163937:N69915
R-MAMMA1002347//ESTs//1.5e-42:326:83//Hs.111723:H57439	R-MAMMA1002650//ESTs//1.6e-102:547:94//Hs.57841:W63776
R-MAMMA1002351//ESTs//3.0e-112:545:97//Hs.26209:AI143127	R-MAMMA1002655
R-MAMMA1002352//Homo sapiens mRNA for leukemia associated gene 2//1.5e-58:259:92//Hs.43628:Y15228	R-MAMMA1002662//Homo sapiens KIAA0426 mRNA, complete cds//2.2e-46:462:75//Hs.97476:AB007886
R-MAMMA1002353//Human mRNA for KIAA0392 gene, partial cds//4.5e-40:360:77//Hs.40100:AB002390	R-MAMMA1002665//Human mRNA for KIAA0118 gene, partial cds//9.1e-51:376:82//Hs.154326:D42087
R-MAMMA1002355//ESTs//1.4e-29:307:75//Hs.3769:AI085367	R-MAMMA1002671//ESTs. Weakly similar to coded for by C. elegans CDNA yk520.5 [C.elegans]//5.3e-108:544:96//Hs.16464:W19606
R-MAMMA1002356//Clathrin, light polypeptide (Lcb)//4.9e-31:217:88//Hs.73919:X81637	R-MAMMA1002673//EST//3.3e-35:169:79//Hs.140046:AA668213
R-MAMMA1002359//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-70:483:84//Hs.113283:AF018080	R-MAMMA1002684//Homo sapiens mRNA for KIAA0214 protein, complete cds//4.6e-109:544:96//Hs.3363:D86987
R-MAMMA1002360//ESTs//3.5e-19:301:69//Hs.124701:AA701475	R-MAMMA1002685//EST//1.9e-31:223:86//Hs.112540:AA601385
R-MAMMA1002361//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//2.6e-30:244:81//Hs.129727:AF035587	R-MAMMA1002698//ESTs//5.9e-43:292:85//Hs.144660:AA652675
R-MAMMA1002362//ESTs//2.3e-43:241:88//Hs.150727:AI292236	R-MAMMA1002699//ESTs//3.2e-25:134:100//Hs.126049:F22510
R-MAMMA1002380//ESTs//5.1e-36:322:79//Hs.136994:AA843542	R-MAMMA1002701//ESTs. Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.9e-70:353:96//Hs.138404:R70986
R-MAMMA1002384//Small inducible cytokine A5 (RANTES)//1.8e-42:298:84//Hs.155464:AF088219	R-MAMMA1002708//ESTs//2.1e-76:413:94//Hs.57932:W69234
R-MAMMA1002385//ESTs//0.57:203:63//Hs.146303:AA579061	R-MAMMA1002711//ESTs//1.9e-44:236:96//Hs.138575:H67858
R-MAMMA1002392//Human mRNA for platelet-activating factor acetylhydrolase 2, complete cds//5.8e-41:305:83//Hs.86188:D87845	R-MAMMA1002721//Homo sapiens DEC-205 mRNA, complete cds//2.7e-43:73:89//Hs.153563:AF011333
R-MAMMA1002411//ESTs//4.4e-68:385:92//Hs.53478:N92294	R-MAMMA1002727//ESTs//2.9e-84:395:100//Hs.162826:AA679571
R-MAMMA1002413//Homo sapiens mRNA for small GTP-binding protein, complete cds//3.3e-14:138:75//Hs.115325:D84488	R-MAMMA1002728//Small inducible cytokine A5 (RANTES)//3.4e-42:266:88//Hs.155464:AF088219
R-MAMMA1002417//ESTs//1.6e-98:475:98//Hs.96345:W22588	R-MAMMA1002744//ESTs//4.2e-18:473:63//Hs.42826:AA846757
R-MAMMA1002427//ESTs//3.1e-39:274:79//Hs.141130:H28477	R-MAMMA1002746//ESTs//1.8e-100:473:99//Hs.117558:AA779907
R-MAMMA1002428//ESTs//8.4e-11:215:66//Hs.141022:H06475	R-MAMMA1002748//Human melanoma antigen recognized by T-cells (MART-1) mRNA//5.8e-40:330:80//Hs.154069:U06452
R-MAMMA1002434//ESTs. Moderately similar to !!!! ALU SUBFAMILY SP WARNING ENTRY !!!! [H.sapiens]//2.5e-106:521:98//Hs.112152:AA487348	R-MAMMA1002754//ESTs. Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//4.5e-40:369:77//Hs.105292:AA504776
R-MAMMA1002446//ESTs. Weakly similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//4.7e-37:374:68//Hs.157142:U85996	R-MAMMA1002758
R-MAMMA1002454//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0485//2.0e-60:323:81//Hs.89121:AB007954	R-MAMMA1002764//ESTs//4.2e-103:486:99//Hs.159909:AI393281
R-MAMMA1002461//ESTs//4.7e-111:548:97//Hs.104281:AA147076	R-MAMMA1002765//ESTs//1.6e-37:338:76//Hs.37573:H59651
R-MAMMA1002470//ESTs. Highly similar to HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION [Saccharomyces cerevisiae]//8.5e-104:544:93//Hs.94570:AI192106	R-MAMMA1002769//ESTs//0.72:409:57//Hs.141376:AI301272
	R-MAMMA1002780//ESTs//1.6e-52:292:92//Hs.135985:AA342750
	R-MAMMA1002782//ESTs//1.0e-31:157:80//Hs.159510:AA297145
	R-MAMMA1002796//ESTs//3.8e-49:284:92//Hs.156479:AA513812

【表613】

R-MAMMA1002807//Archain//1.4e-39:315:80//Hs.33642:X81198	87:94//Hs.108112:AF070640
R-MAMMA1002820//ESTs//5.0e-14:192:74//Hs.134635:AA226260	R-NT2RM4000024//ESTs//2.9e-98:523:94//Hs.26641:R59312
R-MAMMA1002830//EST//4.0e-50:255:97//Hs.160674:A1248319	R-NT2RM4000027
R-MAMMA1002833//EST//1.2e-48:306:88//Hs.149580:A1281881	R-NT2RM4000030//ESTs//1.6e-96:482:96//Hs.90625:T03663
R-MAMMA1002835	R-NT2RM4000046//ESTs//1.6e-91:461:97//Hs.151237:A1186169
R-MAMMA1002838//EST//2.7e-12:161:76//Hs.163252:AA828723	R-NT2RM4000061//ESTs//4.3e-31:167:97//Hs.110821:Z78379
R-MAMMA1002842//ESTs//1.7e-41:366:78//Hs.141899:N22395	R-NT2RM4000085//Homo sapiens clone 24700 unknown mRNA, partial cds
R-MAMMA1002843//Von Hippel-Lindau syndrome//8.8e-38:258:79//Hs.78160:AF010238	//4.0e-113:549:97//Hs.95665:AF070639
R-MAMMA1002844//ESTs//3.5e-51:250:99//Hs.151445:AA351081	R-NT2RM4000086//EST//2.7e-17:212:76//Hs.137041:AA877817
R-MAMMA1002858//H.sapiens ERF-1 mRNA 3' end//9.0e-101:361:91//Hs.85155:X79067	R-NT2RM4000104//ESTs//3.0e-85:452:94//Hs.101750:H19708
R-MAMMA1002868//ESTs//2.1e-38:301:80//Hs.132717:AA171941	R-NT2RM4000139//EST//3.3e-05:156:66//Hs.133228:A1052312
R-MAMMA1002871//EST//6.0e-88:413:99//Hs.149057:A1243592	R-NT2RM4000155//ESTs. Moderately similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [H.sapiens]//1.9e-99:536:92//Hs.127810:A1246301
R-MAMMA1002880//ESTs//6.5e-100:506:96//Hs.163533:N52194	R-NT2RM4000156//EST//0.89:169:62//Hs.162967:AA676397
R-MAMMA1002881//EST//1.1e-40:335:80//Hs.160895:A1365871	R-NT2RM4000167//ESTs//1.0:214:61//Hs.119370:W52962
R-MAMMA1002886//Small inducible cytokine A5 (RANTES)//3.4e-36:228:88//Hs.155464:AF088219	R-NT2RM4000169//ESTs//5.4e-82:440:93//Hs.159379:A1382160
R-MAMMA1002887//ESTs//4.7e-87:409:99//Hs.152155:AA424811	R-NT2RM4000191//ESTs. Weakly similar to P68 PROTEIN [H.sapiens]//4.1e-99:542:93//Hs.6366:AA614113
R-MAMMA1002890//ESTs. Weakly similar to coded for by C. elegans cD NA CEE5882F [C. elegans]//4.2e-92:438:99//Hs.155871:AA533783	R-NT2RM4000197//ESTs//5.4e-113:567:96//Hs.22975:AA156723
R-MAMMA1002892//Homo sapiens EV15 homolog mRNA, complete cds//4.9e-62:322:80//Hs.26929:AF008915	R-NT2RM4000199//ESTs//0.020:95:65//Hs.146203:A1254528
R-MAMMA1002895//ESTs//7.2e-32:330:76//Hs.139132:AA211087	R-NT2RM4000200//ESTs//1.4e-100:488:97//Hs.126538:AA931876
R-MAMMA1002908//Calcium modulating ligand//4.6e-48:313:86//Hs.13572:AF068179	R-NT2RM4000202//Small inducible cytokine A5 (RANTES)//4.3e-37:330:77//Hs.155464:AF088219
R-MAMMA1002909//Human mRNA for KIAA0180 gene, partial cds//3.4e-09:132:76//Hs.90981:D80002	R-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds//1.7e-103:546:94//Hs.111138:AB018255
R-MAMMA1002930//EST//4.9e-44:260:91//Hs.149580:A1281881	R-NT2RM4000215
R-MAMMA1002938	R-NT2RM4000229//ESTs//7.1e-92:457:97//Hs.162074:AA477760
R-MAMMA1002941//Human Line-1 repeat mRNA with 2 open reading frame s//1.1e-83:556:85//Hs.23094:W19503	R-NT2RM4000233//Fms-related tyrosine kinase 1 (vascular endothelial growth factor/vascular permeability factor receptor)//0.00020:174:66//Hs.235:X51602
R-MAMMA1002947//ESTs//7.0e-22:222:80//Hs.103395:T79243	R-NT2RM4000244//ESTs//6.6e-61:320:95//Hs.108646:AA613031
R-MAMMA1002954//Human mRNA for KIAA0355 gene, complete cds//1.6e-44:427:77//Hs.153014:AB002353	R-NT2RM4000251//Homo sapiens mRNA for TRIP6 (thyroid receptor interacting protein)//0.63:219:62//Hs.119498:AF000974
R-MAMMA1002970//Thromboxane A2 receptor//7.9e-48:300:84//Hs.89887:D38081	R-NT2RM4000265//ESTs//8.8e-105:489:99//Hs.131001:A1378742
R-MAMMA1002972//ESTs. Weakly similar to KIAA0371 [H.sapiens]//9.6e-104:525:95//Hs.94396:AA399630	R-NT2RM4000290//ESTs//4.0e-87:435:96//Hs.162592:AA594128
R-MAMMA1002973//ESTs//4.4e-40:257:87//Hs.163580:H15835	R-NT2RM4000324//ESTs//2.2e-80:413:96//Hs.12313:R43673
R-MAMMA1002982//ESTs//2.5e-28:115:87//Hs.141694:W15279	R-NT2RM4000327//Small inducible cytokine A5 (RANTES)//3.2e-45:286:87//Hs.155464:AF088219
R-MAMMA1002987//Homo sapiens DNA fragmentation factor 40 kDa subunit (DFF40) mRNA, complete cds//2.1e-41:402:67//Hs.133089:AF064019	R-NT2RM4000344//Clathrin, light polypeptide (Lcb)//8.6e-60:452:84//Hs.73919:X81637
R-MAMMA1003003//Calcium modulating ligand//1.9e-45:380:79//Hs.13572:AF068179	R-NT2RM4000349//ESTs. Weakly similar to KIAA0005 [H.sapiens]//2.5e-117:579:96//Hs.5216:AA534881
R-MAMMA1003004//ESTs//3.0e-07:378:60//Hs.61885:A1127857	R-NT2RM4000354//ESTs//2.1e-85:406:99//Hs.126774:A1224479
R-MAMMA1003007//ESTs//2.0e-47:404:80//Hs.146314:R99617	R-NT2RM4000356//ESTs//7.9e-109:548:96//Hs.44278:AA418053
R-MAMMA1003011//ESTs. Highly similar to HISTONE MACRO-H2A.1 [Rattus norvegicus]//1.4e-53:320:90//Hs.92023:A1022248	R-NT2RM4000366//Homo sapiens mRNA for KIAA0642 protein, partial cds//2.8e-113:577:95//Hs.8152:AB014542
R-MAMMA1003015//ESTs//1.5e-42:363:79//Hs.155184:AA573189	R-NT2RM4000368//ESTs//2.2e-61:310:97//Hs.143611:W78140
R-MAMMA1003019//ESTs//4.8e-10:232:66//Hs.111341:AA251268	R-NT2RM4000386//ESTs. Weakly similar to tenascin-like protein [D.melanogaster]//1.0e-93:521:92//Hs.41793:AA775879
R-MAMMA1003026//ESTs//2.3e-83:394:99//Hs.24668:AA897315	R-NT2RM4000395//ESTs. Highly similar to HYPOTHETICAL 52.9 KD PROTEIN IN SAPISS-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//1.9e-99:524:94//Hs.5249:U55977
R-MAMMA1003031//ESTs. Moderately similar to !!!! ALU SUBFAMILY J W ARNING ENTRY !!!! [H.sapiens]//3.5e-27:257:77//Hs.96337:AA225358	R-NT2RM4000414//EST//2.7e-06:196:64//Hs.136648:AA688285
R-MAMMA1003035//ESTs//1.3e-94:481:94//Hs.92411:AA603321	R-NT2RM4000421//ESTs. Weakly similar to No definition line found [C. elegans]//5.4e-75:470:90//Hs.69235:AA192359
R-MAMMA1003039//EST//0.56:210:61//Hs.162248:AA552160	R-NT2RM4000425//H.sapiens mRNA for MACH-alpha-2 protein//0.17:112:69//Hs.19949:X98173
R-MAMMA1003040//ESTs//2.1e-17:261:70//Hs.46980:W55940	R-NT2RM4000433//ESTs//2.7e-100:479:98//Hs.24553:A1150687
R-MAMMA1003044//EST//2.4e-18:124:91//Hs.130321:A1002941	R-NT2RM4000457//ESTs//5.1e-107:535:95//Hs.7579:AA775865
R-MAMMA1003047//ESTs//1.0e-20:209:78//Hs.15916:H12862	R-NT2RM4000471//ESTs. Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//6.0e-99:492:96//Hs.21090:AA418587
R-MAMMA1003049//14-3-3 PROTEIN SIGMA//0.94:184:60//Hs.2510:X57348	R-NT2RM4000486//ESTs. Moderately similar to unnamed protein product [H.sapiens]//2.2e-102:493:97//Hs.111279:W84558
R-MAMMA1003055//EST//1.0e-49:281:92//Hs.149580:A1281881	R-NT2RM4000496
R-MAMMA1003056//ESTs//0.99:107:66//Hs.30348:A1038559	R-NT2RM4000511//EST//5.1e-43:326:81//Hs.157658:A1358465
R-MAMMA1003057//ESTs. Highly similar to hypothetical protein MD6 [M.musculus]//1.1e-102:545:93//Hs.13755:AA878911	R-NT2RM4000514//ESTs//1.7e-112:552:96//Hs.6686:AA205496
R-MAMMA1003066//H.sapiens mRNA for urea transporter//8.1e-45:322:83//Hs.66710:X96969	R-NT2RM4000515//ESTs. Weakly similar to HYPOTHETICAL 85.0 KD PROTEIN IN CPA2-ATP2 INTERGENIC REGION [Saccharomyces cerevisiae]//1.4e-60:343:93//Hs.16014:AA074879
R-MAMMA1003089//ESTs. Weakly similar to !!!! ALU SUBFAMILY SQ WARMING ENTRY !!!! [H.sapiens]//1.4e-34:421:70//Hs.161959:AA493652	R-NT2RM4000520//ESTs//2.7e-55:266:100//Hs.99838:AA204731
R-MAMMA1003099//ESTs//1.1e-43:379:79//Hs.37573:H59651	R-NT2RM4000531//ESTs//2.0e-88:502:91//Hs.13110:T67461
R-MAMMA1003104//ESTs//2.1e-97:498:96//Hs.9299:T51283	R-NT2RM4000532//ESTs//0.47:290:58//Hs.148753:T91777
R-MAMMA1003113//EST//3.7e-29:457:70//Hs.123616:AA815366	R-NT2RM4000534//EST//0.00025:303:60//Hs.162809:AA632198
R-MAMMA1003127//ESTs//2.6e-41:283:86//Hs.146811:AA410788	R-NT2RM4000585//EST//0.28:63:77//Hs.150024:A1291981
R-MAMMA1003135//ESTs//7.2e-101:504:97//Hs.87729:AA863125	R-NT2RM4000590//ESTs//5.8e-65:320:98//Hs.116017:AA613437
R-MAMMA1003140//ESTs//4.3e-44:200:89//Hs.152093:A1149537	R-NT2RM4000595//Homo sapiens KIAA0431 mRNA, partial cds//0.99:189:64//Hs.16349:AB007891
R-MAMMA1003146//Wingless-type MMTV integration site 5A, human homolog//0.020:413:61//Hs.152213:L20861	R-NT2RM4000603//ESTs//4.6e-68:356:96//Hs.48855:AA134589
R-MAMMA1003150	R-NT2RM4000611//ESTs//1.5e-89:431:97//Hs.26117:W16697
R-MAMMA1003166//ESTs. Moderately similar to PEANUT PROTEIN [Drosophila melanogaster]//2.0e-87:524:89//Hs.6884:W30736	R-NT2RM4000616//ESTs. Highly similar to ACETYL-COENZYME A SYNTHET
R-NT2RM2002580//Homo sapiens clone 24781 mRNA sequence//1.6e-111:5	

【0916】

【表614】

ASE [Escherichia coli]//1.4e-102:519:96//Hs.14779:N64822	r protein Lnk [M.musculus]//4.0e-102:539:94//Hs.15744:A1055859
R-NT2RM4000674//ESTs//5.1e-78:398:97//Hs.8268:N70144	R-NT2RM4000412
R-NT2RM4000689//ESTs, Weakly similar to T01G9.4 [C.elegans]//2.9e-115:550:98//Hs.11820:AA205531	R-NT2RM4001414//ESTs//6.5e-35:226:88//Hs.121727:AA75895
R-NT2RM4000698//ESTs//2.0e-17:130:87//Hs.86420:AA927510	R-NT2RM4001437//EST//0.017:169:67//Hs.13207:F10054
R-NT2RM4000700	R-NT2RM4001444//ESTs, Weakly similar to ISOLEUCYL-TRNA SYNTHETASE, MITOCHONDRIAL [S.cerevisiae]//7.4e-108:544:94//Hs.7558:AA526812
R-NT2RM4000712//EST//0.99:103:65//Hs.114039:AA701128	R-NT2RM4001454//ESTs//4.7e-108:517:98//Hs.32295:N32277
R-NT2RM4000717//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//2.2e-103:519:95//Hs.6823:W18181	R-NT2RM4001455//EST//9.6e-81:395:97//Hs.127978:AA69739
R-NT2RM4000733//ESTs//8.7e-88:429:98//Hs.72185:AA465311	R-NT2RM4001483//Human mRNA for KIAA0033 gene, partial cds//1.8e-58:324:85//Hs.22271:D26067
R-NT2RM4000734//Homo sapiens mRNA for KIAA0760 protein, partial cds//3.6e-105:536:95//Hs.137168:AB018303	R-NT2RM4001489//Homo sapiens mRNA for KIAA0685 protein, complete cds//7.0e-104:547:93//Hs.153121:AB014585
R-NT2RM4000741//ESTs//0.99:266:58//Hs.142718:AA034046	R-NT2RM4001519//Histatin 1//0.53:340:59//Hs.119101:M26664
R-NT2RM4000751//ESTs//1.6e-20:351:66//Hs.43145:AA776988	R-NT2RM4001522//Small inducible cytokine A5 (RANTES)//8.4e-55:306:80//Hs.155464:AF088219
R-NT2RM4000764	R-NT2RM4001557//ESTs, Weakly similar to FliA10.4 [C.elegans]//6.1e-21:165:83//Hs.29134:H43072
R-NT2RM4000778//EST//0.066:254:61//Hs.148232:AA904174	R-NT2RM4001565//ESTs//2.0e-103:483:99//Hs.121273:AA758027
R-NT2RM4000779//Homo sapiens mRNA for KIAA0451 protein, complete cds//9.3e-106:546:94//Hs.18586:AB007920	R-NT2RM4001566//Human DNA sequence from clone 1409 on chromosome X p11.1-11.4. Contains a Inter-Alpha-Trypsin Inhibitor Heavy Chain 1 LIKE gene, a alternatively spliced Melanoma-Associated Antigen MAGE
R-NT2RM4000787//Human melanoma antigen recognized by T-cells (MART-1) mRNA//6.5e-40:424:73//Hs.154069:U06452	LIKE gene and a 6-Phosphofructo-2-kinase (Fructose-2,6-bisphosphatase) LIKE pseudogene. Contains ESTs, STSs and genomic marker DXS8
R-NT2RM4000790//EST//9.0e-48:259:94//Hs.159694:A1417008	032//2.7e-43:446:72//Hs.4943:Z98046
R-NT2RM4000795//Human mRNA for KIAA0087 gene, complete cds//1.0e-20:3:63//Hs.20991:D31891	R-NT2RM4001569//ESTs//3.6e-37:186:100//Hs.85959:AA888009
R-NT2RM4000796//ESTs//7.0e-106:506:98//Hs.43559:A1003520	R-NT2RM4001582//ESTs//1.2e-96:459:98//Hs.114432:N52946
R-NT2RM4000798//Human polymorphic epithelial mucin core protein mRNA, 3' end//2.5e-28:158:96//Hs.118249:M21868	R-NT2RM4001592
R-NT2RM4000813	R-NT2RM4001594//ESTs//1.6e-83:404:98//Hs.134740:AA282171
R-NT2RM4000820//ESTs, Weakly similar to hypothetical protein [H.sapiens]//1.3e-109:539:97//Hs.99636:A1219667	R-NT2RM4001597//ESTs//6.9e-111:558:96//Hs.11408:A1358871
R-NT2RM4000833//ESTs, Moderately similar to ZK863.3 [C.elegans]//4.0e-112:448:99//Hs.20223:AA482031	R-NT2RM4001605//Homo sapiens mRNA for KIAA0791 protein, complete cds//2.1e-112:565:95//Hs.23255:AB018334
R-NT2RM4000848//ESTs//8.1e-97:476:97//Hs.16036:AA883864	R-NT2RM4001611//EST//5.9e-74:353:99//Hs.125318:AA837079
R-NT2RM4000852//ESTs//6.4e-94:467:97//Hs.11556:A1309597	R-NT2RM4001629//ESTs//6.1e-95:453:99//Hs.115765:AA485957
R-NT2RM4000855//ESTs//2.9e-95:544:90//Hs.106525:A1283343	R-NT2RM4001650
R-NT2RM4000887	R-NT2RM4001662
R-NT2RM4000895//ESTs, Moderately similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]//9.3e-96:450:99//Hs.142076:AA604514	R-NT2RM4001666//Homo sapiens mRNA for KIAA0469 protein, complete cds//3.6e-36:230:70//Hs.7764:AB007938
R-NT2RM4000950//ESTs//2.6e-91:438:98//Hs.43827:AA455262	R-NT2RM4001682//EST//4.3e-68:393:90//Hs.157362:A1367496
R-NT2RM4000971//EST//2.9e-96:461:99//Hs.139709:AA227887	R-NT2RM4001710//ESTs//4.3e-48:235:99//Hs.7299:AA203440
R-NT2RM4000979//EST//1.6e-67:329:98//Hs.96927:AA349647	R-NT2RM4001714//ESTs//0.0014:568:58//Hs.50458:AA868686
R-NT2RM4000996//ESTs, Weakly similar to ZINC FINGER PROTEIN 91 [H.sapiens]//1.7e-82:414:96//Hs.115342:AA650126	R-NT2RM4001715//ESTs//6.5e-104:487:99//Hs.153581:AA630465
R-NT2RM4001002//Homo sapiens mRNA for KIAA0729 protein, partial cds//3.8e-114:545:97//Hs.19542:AB018272	R-NT2RM4001731//ESTs, Weakly similar to No definition line found [C.elegans]//3.1e-108:563:94//Hs.18510:AA522887
R-NT2RM4001016//Homo sapiens mRNA for KIAA0639 protein, partial cds//2.5e-114:556:97//Hs.15711:AB014539	R-NT2RM4001741//T3 receptor-associating cofactor-1 [human, fetal liver, mRNA, 2930 nt]//0.083:124:68//Hs.120980:S83390
R-NT2RM4001032//ESTs//7.8e-17:132:84//Hs.138720:N53352	R-NT2RM4001746//ESTs//6.1e-90:420:100//Hs.139003:AA948200
R-NT2RM4001047//Homo sapiens UKLF mRNA for ubiquitous Kruppel like factor, complete cds//0.42:133:67//Hs.32170:AB015132	R-NT2RM4001754//Human knpi repeat mRNA (cdna clone pcd-kpni-4), 3' end//5.4e-59:504:78//Hs.139107:K00629
R-NT2RM4001054//ESTs//1.7e-84:404:99//Hs.116407:AA815300	R-NT2RM4001758//ESTs//8.9e-27:140:100//Hs.149973:A1290740
R-NT2RM4001084//ESTs//3.4e-91:439:99//Hs.103177:W72798	R-NT2RM4001776//Homo sapiens mRNA for KIAA0727 protein, partial cds//6.4e-24:236:80//Hs.39871:AB018270
R-NT2RM4001092//ESTs//1.4e-86:517:89//Hs.132969:Z78324	R-NT2RM4001783//ESTs//9.9e-30:156:99//Hs.115260:AA314956
R-NT2RM4001116//ESTs//5.2e-57:275:100//Hs.131115:A1016962	R-NT2RM4001810//ESTs//1.3e-65:346:95//Hs.131915:W22567
R-NT2RM4001140//ESTs//5.5e-96:461:98//Hs.86965:AA252276	R-NT2RM4001813//ESTs//5.7e-102:473:100//Hs.87574:A1089920
R-NT2RM4001151//ESTs//0.40:263:58//Hs.113189:R08311	R-NT2RM4001823//ESTs//3.8e-62:324:95//Hs.124109:AA888839
R-NT2RM4001155//ESTs//8.3e-105:544:94//Hs.29647:W60848	R-NT2RM4001828//ESTs//1.3e-119:563:98//Hs.102397:AA706551
R-NT2RM4001160//EST//7.6e-25:380:68//Hs.147405:A1209085	R-NT2RM4001836//ESTs//5.5e-16:92:100//Hs.26996:AA551070
R-NT2RM4001187//ESTs, Moderately similar to !!! ALU SUBFAMILY SC WARNING ENTRY !!! [H.sapiens]//9.2e-43:273:91//Hs.109005:N31174	R-NT2RM4001841//ESTs//1.3e-99:540:94//Hs.42322:AA082619
R-NT2RM4001191//Cytochrome P450, 51 (lanosterol 14-alpha-demethylase) //3.1e-32:274:70//Hs.2379:U23942	R-NT2RM4001842//ESTs, Weakly similar to !!! ALU SUBFAMILY SQ WARNING ENTRY !!! [H.sapiens]//4.1e-10:274:62//Hs.161959:AA493652
R-NT2RM4001200//ESTs//4.5e-102:494:97//Hs.31844:N32849	R-NT2RM4001856//ESTs, Weakly similar to contains similarity to ATP/GTP-binding site motif [C.elegans]//3.0e-43:292:86//Hs.14202:N46000
R-NT2RM4001203	R-NT2RM4001858//ESTs//6.2e-104:495:98//Hs.118686:AA682280
R-NT2RM4001204//ESTs//9.8e-88:468:93//Hs.4990:T65307	R-NT2RM4001865//Homo sapiens mRNA for atopy related autoantigen CALC//1.6e-120:592:97//Hs.61628:Y17711
R-NT2RM4001217//ESTs//1.2e-75:396:94//Hs.25042:R72410	R-NT2RM4001876//ESTs//2.9e-98:532:92//Hs.100734:AA158252
R-NT2RM4001256//ESTs//1.0:157:62//Hs.65377:AA994677	R-NT2RM4001880//ESTs//2.5e-29:224:86//Hs.6193:AA045149
R-NT2RM4001258//ESTs//9.6e-41:260:88//Hs.27633:N76184	R-NT2RM4001905//ESTs//5.6e-109:565:95//Hs.9536:AA114178
R-NT2RM4001309	R-NT2RM4001922//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARNING ENTRY !!! [H.sapiens]//1.2e-105:535:95//Hs.30991:AA994438
R-NT2RM4001313//EST//0.0022:150:66//Hs.161573:W84857	R-NT2RM4001930//ESTs//4.1e-84:425:96//Hs.80042:N63143
R-NT2RM4001316//ESTs//3.5e-26:139:99//Hs.23100:A1128899	R-NT2RM4001938//EST//0.00040:241:60//Hs.147235:A1205893
R-NT2RM4001320//ESTs//1.6e-97:308:99//Hs.112024:A1042352	R-NT2RM4001940//Homo sapiens timeless homolog mRNA, complete cds//2.0e-110:556:95//Hs.118631:AF098162
R-NT2RM4001340//ESTs, Highly similar to UTR4 PROTEIN [Saccharomyces cerevisiae]//1.9e-105:522:97//Hs.18442:A1129307	R-NT2RM4001953//ESTs//5.3e-65:338:96//Hs.33718:AA453268
R-NT2RM4001344//EST//1.1e-90:436:99//Hs.95900:AA160339	R-NT2RM4001965//ESTs, Weakly similar to T1484.2 gene product [C.elegans]//5.7e-62:326:95//Hs.3385:N25917
R-NT2RM4001347//EST//0.17:186:61//Hs.16751:T90476	R-NT2RM4001969//ESTs, Weakly similar to IP63 protein [R.norvegicus]//1.9e-21:121:98//Hs.8772:AA521097
R-NT2RM4001371//EST//0.0069:270:62//Hs.99239:AA450211	
R-NT2RM4001382	
R-NT2RM4001384//ESTs//9.6e-91:445:98//Hs.55000:AA805507	
R-NT2RM4001410//EST//0.13:50:82//Hs.157675:A1358790	
R-NT2RM4001411//ESTs, Weakly similar to lymphocyte specific adapt	

【0917】

【表615】

R-NT2RM4001979//ESTs//1.4e-96:465:98//Hs.157103:W60265	R-NT2RM4002623//ESTs. Weakly similar to ASPARTYL-TRNA SYNTHETASE [Thermus aquaticus thermophilus]//9.6e-28:194:87//Hs.59346:AI12680
R-NT2RM4001984	2
R-NT2RM4001987	R-NT2RP2000001//ESTs//2.6e-80:386:99//Hs.105061:N45096
R-NT2RM4002013//EST//2.2e-14:110:90//Hs.160835:AI345528	R-NT2RP2000006//Thromboxane A2 receptor//7.2e-37:253:84//Hs.89887:038081
R-NT2RM4002018	R-NT2RP2000008//Zinc finger protein 37a (KOX 21)//5.2e-25:366:67//Hs.54488:X69115
R-NT2RM4002034//Human mRNA for KIAA0118 gene, partial cds//9.4e-46:293:87//Hs.154326:D42087	R-NT2RP2000027//ESTs//9.5e-74:377:96//Hs.96557:AA286713
R-NT2RM4002044//ESTs//2.8e-107:537:96//Hs.24078:W44435	R-NT2RP2000040//Homo sapiens mRNA for KIAA0747 protein, partial cds//2.7e-42:223:96//Hs.8309:AB018290
R-NT2RM4002054//ESTs//3.7e-88:482:94//Hs.4243:T78226	R-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//4.3e-64:309:98//Hs.6216:AF061749
R-NT2RM4002062//ESTs//1.4e-55:377:85//Hs.152592:AA587887	R-NT2RP2000054//EST//1.2e-71:375:96//Hs.98835:AA435798
R-NT2RM4002063//Calcium modulating ligand//1.8e-43:385:78//Hs.13572:AF068179	R-NT2RP2000056//EST//2.8e-28:342:69//Hs.135526:AI094910
R-NT2RM4002066//Homo sapiens OPA-containing protein mRNA, complete cds//5.5e-42:554:68//Hs.85313:AF071309	R-NT2RP2000067//ESTs. Weakly similar to tenascin-like protein [D. melanogaster]//2.3e-35:199:94//Hs.41793:AA775879
R-NT2RM4002067//Human knp1 repeat rna (cdna clone pcd-knp1-4), 3' end//2.3e-43:468:73//Hs.139107:K00629	R-NT2RP2000070//ESTs. Weakly similar to proto-cadherin 3 [R. norvegicus]//1.4e-78:383:98//Hs.58254:W72881
R-NT2RM4002073//ESTs. Weakly similar to very-long-chain acyl-CoA synthetase [H. sapiens]//6.8e-57:290:96//Hs.109274:AA193416	R-NT2RP2000076//EST//0.0014:227:63//Hs.136761:AA738097
R-NT2RM4002075//ESTs//0.078:267:61//Hs.163563:AA641655	R-NT2RP2000077//Homo sapiens growth arrest specific 11 (GAS11) mRNA, complete cds//1.1e-78:379:97//Hs.54877:AF050078
R-NT2RM4002093//ESTs//1.2e-64:316:99//Hs.34956:AI052528	R-NT2RP2000079//Homo sapiens RET finger protein-like 1 antisense transcript, partial//2.9e-21:232:75//Hs.102576:AJ010230
R-NT2RM4002109//ESTs//1.0:95:69//Hs.25897:W65409	R-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds//1.8e-75:378:96//Hs.22926:AB018338
R-NT2RM4002128//Homo sapiens mRNA for BCL9 gene//0.51:258:60//Hs.122607:Y13620	R-NT2RP2000091//Carcinoembryonic antigen gene family member 6//0.030:236:63//Hs.41:D90064
R-NT2RM4002140//ESTs//5.5e-46:187:94//Hs.8737:W22712	R-NT2RP2000097//ESTs//4.2e-15:92:97//Hs.7432:AA281757
R-NT2RM4002145//ESTs//4.6e-70:374:94//Hs.141082:H18987	R-NT2RP2000098//ESTs//9.0e-53:279:94//Hs.87807:AA813827
R-NT2RM4002146//ESTs//1.9e-93:439:99//Hs.119295:AA442090	R-NT2RP2000108//EST//1.5e-75:378:96//Hs.162105:AA524419
R-NT2RM4002161//Homo sapiens laforin (EPM2A) mRNA, partial cds//1.5e-111:560:96//Hs.22464:AF084535	R-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds//5.8e-76:386:95//Hs.17705:AB018356
R-NT2RM4002174//Homo sapiens LIM protein mRNA, complete cds//3.2e-46:552:72//Hs.154103:AF061258	R-NT2RP2000120//ESTs. Weakly similar to HYPOTHETICAL 68.7 KD PROTEIN ZK757.1 IN CHROMOSOME III [C. elegans]//1.9e-19:153:86//Hs.5268:W22670
R-NT2RM4002189//ESTs//9.6e-75:352:100//Hs.98350:H15400	R-NT2RP2000126//ESTs//1.0e-55:293:95//Hs.14570:AI422099
R-NT2RM4002194//EST//0.22:68:72//Hs.149104:AI244343	R-NT2RP2000133//ESTs//0.24:354:59//Hs.157564:AI356513
R-NT2RM4002205//EST//0.00028:103:72//Hs.130032:AA897678	R-NT2RP2000147//ESTs. Highly similar to CLATHRIN COAT ASSEMBLY PROTEIN AP47 [Mus musculus]//3.0e-89:457:95//Hs.3832:AI208601
R-NT2RM4002213//ESTs//3.3e-15:160:78//Hs.63304:W22079	R-NT2RP2000153//EST//0.0039:93:68//Hs.140386:AA773548
R-NT2RM4002226//ESTs. Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]//5.1e-112:569:95//Hs.23900:U82984	R-NT2RP2000157//ESTs//1.1e-53:322:91//Hs.6877:AA040820
R-NT2RM4002251//ESTs. Weakly similar to similar to alpha-1,3-mannosyl-glycoprotein beta-1, 2-N-acetylglucosaminyltransferase [C. elegans]//1.1e-100:544:93//Hs.27567:W2190	R-NT2RP2000161//ESTs//1.6e-99:492:97//Hs.21738:AI188190
R-NT2RM4002256//Small inducible cytokine A5 (RANTES)//1.0e-44:341:81//Hs.155464:AF088219	R-NT2RP2000175//ESTs//1.4e-98:489:96//Hs.4849:AI143741
R-NT2RM4002266//ESTs//2.6e-100:539:93//Hs.57976:AA535864	R-NT2RP2000183//ESTs//9.0e-72:358:96//Hs.4856:MS1373
R-NT2RM4002278//ESTs//1.8e-112:569:95//Hs.87281:AA128263	R-NT2RP2000195//ESTs//3.9e-92:439:98//Hs.145091:AA814510
R-NT2RM4002280//ESTs//4.9e-20:187:80//Hs.141203:HS2638	R-NT2RP2000205//ESTs. Moderately similar to !!! ALU SUBFAMILY J W ARNING ENTRY !!! [H. sapiens]//1.4e-80:415:95//Hs.11807:T86897
R-NT2RM4002287//ESTs//7.9e-84:388:94//Hs.33977:MS2461	R-NT2RP2000224//RNA polymerase II, polypeptide C (33kd)//1.1e-57:306:94//Hs.79402:AC004382
R-NT2RM4002294	R-NT2RP2000232
R-NT2RM4002301//ESTs//4.5e-111:556:96//Hs.85916:AA194164	R-NT2RP2000233//ESTs//1.1e-08:63:96//Hs.124861:AI090683
R-NT2RM4002323//ESTs//4.5e-102:498:97//Hs.85782:AA191498	R-NT2RP2000239//ESTs//5.3e-87:427:96//Hs.86211:AA604379
R-NT2RM4002339//ESTs//5.0e-59:283:100//Hs.125048:AA682913	R-NT2RP2000248//ESTs. Weakly similar to O-linked GlcNAc transferase [H. sapiens]//1.3e-95:454:99//Hs.102057:AA649005
R-NT2RM4002344//V-akt murine thymoma viral oncogene homolog 2//0.29:153:66//Hs.155129:W77198	R-NT2RP2000257//ESTs//5.1e-58:282:99//Hs.122565:AI126840
R-NT2RM4002373//Homo sapiens mRNA for KIAA0649 protein, complete cds//2.8e-122:593:97//Hs.26163:AB014549	R-NT2RP2000258//EST//1.0:67:68//Hs.61812:AA035649
R-NT2RM4002374//ESTs//3.3e-40:505:70//Hs.95115:AA206594	R-NT2RP2000270//ESTs. Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [Homo sapiens]//8.4e-59:298:96//Hs.16085:AI261382
R-NT2RM4002383//ESTs//2.7e-93:455:97//Hs.134278:AA648884	R-NT2RP2000274//ESTs//7.5e-61:296:98//Hs.86081:AA196635
R-NT2RM4002390//ESTs//3.3e-93:481:95//Hs.48764:AA613328	R-NT2RP2000288//ESTs//1.8e-56:305:93//Hs.7579:AA775865
R-NT2RM4002409//ESTs. Weakly similar to coded for by C. elegans CDNA yk52e10.5 [C. elegans]//1.3e-97:473:98//Hs.16464:W19606	R-NT2RP2000289
R-NT2RM4002438//ESTs//0.74:162:61//Hs.65377:AA994677	R-NT2RP2000297//ESTs. Highly similar to MKR2 PROTEIN [Mus musculus]//9.8e-106:494:99//Hs.102951:AA574249
R-NT2RM4002446	R-NT2RP2000298//ESTs//2.1e-62:256:90//Hs.8737:W22712
R-NT2RM4002452//EST//1.0:164:60//Hs.116619:AA668142	R-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds//2.8e-39:222:93//Hs.58218:U82381
R-NT2RM4002457	R-NT2RP2000327//Homo sapiens DNA sequence from PAC 434014 on chromosome 1q32.3.-41. Contains the HSD11B1 gene for Hydroxysteroid (11-beta) Dehydrogenase 1, the ADORA2B adenosine A2b receptor LIKE pseudogene, the IRF6 gene for Interferon Regulatory Factor 6 and two unknown genes. Contains ESTs and GSSs//2.9e-71:342:98//Hs.8768:AL022398
R-NT2RM4002460//ESTs//3.0e-74:385:96//Hs.6933:R07890	R-NT2RP2000329//ESTs. Highly similar to GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL [Bos taurus]//3.4e-69:371:94//Hs.43436:N32441
R-NT2RM4002479//Homo sapiens RNA helicase-related protein mRNA, complete cds//1.6e-103:507:97//Hs.8765:AF083255	R-NT2RP2000337//ESTs//5.2e-79:411:95//Hs.101799:AI276062
R-NT2RM4002482//Homo sapiens mRNA for KIAA0691 protein, complete cds//2.3e-32:172:98//Hs.94781:AB014591	R-NT2RP2000346//Homo sapiens apoptosis associated protein (CADD34) mRNA, complete cds//1.1e-47:262:94//Hs.76556:U83981
R-NT2RM4002493//ESTs//6.4e-73:366:97//Hs.157114:T58884	R-NT2RP2000369//ESTs//4.3e-102:531:94//Hs.15855:H98103
R-NT2RM4002499//ESTs//3.5e-61:307:97//Hs.117737:AI088029	
R-NT2RM4002504//ESTs//2.1e-55:306:94//Hs.10949:AA644464	
R-NT2RM4002527//ESTs. Weakly similar to peroxisome targeting signal 2 receptor [H. sapiens]//1.4e-73:360:91//Hs.31030:HS0467	
R-NT2RM4002532//ESTs//1.3e-21:191:78//Hs.146811:AA410788	
R-NT2RM4002534//ESTs//1.8e-99:512:95//Hs.13526:AI417057	
R-NT2RM4002567//ESTs//7.6e-41:272:87//Hs.7114:R24312	
R-NT2RM4002571//ESTs. Highly similar to POLYPEPTIDE N-ACETYLGLYCOSAMINYLTRANSFERASE [Bos taurus]//2.3e-89:435:97//Hs.15830:AA165698	
R-NT2RM4002593//ESTs//2.3e-109:552:96//Hs.17424:AA190569	

【0918】

【表616】

R-NT2RP2000414//Homo sapiens HnRNP F protein mRNA, complete cds// 8.4e-09:93:83//Hs.808:L28010	R-NT2RP2001290//ESTs//2.4e-91:501:92//Hs.12600:AA044775
R-NT2RP2000420//ESTs//8.2e-24:142:94//Hs.144893:AI222324	R-NT2RP2001295//ESTs//1.4e-70:337:99//Hs.123854:AA412665
R-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//4.2e-20:140:90//Hs.5819:AF102265	R-NT2RP2001312//ESTs//4.6e-53:276:95//Hs.7961:AA401205
R-NT2RP2000438//ESTs, Weakly similar to misato [O.melanogaster]// 1.3e-65:362:93//Hs.22197:AI151425	R-NT2RP2001327//ESTs, Moderately similar to tumor necrosis factor- alpha-induced protein B12 [H.sapiens]//2.3e-43:238:93//Hs.106632:N 25679
R-NT2RP2000448//ESTs, Highly similar to HYPOTHETICAL 51.6 KD PROT EIN IN PAP1-MRPL13 INTERGENIC REGION [Saccharomyces cerevisiae]// 3.6e-75:435:92//Hs.21938:W81045	R-NT2RP2001328//ESTs//5.1e-99:499:96//Hs.34868:AI341138
R-NT2RP2000459//ESTs//2.8e-95:527:93//Hs.103422:AI352013	R-NT2RP2001347//ESTs//6.7e-05:100:77//Hs.9536:AA114178
R-NT2RP2000498//ESTs//2.3e-17:119:79//Hs.161714:AA229078	R-NT2RP2001378//ESTs//4.2e-83:456:93//Hs.10554:N50028
R-NT2RP2000503//ESTs//5.2e-91:438:98//Hs.152335:AI290215	R-NT2RP2001381//ESTs//1.1e-26:148:96//Hs.161859:AA444038
R-NT2RP2000510//Homo sapiens KIAA0436 mRNA, partial cds//0.13:455: 58//Hs.110:AB007896	R-NT2RP2001392//ESTs, Weakly similar to MITOCHONDRIAL LON PROTEASE HOMOLOG PRECURSOR [H.sapiens]//3.9e-74:411:93//Hs.47305:AA195153
R-NT2RP2000516//ESTs//9.9e-63:376:89//Hs.47546:AA181348	R-NT2RP2001397//ESTs, Highly similar to G2/MITOTIC-SPECIFIC CYCLI N B2 [Mesocricetus auratus]//5.2e-97:469:97//Hs.20483:AA522505
R-NT2RP2000523	R-NT2RP2001420//ESTs//1.6e-49:228:88//Hs.163602:N32030
R-NT2RP2000603//Homo sapiens mRNA for KIAA0572 protein, partial cd s//3.5e-30:167:97//Hs.14409:AB011144	R-NT2RP2001423//ESTs//2.0e-37:190:99//Hs.101565:R35431
R-NT2RP2000617//ESTs//9.5e-103:493:98//Hs.9412:W72446	R-NT2RP2001427//EST//1.7e-11:107:84//Hs.148584:AI201728
R-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cd s//8.1e-66:335:96//Hs.7314:AB014514	R-NT2RP2001436//ESTs, Weakly similar to F0208.3 [C.elegans]//2.9e- 114:558:97//Hs.7627:AI341556
R-NT2RP2000644//ESTs//1.1e-18:372:63//Hs.82419:AA789222	R-NT2RP2001440//EST//0.17:192:58//Hs.133442:AI061394
R-NT2RP2000656//ESTs//1.0e-10:128:80//Hs.23977:AA115275	R-NT2RP2001445//ESTs//1.1e-43:215:100//Hs.145497:AA501453
R-NT2RP2000658//ESTs//0.31:278:59//Hs.15661:W02396	R-NT2RP2001449//ESTs//4.1e-08:234:61//Hs.134067:AI076765
R-NT2RP2000668//ESTs//8.2e-40:255:88//Hs.113310:R16767	R-NT2RP2001450//ESTs//9.5e-65:356:94//Hs.61829:AI079539
R-NT2RP2000678//ESTs//2.6e-53:271:96//Hs.23790:N99347	R-NT2RP2001467//Small inducible cytokine A5 (RANTES)//1.2e-34:255: 83//Hs.155464:AF088219
R-NT2RP2000710//ESTs//0.49:190:63//Hs.145521:AI261368	R-NT2RP2001506//ESTs//2.9e-23:170:88//Hs.7147:T23513
R-NT2RP2000715//EST//1.2e-87:418:99//Hs.139425:AA429279	R-NT2RP2001511//ESTs//2.0e-08:59:100//Hs.57660:AA251146
R-NT2RP2000731//EST//5.3e-65:322:97//Hs.136754:AA713965	R-NT2RP2001520//Homo sapiens mRNA for mitochondrial carrier protei n ARALAR1//6.7e-108:545:95//Hs.4277:Y14494
R-NT2RP2000758//ESTs//1.0:187:61//Hs.10545:N62642	R-NT2RP2001526//ESTs//3.7e-23:295:72//Hs.8514:AF039240
R-NT2RP2000764//ESTs//5.8e-84:485:91//Hs.121816:AA775419	R-NT2RP2001536//Homo sapiens X-ray repair cross-complementing prot ein 3 (XRCC3) mRNA, complete cds//1.9e-15:99:95//Hs.99742:AF035586
R-NT2RP2000809	R-NT2RP2001560//ESTs//2.2e-58:310:94//Hs.87454:AA732816
R-NT2RP2000812//ESTs//1.2e-45:231:97//Hs.121028:AA902745	R-NT2RP2001569//Homo sapiens mRNA, chromosome 1 specific transcrip t KIAA0488//2.0e-76:387:96//Hs.67619:AB007957
R-NT2RP2000814//ESTs//6.3e-87:433:97//Hs.145479:AA969404	R-NT2RP2001576//Human mRNA for KIAA0105 gene, complete cds//0.17:1 93:60//Hs.119:D14661
R-NT2RP2000816//ESTs//0.45:100:69//Hs.147529:AA458918	R-NT2RP2001581//ESTs//5.1e-08:107:78//Hs.157114:T58884
R-NT2RP2000819	R-NT2RP2001597//EST//5.2e-22:151:88//Hs.158613:AI369995
R-NT2RP2000841//ESTs//1.9e-73:351:99//Hs.116385:AI224511	R-NT2RP2001601//ESTs//1.5e-78:373:99//Hs.137558:AI393767
R-NT2RP2000842//TUMOR NECROSIS FACTOR-INDUCIBLE PROTEIN TSG-6 PREC URSOR//4.6e-10:247:66//Hs.29352:M31165	R-NT2RP2001613
R-NT2RP2000845//ESTs//2.8e-91:443:97//Hs.66810:AI206552	R-NT2RP2001628//EST//0.99:195:60//Hs.144238:W52294
R-NT2RP2000863//ESTs//4.3e-49:310:88//Hs.104336:W07345	R-NT2RP2001663//ESTs//4.0e-37:282:84//Hs.12319:W56090
R-NT2RP2000880//Homo sapiens mRNA for KIAA0741 protein, complete c ds//2.8e-43:277:89//Hs.3615:AB018284	R-NT2RP2001677//ESTs//1.4e-44:232:96//Hs.159387:AI370845
R-NT2RP2000892//ESTs//2.8e-50:258:96//Hs.119238:AA476267	R-NT2RP2001678//ESTs//0.91:124:60//Hs.10593:AI201336
R-NT2RP2000931//MATRIN 3//7.2e-57:290:96//Hs.78825:AB018266	R-NT2RP2001699//EST//0.0033:230:61//Hs.146544:AI125323
R-NT2RP2000938//ESTs, Highly similar to HYPOTHETICAL 6.3 KD PROTE IN XK652.2 IN CHROMOSOME III [Caenorhabditis elegans]//3.9e-37:19 9:95//Hs.112318:AA186477	R-NT2RP2001720//ESTs//1.8e-52:255:99//Hs.101064:AA290579
R-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete c ds//9.8e-98:494:96//Hs.19822:AB018298	R-NT2RP2001721//ESTs//7.0e-101:479:99//Hs.129750:AA987538
R-NT2RP2000965//EST//0.22:223:60//Hs.105703:AA487021	R-NT2RP2001740//ESTs//3.3e-76:379:96//Hs.144704:AI147100
R-NT2RP2000970//EST//8.7e-06:255:62//Hs.149202:AI246481	R-NT2RP2001748//ESTs//1.4e-44:352:81//Hs.142259:AA828840
R-NT2RP2000985//ESTs, Weakly similar to HYPOTHETICAL 96.8 KD PROTE IN IN S152-MTD1 INTERGENIC REGION [S.cerevisiae]//7.8e-92:468:95// Hs.12124:AA522537	R-NT2RP2001762//Homo sapiens exonuclease 1a (EXO1a) mRNA, complete cds//2.1e-105:519:96//Hs.47504:AF091754
R-NT2RP2000987//ESTs//4.5e-78:419:93//Hs.21968:H97521	R-NT2RP2001813//ESTs//6.3e-78:406:95//Hs.21902:R44037
R-NT2RP2001036//EST//2.0e-33:148:82//Hs.163196:AA767643	R-NT2RP2001861
R-NT2RP2001044//ESTs//5.6e-95:493:95//Hs.21958:AA453660	R-NT2RP2001869//EST//2.8e-21:173:82//Hs.130321:AI002941
R-NT2RP2001065//ESTs//3.6e-28:153:96//Hs.119314:AA432108	R-NT2RP2001876//ESTs//6.1e-102:526:95//Hs.4944:AA533088
R-NT2RP2001070//EST//0.30:94:67//Hs.94289:N73665	R-NT2RP2001883//ESTs, Weakly similar to No definition line found [C.elegans]//6.9e-110:556:95//Hs.23159:AA113849
R-NT2RP2001094//EST//0.75:101:69//Hs.161040:H82068	R-NT2RP2001900//ESTs//6.9e-85:442:95//Hs.154220:AA171724
R-NT2RP2001119	R-NT2RP2001907//ESTs//2.1e-82:432:94//Hs.142257:AA188423
R-NT2RP2001127//Homo sapiens mRNA for HRIHF2060, partial cds//1.5 e-56:304:94//Hs.146282:AB015348	R-NT2RP2001926//EST//2.3e-24:299:71//Hs.135085:AI097268
R-NT2RP2001137	R-NT2RP2001936//ESTs//1.1e-45:265:92//Hs.112482:T66087
R-NT2RP2001149//ESTs//5.1e-66:324:97//Hs.27475:AA704512	R-NT2RP2001943//EST//1.4e-05:246:61//Hs.144096:AI032180
R-NT2RP2001168//ESTs//2.0e-98:539:92//Hs.77870:AI188145	R-NT2RP2001946//ESTs//3.6e-87:410:99//Hs.20242:W72594
R-NT2RP2001173//Homo sapiens mRNA for KIAA0480 protein, complete c ds//1.5e-96:490:96//Hs.26247:AB007949	R-NT2RP2001947//ESTs//1.9e-55:338:88//Hs.58582:T72588
R-NT2RP2001174//ESTs//2.2e-63:354:93//Hs.24266:R28287	R-NT2RP2001969
R-NT2RP2001196//ESTs//1.4e-83:463:93//Hs.124304:AA825510	R-NT2RP2001976//ESTs//1.2e-98:499:95//Hs.121028:AA902745
R-NT2RP2001218//ESTs//1.4e-100:506:96//Hs.93391:AI188402	R-NT2RP2001985//ESTs, Weakly similar to GTPASE-ACTIVATING PROTEIN SPA-1 [M.musculus]//8.3e-15:118:89//Hs.18760:AA166678
R-NT2RP2001226//EST//0.0074:154:63//Hs.128612:AA909358	R-NT2RP2002025//ESTs//2.1e-82:393:98//Hs.159488:AI378233
R-NT2RP2001233//ESTs, Highly similar to ZINC FINGER PROTEIN ZFP-3 6 [Homo sapiens]//3.7e-65:538:80//Hs.44014:AA632298	R-NT2RP2002032//ESTs//4.4e-98:531:91//Hs.93836:AA813332
R-NT2RP2001245//ESTs//5.2e-90:447:97//Hs.14559:H92996	R-NT2RP2002033//ESTs//3.5e-43:229:96//Hs.30563:AA102627
R-NT2RP2001268//Homo sapiens mRNA for KIAA0810 protein, partial cd s//1.5e-112:544:97//Hs.7513:AB018353	R-NT2RP2002041
R-NT2RP2001277//ESTs//2.0e-81:387:99//Hs.13751:AA908229	R-NT2RP2002046//ESTs//1.6e-101:476:99//Hs.101107:AA825938
	R-NT2RP2002047//ESTs//9.1e-85:431:95//Hs.116750:AA629895
	R-NT2RP2002058//ESTs//1.3e-31:163:99//Hs.33085:AA258068
	R-NT2RP2002066//ESTs//1.9e-87:459:93//Hs.118871:AA846091
	R-NT2RP2002070//ESTs//4.1e-63:332:96//Hs.156446:T92265
	R-NT2RP2002076//Homo sapiens clone 24804 mRNA sequence//1.7e-26:17

【0919】

【表617】

8:87//Hs.11039:AF052183	R-NT2RP2002839//ESTs. Moderately similar to !!!! ALU SUBFAMILY J W
R-NT2RP2002079//ESTs//1.2e-79:389:97//Hs.135214:AI350524	ARNING ENTRY !!!! [H.sapiens]//1.6e-100:501:97//Hs.136202:AA206578
R-NT2RP2002099//Homo sapiens mRNA for E1B-55kDa-associated protein	R-NT2RP2002857//ESTs//4.3e-94:463:97//Hs.134292:AA603031
//1.5e-60:376:89//Hs.155218:AJ007509	R-NT2RP2002862//ESTs//2.3e-42:302:82//Hs.117969:H94870
R-NT2RP2002105//ESTs//8.4e-54:313:90//Hs.98702:AI123000	R-NT2RP2002880
R-NT2RP2002124//ESTs//6.6e-81:431:93//Hs.127326:AA525134	R-NT2RP2002891
R-NT2RP2002137//Deoxyctidine kinase//0.29:183:62//Hs.709:M60527	R-NT2RP2002925//ESTs//1.3e-103:564:92//Hs.142079:AA182894
R-NT2RP2002154//ESTs//9.6e-97:539:91//Hs.18624:AA523268	R-NT2RP2002928//ESTs//3.9e-108:502:99//Hs.29105:AA574143
R-NT2RP2002172//EST//0.69:53:75//Hs.156238:AI334495	R-NT2RP2002929//ESTs//4.1e-106:499:99//Hs.44743:AA837096
R-NT2RP2002185//ESTs. Weakly similar to F15C11.2 [C.elegans]//1.4	R-NT2RP2002954//ESTs//2.6e-88:417:99//Hs.100824:AI308771
e-54:269:98//Hs.107201:W52859	R-NT2RP2002959//ESTs//7.5e-101:489:97//Hs.32690:M57480
R-NT2RP2002192//ESTs. Moderately similar to !!!! ALU SUBFAMILY J W	R-NT2RP2002979//ESTs//5.4e-06:197:65//Hs.146726:AI147060
ARNING ENTRY !!!! [H.sapiens]//3.9e-15:245:71//Hs.87578:AI125363	R-NT2RP2002980//ESTs//1.0e-110:562:96//Hs.28444:AA083213
R-NT2RP2002193//ESTs//3.5e-79:453:90//Hs.76578:AI290672	R-NT2RP2002986//ESTs. Highly similar to RING CANAL PROTEIN [Drosophila melanogaster]//3.1e-119:578:97//Hs.106290:AI125291
R-NT2RP2002208//ESTs//2.0e-72:347:99//Hs.164028:AI003946	R-NT2RP2002987//Human mRNA for KIAA0331 gene, complete cds//1.0:7
R-NT2RP2002219//EST//0.039:229:63//Hs.149830:AI287499	8:74//Hs.146395:AB002329
R-NT2RP2002231//ESTs//3.3e-64:337:94//Hs.79828:AA642341	R-NT2RP2002993//ESTs. Weakly similar to DNA-DIRECTED RNA POLYMERASE
R-NT2RP2002252//ESTs. Highly similar to co-repressor protein [M.musculus]//5.4e-48:238:99//Hs.22583:AA188168	E1140 KD POLYPEPTIDE [H.sapiens]//2.4e-98:467:98//Hs.85337:AA14
R-NT2RP2002256//Homo sapiens retinoic acid hydroxylase mRNA, complete cds//1.6e-15:131:83//Hs.150595:AF005418	9311
R-NT2RP2002259//Human L-myc protein gene, complete cds//5.3e-99:54	R-NT2RP2003000//ESTs//0.0070:400:61//Hs.138506:U85642
8:91//Hs.92137:M19720	R-NT2RP2003034//ESTs//9.3e-87:408:96//Hs.164042:HI2594
R-NT2RP2002270//ESTs. Weakly similar to AF-9 PROTEIN [H.sapiens]//	R-NT2RP2003073//Human transporter protein (glt) mRNA, complete cds
4.8e-100:550:91//Hs.4029:Z78373	//0.95:259:61//Hs.76460:U49082
R-NT2RP2002292//ESTs. Weakly similar to F13B12.1 [C.elegans]//3.2	R-NT2RP2003099//Thromboxane A2 receptor//2.6e-42:328:81//Hs.89887:
e-92:482:93//Hs.5570:AI377863	D38081
R-NT2RP2002312//Homo sapiens CDP-diacylglycerol synthase 2 (CDS2)	R-NT2RP2003108//ESTs//2.3e-82:398:98//Hs.5105:AA115512
mRNA, partial cds//4.1e-103:527:94//Hs.24812:AF069532	R-NT2RP2003117//Human mRNA for KIAA0347 gene, complete cds//2.4e-4
R-NT2RP2002316//ESTs//4.2e-91:425:100//Hs.3350:AI368015	9:336:86//Hs.101996:AB002345
R-NT2RP2002325//Homo sapiens peroxisomal biogenesis factor (PEX11a)	R-NT2RP2003121//ESTs//2.0e-75:380:96//Hs.133127:AA133355
mRNA, complete cds//1.2e-112:567:95//Hs.31034:AB015594	R-NT2RP2003125
R-NT2RP2002333//ESTs//1.9e-86:483:91//Hs.155198:AA767372	R-NT2RP2003129//EST//0.68:115:69//Hs.122196:AA780986
R-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds//1.2e-103:600:89//Hs.109051:AF038958	R-NT2RP2003137//ESTs//2.1e-37:259:85//Hs.63169:N78506
R-NT2RP2002394//EST//0.11:158:65//Hs.28792:AI343467	R-NT2RP2003161//ESTs//2.5e-88:451:96//Hs.29041:W37379
R-NT2RP2002408//ESTs//1.5e-51:278:93//Hs.6044:W22815	R-NT2RP2003164//ESTs//4.3e-113:543:97//Hs.8980:AA629067
R-NT2RP2002426//Homo sapiens mRNA for KIAA0563 protein, complete cds//1.7e-33:285:80//Hs.15731:AB011135	R-NT2RP2003165//ESTs//6.9e-83:486:89//Hs.138632:H97952
R-NT2RP2002439//ESTs//3.2e-12:134:76//Hs.32246:AA464020	R-NT2RP2003177//ESTs//0.47:38:100//Hs.61790:AA421156
R-NT2RP2002457//ESTs//4.7e-52:282:94//Hs.21968:H97521	R-NT2RP2003194//ESTs//4.7e-118:582:96//Hs.27266:AA053816
R-NT2RP2002464//ESTs//5.3e-27:148:98//Hs.115660:AI362230	R-NT2RP2003206//ESTs//0.032:388:58//Hs.122148:AA442074
R-NT2RP2002475//ESTs//3.9e-85:439:94//Hs.9873:W27233	R-NT2RP2003230//ESTs//8.8e-103:478:99//Hs.40140:AI079253
R-NT2RP2002479//Homo sapiens mRNA for ABC transporter T protein, complete cds//9.9e-115:605:92//Hs.125856:AB005289	R-NT2RP2003237//ESTs//2.7e-76:392:96//Hs.106278:R37661
R-NT2RP2002498//ESTs//6.3e-37:227:93//Hs.108779:N73180	R-NT2RP2003243//ESTs//3.6e-53:300:92//Hs.118793:AA192438
R-NT2RP2002503//ESTs//1.9e-54:358:86//Hs.57800:W60838	R-NT2RP2003265//ESTs. Highly similar to protein NGD5 [M.musculus]//
R-NT2RP2002504//Homo sapiens mRNA for KIAA0791 protein, complete cds//8.5e-107:583:91//Hs.23255:AB018334	3.3e-110:557:96//Hs.24994:AA236937
R-NT2RP2002520//ESTs//4.2e-99:509:94//Hs.32368:AA205305	R-NT2RP2003272//ESTs. Weakly similar to F15C11.2 [C.elegans]//1.2
R-NT2RP2002537//ESTs//4.2e-105:552:93//Hs.154363:AA533090	e-34:228:89//Hs.107201:W52859
R-NT2RP2002546//Homo sapiens clone TUA8 Cri-du-chat region mRNA//	R-NT2RP2003277//Homo sapiens mRNA for KIAA0625 protein, partial cds//1.4e-111:565:95//Hs.154919:AB014525
2.6e-109:570:93//Hs.49476:AF009314	R-NT2RP2003280//ESTs//2.6e-101:541:94//Hs.6982:AA622427
R-NT2RP2002549//DNA polymerase gamma//1.1e-35:189:86//Hs.80961:U60	R-NT2RP2003286//ESTs//1.2e-104:497:98//Hs.113052:AI222106
325	R-NT2RP2003293//Human mRNA for KIAA0118 gene, partial cds//9.1e-4
R-NT2RP2002591//ESTs. Weakly similar to ZINC FINGER PROTEIN 84 [H.sapiens]//7.1e-118:564:97//Hs.94549:AA149547	4:458:74//Hs.154326:D42087
R-NT2RP2002595//EST//1.4e-15:101:95//Hs.129528:AA994783	R-NT2RP2003295//Protein serine/threonine kinase stk2//0.31:321:57//
R-NT2RP2002606//ESTs//4.5e-99:475:98//Hs.45046:N40170	Hs.1087:L20321
R-NT2RP2002609//ESTs//1.9e-104:568:92//Hs.9175:AI184220	R-NT2RP2003297//ESTs//3.0e-15:118:87//Hs.16621:AA098874
R-NT2RP2002618//ESTs//0.014:493:57//Hs.96322:AA541615	R-NT2RP2003308//ESTs. Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]//4.8e-109:553:96//Hs.26089:AA195126
R-NT2RP2002621//EST//4.4e-36:252:84//Hs.149580:AI281881	R-NT2RP2003329//ESTs//0.99:208:62//Hs.143607:AI424948
R-NT2RP2002643//ESTs//6.9e-32:247:74//Hs.33354:AA179944	R-NT2RP2003339//ESTs//1.3e-85:441:96//Hs.24115:N32618
R-NT2RP2002672	R-NT2RP2003347//ESTs//1.5e-70:365:96//Hs.155773:AI312825
R-NT2RP2002701//N-acetylglucosaminidase, alpha- (Sanfilippo disease e1118//0.99:184:63//Hs.50727:U43572	R-NT2RP2003367//EST//5.8e-80:376:100//Hs.112500:AA599014
R-NT2RP2002706//EST//2.8e-41:148:86//Hs.161917:AA483223	R-NT2RP2003391//ESTs//2.8e-98:484:97//Hs.5842:AA534476
R-NT2RP2002710//EST//0.34:105:71//Hs.136747:AA749210	R-NT2RP2003393//ESTs//2.0e-96:510:93//Hs.75844:AA115502
R-NT2RP2002727//ESTs//8.7e-68:368:94//Hs.14366:T78626	R-NT2RP2003394//EST//5.2e-06:264:63//Hs.144234:W52249
R-NT2RP2002736//ESTs//9.7e-98:457:99//Hs.74899:AA993300	R-NT2RP2003401//ESTs//6.1e-25:161:90//Hs.155360:AA984683
R-NT2RP2002740//Homo sapiens mRNA for KIAA0536 protein, partial cds//0.66:360:59//Hs.119139:AB011108	R-NT2RP2003433//ESTs. Highly similar to PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT [Canis familiaris]//1.2e-106:508:98//Hs.13184
R-NT2RP2002741//ESTs//3.1e-102:489:98//Hs.112024:AI042352	0:AI016073
R-NT2RP2002750//EST//3.6e-43:166:86//Hs.162404:AA573131	R-NT2RP2003445//ESTs. Moderately similar to !!!! ALU SUBFAMILY J W
R-NT2RP2002752//ESTs//5.0e-56:355:89//Hs.95867:M62042	ARNING ENTRY !!!! [H.sapiens]//5.6e-21:161:70//Hs.43153:N22360
R-NT2RP2002753//ESTs//1.7e-49:262:96//Hs.49005:W89124	R-NT2RP2003446//ESTs. Weakly similar to C27H6.4 [C.elegans]//6.0e-
R-NT2RP2002769//ESTs//1.3e-49:376:88//Hs.4046:M03587	105:529:96//Hs.8055:W60903
R-NT2RP2002778//Homo sapiens clone 24606 mRNA sequence//4.0e-65:34	R-NT2RP2003456//ESTs//7.5e-96:449:99//Hs.25362:AI277332
1:94//Hs.17481:AF070537	R-NT2RP2003480//ESTs//1.6e-116:583:96//Hs.59757:AA176121
R-NT2RP2002800//ESTs//6.5e-08:79:84//Hs.153262:AA551124	R-NT2RP2003499//ESTs. Weakly similar to elastin like protein [Drosophila melanogaster]//7.0e-71:365:95//Hs.101056:R52777
	R-NT2RP2003506//ESTs. Weakly similar to ORF YPL207w [S.cerevisiae]//2.2e-115:577:96//Hs.16277:N36831
	R-NT2RP2003511//ESTs//1.6e-22:182:85//Hs.28249:AA203733
	R-NT2RP2003513//Human mRNA for KIAA0270 gene, partial cds//1.3e-10

【表618】

R-566:94//Hs.78482:Y16270	R-NT2RP2004226//ESTs//8.8e-18:252:71//Hs.11924:W26972
R-NT2RP2003517//Platelet-derived growth factor beta polypeptide (s	R-NT2RP2004232//ESTs. Highly similar to protein kinase C mu [H. sap
ian sarcoma viral (v-sis) oncogene homolog//4.9e-62:518:79//Hs.	iens//5.2e-105:499:98//Hs.143460:AA483305
1976:W12783	R-NT2RP2004239//ESTs//1.2e-16:171:80//Hs.16134:AA203116
R-NT2RP2003522//ESTs//2.0e-97:462:99//Hs.24512:D60170	R-NT2RP2004240//Homo sapiens antigen NY-CO-1 (NY-CO-1) mRNA, compl
R-NT2RP2003533//ESTs//4.4e-45:273:78//Hs.140225:AA704101	ete cds//3.4e-103:530:93//Hs.54900:AF039687
R-NT2RP2003543//EST//1.0:80:68//Hs.65646:F13684	R-NT2RP2004242//ESTs//1.3e-85:460:93//Hs.104535:AA211483
R-NT2RP2003559//ESTs. Moderately similar to !!!! ALU SUBFAMILY J W	R-NT2RP2004245//ESTs//6.4e-117:575:97//Hs.23744:AA035744
ARNING ENTRY !!!! [H. sapiens]//1.8e-58:316:94//Hs.28891:W72439	R-NT2RP2004270//ESTs//1.0:95:69//Hs.141371:H92187
R-NT2RP2003564//ESTs//3.2e-112:528:99//Hs.53940:N46696	R-NT2RP2004300//ESTs//4.4e-80:379:99//Hs.130874:AA905056
R-NT2RP2003581//ESTs//1.3e-88:506:93//Hs.16157:AA203719	R-NT2RP2004316//Homo sapiens EXT-like protein 2 (EXTL2) mRNA, comp
R-NT2RP2003596//ESTs. Weakly similar to No definition line found	lete cds//4.7e-110:544:96//Hs.61152:AF000416
[C. elegans]//4.7e-101:495:98//Hs.34627:AA126463	R-NT2RP2004321//ESTs//2.1e-18:104:99//Hs.107207:AA044788
R-NT2RP2003604//Homo sapiens alpha-catenin related protein (ACRP)	R-NT2RP2004339//EST//1.4e-47:309:86//Hs.161917:AA483223
mRNA, complete cds//1.7e-103:501:97//Hs.58488:U97067	R-NT2RP2004347
R-NT2RP2003620//EST//0.032:440:59//Hs.135297:A1038981	R-NT2RP2004364//ESTs//1.1e-113:566:96//Hs.25880:A1268173
R-NT2RP2003643//ESTs. Weakly similar to HYPOTHETICAL 14.1 KD PROTE	R-NT2RP2004365//ESTs//0.022:271:62//Hs.38897:A1129310
IN IN MURZ-RPON INTERGENIC REGION [E. coli]//9.1e-62:359:92//Hs.124	R-NT2RP2004366//ESTs//9.5e-71:335:100//Hs.91867:A1218624
92:AA203188	R-NT2RP2004373//ESTs//4.2e-25:172:87//Hs.83243:N32192
R-NT2RP2003668//EST//9.4e-110:535:97//Hs.116279:AA628951	R-NT2RP2004389//ESTs. Highly similar to HYPOTHETICAL 70.7 KD PROT
R-NT2RP2003681//EST//5.9e-05:196:65//Hs.139064:AA35523	EIN F09C8.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.4e-11:10
R-NT2RP2003691//ESTs. Weakly similar to F59C6.9 [C. elegans]//1.0:2	8:82//Hs.30490:AA146916
02:62//Hs.65539:A1148540	R-NT2RP2004392//ESTs//3.4e-81:427:94//Hs.5827:AA581646
R-NT2RP2003702//ESTs. Moderately similar to ovarian-specific prote	R-NT2RP2004396//EST//5.6e-06:100:77//Hs.138623:H92473
in [R. norvegicus]//4.3e-99:492:96//Hs.93332:AA811920	R-NT2RP2004399//EST//0.98:337:59//Hs.118446:N67900
R-NT2RP2003704//ESTs//1.0:155:63//Hs.104166:AA740246	R-NT2RP2004400//ESTs//2.1e-90:422:100//Hs.152460:AA602921
R-NT2RP2003706//Homo sapiens mRNA for KIAA0525 protein, partial cd	R-NT2RP2004412//ESTs//1.4e-105:503:98//Hs.15929:AA403121
s//8.4e-47:265:93//Hs.78494:AB011097	R-NT2RP2004425//EST//0.00017:225:60//Hs.146935:A1168124
R-NT2RP2003713//EST//0.81:210:50//Hs.14551:T79401	R-NT2RP2004476//ESTs//1.4e-88:477:94//Hs.4859:N26959
R-NT2RP2003714//ESTs//1.7e-99:495:96//Hs.158101:A1365003	R-NT2RP2004490//Homo sapiens 3-phosphoinositide dependent protein
R-NT2RP2003727//Human 19.8 kDa protein mRNA, complete cds//0.84:22	kinase-1 (PKM1) mRNA, complete cds//8.6e-34:143:98//Hs.154729:AF01
1:60//Hs.2384:U18914	7995
R-NT2RP2003737//ESTs. Highly similar to UBIQUITIN-CONJUGATING ENZ	R-NT2RP2004512//ESTs//2.6e-91:426:100//Hs.94133:A1270700
YME E2-17 KD [Caenorhabditis elegans]//2.4e-50:302:90//Hs.19196:W7	R-NT2RP2004523//ESTs//1.6e-74:377:97//Hs.14217:R61320
4577	R-NT2RP2004538//Thromboxane A2 receptor//1.4e-45:279:89//Hs.89887:
R-NT2RP2003751	D38081
R-NT2RP2003760//ESTs//2.6e-101:548:93//Hs.115987:AA483808	R-NT2RP2004551//ESTs//0.47:147:66//Hs.131519:A1024347
R-NT2RP2003764//EST//8.2e-25:134:98//Hs.64036:AA127709	R-NT2RP2004568//ESTs//1.3e-107:567:94//Hs.65234:AA195470
R-NT2RP2003769//ESTs//1.7e-108:545:95//Hs.56847:AA541606	R-NT2RP2004580//ESTs//5.9e-29:156:98//Hs.147801:A1221661
R-NT2RP2003770//Homo sapiens sperm acrosomal protein mRNA, complet	R-NT2RP2004587//ESTs//1.0e-102:495:97//Hs.91662:AA781126
e cds//6.0e-106:531:96//Hs.90436:AF047437	R-NT2RP2004594//ESTs//4.1e-56:298:95//Hs.24641:AA954666
R-NT2RP2003777//ESTs//2.6e-59:323:94//Hs.10101:A1381811	R-NT2RP2004600//ESTs//4.8e-67:374:93//Hs.49762:N69862
R-NT2RP2003781//ESTs//2.0e-25:269:75//Hs.144951:N34836	R-NT2RP2004602//ESTs. Weakly similar to !!!! ALU SUBFAMILY J WARNI
R-NT2RP2003793//ESTs//8.7e-94:466:97//Hs.93949:AA782955	NG ENTRY !!!! [H. sapiens]//4.5e-07:149:76//Hs.12845:N28835
R-NT2RP2003840//ESTs//3.4e-97:533:93//Hs.16130:AA195077	R-NT2RP2004614//ESTs//1.0e-111:557:96//Hs.37892:N53497
R-NT2RP2003857//H. sapiens mRNA for C9A//2.8e-23:351:65//Hs.75196:X	R-NT2RP2004655//Homo sapiens mRNA for leucine rich protein//2.4e-1
69838	18:587:96//Hs.5198:AJ006291
R-NT2RP2003859//ESTs//3.0e-07:96:81//Hs.153262:AA551124	R-NT2RP2004664//Homo sapiens mRNA for KIAA0460 protein, partial cd
R-NT2RP2003871//ESTs//1.9e-102:509:97//Hs.25726:AA430167	s//5.9e-107:520:96//Hs.29956:AB007929
R-NT2RP2003885//ESTs//1.0e-102:502:97//Hs.36353:AA702341	R-NT2RP2004675//ESTs//2.7e-82:407:97//Hs.116113:F18930
R-NT2RP2003912//EST//1.2e-38:336:76//Hs.134975:A1094611	R-NT2RP2004681//NUCLEOLIN//0.34:387:58//Hs.79110:M60858
R-NT2RP2003952//Homo sapiens DNA-binding protein (CROC-1B) mRNA, c	R-NT2RP2004689//Homo sapiens mRNA for KIAA0625 protein, partial cd
omplete cds//0.90:190:60//Hs.75875:U49278	s//5.0e-120:600:96//Hs.154919:AB014525
R-NT2RP2003968//Homo sapiens HUBP mRNA for ubiquitin specific prot	R-NT2RP2004709//ESTs//1.1e-106:511:98//Hs.38034:A1149793
ease, complete cds//7.6e-116:568:97//Hs.35086:AB014458	R-NT2RP2004710//ESTs//9.9e-87:477:93//Hs.6834:AA203433
R-NT2RP2003976//Homo sapiens mRNA for KIAA0447 protein, complete c	R-NT2RP2004736//Homo sapiens mRNA for KIAA0478 protein, complete c
ds//3.6e-109:540:97//Hs.7302:AB007916	ds//1.3e-118:594:96//Hs.4236:AB007947
R-NT2RP2003981//Homo sapiens mRNA for KIAA0804 protein, partial cd	R-NT2RP2004743//ESTs//2.1e-48:327:88//Hs.43635:AA447015
s//2.5e-115:568:96//Hs.7316:AB018347	R-NT2RP2004767//EST//4.0e-57:328:81//Hs.142796:N51423
R-NT2RP2003984	R-NT2RP2004775//ESTs//9.4e-60:326:94//Hs.115339:AA136774
R-NT2RP2003986//ESTs//4.9e-36:272:82//Hs.158268:AA738087	R-NT2RP2004791//ESTs//3.2e-82:367:96//Hs.141911:N64013
R-NT2RP2003988//ESTs. Weakly similar to reverse transcriptase [H. s	R-NT2RP2004799//Homo sapiens ATP-specific succinyl-CoA synthetase
apiens]//3.2e-110:519:99//Hs.36093:A1149968	beta subunit (SCS) mRNA, partial cds//8.0e-116:564:96//Hs.40820:AF
R-NT2RP2004014//ESTs//8.4e-102:483:99//Hs.22867:A1417478	058953
R-NT2RP2004041	R-NT2RP2004802//ESTs//6.5e-111:586:94//Hs.90375:W74579
R-NT2RP2004042//ESTs//1.5e-105:466:97//Hs.7296:N29706	R-NT2RP2004816//Homo sapiens H beta 58 homolog mRNA, complete cds/
R-NT2RP2004066//ESTs//1.4e-110:559:96//Hs.71916:AA219699	//8.7e-120:584:97//Hs.67052:AF054179
R-NT2RP2004081//ESTs//3.7e-105:503:98//Hs.27542:AA977204	R-NT2RP2004841//EST//3.8e-31:323:74//Hs.147714:A1219906
R-NT2RP2004098//EST//7.3e-26:203:87//Hs.21897:R41461	R-NT2RP2004861//EST//0.92:147:63//Hs.23064:R20803
R-NT2RP2004124//ESTs//1.1e-83:435:95//Hs.43299:N23036	R-NT2RP2004897//ESTs//1.7e-46:390:80//Hs.139225:H96567
R-NT2RP2004142//EST//1.3e-06:165:65//Hs.146742:A1147500	R-NT2RP2004936//EST//0.97:176:63//Hs.137436:AA280529
R-NT2RP2004152//ESTs//7.0e-98:455:100//Hs.17731:A1342241	R-NT2RP2004959//ESTs//0.059:137:64//Hs.144109:A1345543
R-NT2RP2004165//ESTs. Highly similar to DYMEIN BETA CHAIN, CILIAR	R-NT2RP2004961//ESTs//1.8e-87:409:100//Hs.138297:AA781941
Y [Anthracidaris crassipinna]//1.0e-118:583:97//Hs.16520:A1224533	R-NT2RP2004962//ESTs//0.0021:292:59//Hs.145917:A1275458
R-NT2RP2004170//ESTs//6.7e-66:407:88//Hs.157138:A1348544	R-NT2RP2004967//Human mRNA for KIAA0118 gene, partial cds//7.4e-5
R-NT2RP2004172//ESTs//1.5e-109:567:95//Hs.159091:AA033974	1:506:75//Hs.154326:042087
R-NT2RP2004187//ESTs//3.6e-92:488:93//Hs.22954:W26589	R-NT2RP2004978//ESTs//0.95:138:63//Hs.13619:W93496
R-NT2RP2004194//ESTs//6.2e-114:585:95//Hs.18778:AA203167	R-NT2RP2004982//ESTs//7.8e-95:468:97//Hs.22545:R43910
R-NT2RP2004196	R-NT2RP2004985
R-NT2RP2004207//ESTs//6.3e-102:488:98//Hs.22678:AA604756	R-NT2RP2004999//ESTs//2.9e-94:450:98//Hs.128766:A1419902

【0921】

【表619】

R-NT2RP2005000	//8.8e-108:560:94//Hs.159597:AJ012449
R-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds//9.6e-113:577:95//Hs.155972:AB014515	R-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds//1.7e-115:583:96//Hs.62515:AB007963
R-NT2RP2005003//EST//1.3e-75:387:96//Hs.140843:R42235	R-NT2RP2005549//EST//0.61:111:62//Hs.147482:A1215572
R-NT2RP2005012//Homo sapiens SEC63 (SEC63) mRNA, complete cds//3.1e-116:568:97//Hs.31575:AF100141	R-NT2RP2005555//ESTs//6.6e-108:507:99//Hs.68613:A1357567
R-NT2RP2005018//ESTs//7.5e-46:280:90//Hs.126857:AA932161	R-NT2RP2005557//ESTs//3.1e-105:495:99//Hs.105985:AA885169
R-NT2RP2005020//ESTs//1.6e-105:554:94//Hs.14846:AA148507	R-NT2RP2005581//ESTs//1.7e-79:445:92//Hs.138152:H03240
R-NT2RP2005031//EST//3.1e-79:379:99//Hs.139709:AA227887	R-NT2RP2005600//ESTs//1.3e-38:192:100//Hs.48329:W92733
R-NT2RP2005037//EST//5.3e-102:551:93//Hs.26516:AA195220	R-NT2RP2005605//ESTs//7.6e-87:409:99//Hs.45005:AA975060
R-NT2RP2005038//ESTs//5.8e-101:566:92//Hs.46964:W49757	R-NT2RP2005620//ESTs//2.9e-96:463:97//Hs.7407:A1376788
R-NT2RP2005108	R-NT2RP2005622//ESTs//1.8e-104:497:98//Hs.22595:AA394229
R-NT2RP2005116//Homo sapiens mRNA for KIAA0664 protein, partial cds//2.7e-105:518:97//Hs.22616:AB014564	R-NT2RP2005637//EST//2.5e-20:163:71//Hs.161164:A148211
R-NT2RP2005126//H. sapiens mRNA for RNA helicase (Myc-regulated dead box protein)//4.6e-69:464:85//Hs.100555:X98743	R-NT2RP2005640//ESTs//5.0e-99:473:98//Hs.23467:AA708740
R-NT2RP2005139//ESTs//1.0e-108:545:95//Hs.21006:AA523383	R-NT2RP2005645//ESTs//9.5e-23:231:77//Hs.5534:AA195173
R-NT2RP2005140//ESTs//4.3e-90:422:99//Hs.62180:A1341261	R-NT2RP2005651//ESTs, Highly similar to XF1N PROTEIN [Xenopus laevis]//2.9e-103:525:96//Hs.70589:AA868470
R-NT2RP2005144//ESTs//0.91:162:62//Hs.52399:A1075744	R-NT2RP2005654//Insulin-like growth factor binding protein 2//0.94:223:60//Hs.162:X16302
R-NT2RP2005147//ESTs//4.6e-100:502:96//Hs.27931:AA633438	R-NT2RP2005669//Homo sapiens nitrilase 1 (NIT1) mRNA, complete cds//2.7e-14:87:100//Hs.146406:AF069987
R-NT2RP2005159//ESTs//7.5e-105:533:95//Hs.109819:A1357582	R-NT2RP2005675//Homo sapiens growth suppressor related (DOC-IR) mRNA, complete cds//5.8e-91:434:98//Hs.25664:AF089814
R-NT2RP2005162//ESTs//6.6e-83:419:96//Hs.113998:H50648	R-NT2RP2005683//ESTs//1.5e-98:494:96//Hs.22595:AA394229
R-NT2RP2005168//Homo sapiens mRNA for E1B-55kDa-associated protein//2.4e-101:513:95//Hs.155218:AJ007509	R-NT2RP2005690//ESTs//4.8e-43:286:86//Hs.150727:A1292236
R-NT2RP2005204//ESTs, Weakly similar to UBQUITIN-ACTIVATING ENZYME E1 HOMOLOG [H. sapiens]//1.9e-115:577:96//Hs.7600:H98166	R-NT2RP2005694//EST//3.1e-82:386:100//Hs.149391:A1273643
R-NT2RP2005227//Homo sapiens LIM protein mRNA, complete cds//1.0e-45:359:82//Hs.154103:AF061258	R-NT2RP2005701//ESTs, Highly similar to BUTYRPHILIN PRECURSOR [Bos taurus]//2.8e-68:376:93//Hs.9095:AA532630
R-NT2RP2005239//ESTs, Highly similar to NIFS-LIKE 54.5 KD PROTEIN [Saccharomyces cerevisiae]//1.0e-47:245:97//Hs.21090:AA418587	R-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds//1.3e-105:503:98//Hs.61638:AB018342
R-NT2RP2005254//ESTs//3.3e-111:581:94//Hs.22549:AA524503	R-NT2RP2005719//ESTs, Weakly similar to GPI-anchored protein p137 precursor [H. sapiens]//5.4e-105:500:98//Hs.14298:A1417523
R-NT2RP2005270//ESTs, Highly similar to HYPOTHETICAL 67.6 KD PROTEIN ZK637.3 IN CHROMOSOME III [Caenorhabditis elegans]//1.1e-79:412:95//Hs.23047:N66596	R-NT2RP2005722//EST//6.5e-76:395:94//Hs.142150:AA223982
R-NT2RP2005276//ESTs//4.6e-85:426:96//Hs.24550:AA316272	R-NT2RP2005723//ESTs//1.5e-84:452:93//Hs.91753:R44455
R-NT2RP2005281//ESTs//1.7e-109:565:94//Hs.61976:A1279001	R-NT2RP2005726//ESTs//3.5e-64:500:82//Hs.100526:A1223153
R-NT2RP2005288//Homo sapiens RCC1-like G exchanging factor RLG mRNA, complete cds//2.4e-125:594:98//Hs.27007:AF060219	R-NT2RP2005741//ESTs//4.7e-60:333:93//Hs.107242:R40258
R-NT2RP2005289//Homo sapiens mRNA for XPR2 protein//4.9e-112:545:96//Hs.44766:AJ007590	R-NT2RP2005748//ESTs//3.4e-102:498:97//Hs.82660:N78064
R-NT2RP2005293//ESTs//5.1e-116:538:99//Hs.62180:A1341261	R-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds//4.3e-42:223:96//Hs.159651:AF068858
R-NT2RP2005315//ESTs//1.4e-82:415:97//Hs.155829:AA018338	R-NT2RP2005753//Homo sapiens l-1 receptor candidate protein mRNA, complete cds//1.2e-104:494:98//Hs.26285:AF082516
R-NT2RP2005325//Human LIM-homeobox domain protein (LIM-2) mRNA, complete cds//2.5e-45:272:91//Hs.1569:U11701	R-NT2RP2005763//ESTs//1.1e-97:456:99//Hs.65412:A1362163
R-NT2RP2005336//ESTs//1.9e-93:444:99//Hs.110966:AA151699	R-NT2RP2005767//ESTs//8.0e-38:204:96//Hs.18460:AA193463
R-NT2RP2005344//Homo sapiens GDP-L-fucose pyrophosphorylase (GFPP) mRNA, complete cds//0.011:463:58//Hs.150926:AF017445	R-NT2RP2005773//ESTs, Highly similar to PYRROLINE-5-CARBOXYLATE REDUCTASE [Homo sapiens]//5.4e-112:559:96//Hs.14214:A1189379
R-NT2RP2005354//ESTs//7.2e-22:148:91//Hs.153783:HI4544	R-NT2RP2005775//ESTs, Highly similar to NEUROLYSIN PRECURSOR [Sus scrofa]//3.0e-108:544:96//Hs.22151:A1214321
R-NT2RP2005360//ESTs//0.048:225:60//Hs.7602:AA099247	R-NT2RP2005781//ESTs//1.7e-43:217:99//Hs.144391:AA365664
R-NT2RP2005393//Homo sapiens mRNA for KIAA0761 protein, partial cds//2.9e-41:248:82//Hs.93121:AB018304	R-NT2RP2005784//EST//0.0071:217:60//Hs.117332:AA699724
R-NT2RP2005407//ESTs, Weakly similar to OSH1 PROTEIN [Saccharomyces cerevisiae]//2.5e-75:461:88//Hs.70849:AA121697	R-NT2RP2005804//ESTs//8.8e-107:512:98//Hs.15496:W44398
R-NT2RP2005436//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN 80495.8 IN CHROMOSOME II [C. elegans]//8.1e-96:491:95//Hs.7194:A1185631	R-NT2RP2005812//ESTs//9.0e-76:359:99//Hs.113937:A1298746
R-NT2RP2005441//ESTs//1.1e-110:548:96//Hs.5209:AA780068	R-NT2RP2005815//ESTs//5.5e-76:363:99//Hs.136230:AA594981
R-NT2RP2005453//ESTs//0.94:352:58//Hs.25870:HI4423	R-NT2RP2005835//ESTs//1.5e-100:541:94//Hs.86813:N25122
R-NT2RP2005457//ESTs//2.1e-46:236:97//Hs.19522:AA975096	R-NT2RP2005841//ESTs//2.8e-105:556:92//Hs.69993:AA628403
R-NT2RP2005464//ESTs//1.8e-72:349:99//Hs.44045:N51307	R-NT2RP2005853//EST//2.0e-13:219:70//Hs.134016:A1076062
R-NT2RP2005465//ESTs//0.0058:322:58//Hs.127009:A1378936	R-NT2RP2005857//ESTs//1.0e-115:576:96//Hs.30663:A1338462
R-NT2RP2005472//ESTs//0.47:309:60//Hs.144838:A1222019	R-NT2RP2005859//ESTs//7.3e-116:571:97//Hs.85986:AA195105
R-NT2RP2005476//ESTs//5.1e-40:205:98//Hs.101577:A1168526	R-NT2RP2005868//EST//0.00023:320:61//Hs.149689:A1284133
R-NT2RP2005490//ESTs//1.3e-70:364:96//Hs.134382:AA083573	R-NT2RP2005890//ESTs//1.0e-96:466:98//Hs.122579:AA766315
R-NT2RP2005491//EST//0.012:220:60//Hs.144448:AA812455	R-NT2RP2005901//ESTs//8.3e-116:548:98//Hs.66296:A1125268
R-NT2RP2005495//ESTs//1.2e-86:501:91//Hs.99445:R93540	R-NT2RP2005908//ESTs, Weakly similar to gastrula zinc finger protein [C. elegans]//2.4e-73:397:94//Hs.16667:192427
R-NT2RP2005496//ESTs//3.2e-34:263:81//Hs.70279:AA757426	R-NT2RP2005933//ESTs, Highly similar to nucleoporin p54 [R. norvegicus]//2.8e-114:560:97//Hs.9082:AA873170
R-NT2RP2005498//ESTs, Highly similar to PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, NEURONAL ISOFORM [Oryctolagus cuniculus]//2.3e-45:284:88//Hs.85752:A1138993	R-NT2RP2005942//ESTs//5.6e-117:582:96//Hs.146123:A1338419
R-NT2RP2005501//ESTs//2.5e-84:404:98//Hs.143812:A1141755	R-NT2RP2005980//ESTs//6.9e-101:478:98//Hs.43145:AA776988
R-NT2RP2005509//ESTs, Highly similar to HYPOTHETICAL 37.2 KD PROTEIN C12C.09C IN CHROMOSOME I [Schizosaccharomyces pombe]//8.2e-36:215:92//Hs.5298:AA725071	R-NT2RP2006023//Homo sapiens PYRIN (MEFV) mRNA, complete cds//8.5e-51:398:80//Hs.113283:AF018080
R-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds//3.2e-110:570:94//Hs.119023:AF092563	R-NT2RP2006038//ESTs//0.025:284:59//Hs.97852:AA404347
R-NT2RP2005525//ESTs, Weakly similar to !!! ALU SUBFAMILY SQ WARMING ENTRY !!! [H. sapiens]//1.3e-84:433:95//Hs.36942:AA524535	R-NT2RP2006043//ESTs, Weakly similar to HYPOTHETICAL 37.0 KD PROTEIN 80495.8 IN CHROMOSOME II [C. elegans]//1.2e-50:278:94//Hs.7194:A1185631
R-NT2RP2005531//EST//0.98:64:70//Hs.146573:A1139856	R-NT2RP2006052//ESTs//5.0e-52:272:95//Hs.99545:AA461492
R-NT2RP2005539//Homo sapiens mRNA for NS1-binding protein (NS1-BP)	R-NT2RP2006069//ESTs//1.8e-90:495:93//Hs.43654:AA527114
	R-NT2RP2006071//ESTs//1.5e-38:218:94//Hs.107882:W72093
	R-NT2RP2006098//ESTs//2.9e-105:540:95//Hs.26860:N56918
	R-NT2RP2006100//Human organic anion transporting polypeptide (OATP) mRNA, complete cds//0.031:254:62//Hs.46440:U21943
	R-NT2RP2006103//ESTs//1.5e-86:416:98//Hs.152114:AA401365
	R-NT2RP2006141//ESTs//5.3e-88:432:98//Hs.77480:AA100522
	R-NT2RP2006166//Homo sapiens LIM protein mRNA, complete cds//2.8e-

【0922】

【表620】

17:255:72//Hs.154103:AF061258	R-NT2RP3000359//EST//4.9e-61:340:92//Hs.126495:AA913741
R-NT2RP2006184//ESTs//8.4e-101:487:98//Hs.58009:W69435	R-NT2RP3000361//ESTs. Weakly similar to PRE-MRNA SPLICING FACTOR P
R-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cd	RP6 [S.cerevisiae]//4.8e-91:439:97//Hs.31334:A114423
s//6.1e-110:553:95//Hs.109299:AB014554	R-NT2RP3000366//EST//0.20:392:57//Hs.149652:A1283303
R-NT2RP2006196//Homo sapiens mRNA sequence//0.0037:48:100//H	R-NT2RP3000397//EST//8.7e-26:150:94//Hs.124617:AA855106
s.151293:U97276	R-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, compl
R-NT2RP2006200//ESTs//6.5e-77:398:96//Hs.163953:R01398	ete cds//4.2e-111:529:98//Hs.28307:AF071185
R-NT2RP2006219//H. sapiens mRNA for DGC86 protein//1.2e-94:532:90//	R-NT2RP3000418//EST//3.3e-09:202:67//Hs.117189:AA682947
Hs.153910:X96484	R-NT2RP3000433
R-NT2RP2006237//ESTs//1.2e-57:305:95//Hs.86149:A1341312	R-NT2RP3000439//ESTs//3.1e-79:426:92//Hs.26548:W26340
R-NT2RP2006238//ESTs. Highly similar to rAB [R.norvegicus]//1.5e-2	R-NT2RP3000441//ESTs//6.3e-84:420:97//Hs.137482:AA421254
9:183:91//Hs.4048:AA04253	R-NT2RP3000449//ESTs//4.9e-93:435:99//Hs.54617:A1379102
R-NT2RP2006250//ESTs//3.2e-87:462:94//Hs.141556:N49928	R-NT2RP3000451//ESTs//2.3e-89:439:97//Hs.9196:AA748492
R-NT2RP2006261//ESTs//3.4e-57:326:92//Hs.22523:W02999	R-NT2RP3000456//Homo Sapiens (clone B3B3E13) chromosome 4p16.3 DNA
R-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds//4.7	fragment//1.8e-23:347:70//Hs.114963:L34408
e-96:481:97//Hs.3404:AF035262	R-NT2RP3000484//Heparin cofactor II//0.98:166:62//Hs.1478:M58600
R-NT2RP2006320//EST//3.4e-21:335:65//Hs.141603:N66015	R-NT2RP3000487//ESTs//0.012:384:60//Hs.88684:AA885141
R-NT2RP2006321//ESTs. Moderately similar to karyopherin beta 3 [H.	R-NT2RP3000512//Homeo box B3//2.0e-69:377:93//Hs.49931:X16667
sapiens]//1.9e-89:460:96//Hs.21889:N78664	R-NT2RP3000526//ESTs//1.6e-91:432:99//Hs.38042:AA187151
R-NT2RP2006323//ESTs//3.5e-91:439:98//Hs.16197:A1081771	R-NT2RP3000527//ESTs//1.2e-100:518:94//Hs.104557:A1078161
R-NT2RP2006333//ESTs//4.9e-38:301:82//Hs.155999:AA196412	R-NT2RP3000531//ESTs. Weakly similar to TH1 protein [D.melanogaste
R-NT2RP2006334//EST//3.1e-45:264:91//Hs.149599:A1282321	r]//0.95:85:71//Hs.5184:AA709151
R-NT2RP2006365//ESTs//2.9e-81:417:95//Hs.11814:W44411	R-NT2RP3000542//ESTs//2.6e-53:375:84//Hs.44158:N30180
R-NT2RP2006393//Cytochrome P450, subfamily I (aromatic compound-in	R-NT2RP3000561//EST//1.1e-13:170:75//Hs.148421:A1198036
ducible), polypeptide 2//3.9e-48:403:77//Hs.1361:M55053	R-NT2RP3000562//Human mRNA for KIAA0233 gene, complete cds//0.97:1
R-NT2RP2006436//Homo sapiens mRNA for small GTP-binding protein, c	41:68//Hs.79077:D87071
omplete cds//1.4e-27:155:76//Hs.115325:D84488	R-NT2RP3000578//ESTs//2.6e-68:324:100//Hs.5445:AA779447
R-NT2RP2006441//ESTs//6.0e-108:529:97//Hs.101282:N45092	R-NT2RP3000582//ESTs//2.1e-25:131:80//Hs.152465:AA563785
R-NT2RP2006454//ESTs//9.2e-20:110:99//Hs.144687:A1341146	R-NT2RP3000584//ESTs//1.8e-97:460:99//Hs.120698:A1241511
R-NT2RP2006456//ESTs//7.1e-91:508:92//Hs.12488:W63595	R-NT2RP3000590//ESTs//2.0e-97:453:100//Hs.105355:AA953817
R-NT2RP2006464//Homo sapiens mRNA for AMD-1 protein//2.1e-109:524:	R-NT2RP3000592//ESTs//2.8e-91:432:99//Hs.144304:A1190916
97//Hs.72160:AJ006266	R-NT2RP3000596//Human mRNA for KIAA0314 gene, partial cds//1.5e-0
R-NT2RP2006467//EST//0.99:140:61//Hs.146958:A1174478	9:447:58//Hs.155045:AB002312
R-NT2RP2006472//ESTs//3.3e-92:473:95//Hs.29216:AA916679	R-NT2RP3000599//ESTs//3.8e-93:437:99//Hs.23971:AA829880
R-NT2RP2006534//EST//3.1e-83:394:99//Hs.162116:AA524947	R-NT2RP3000605//ESTs//4.2e-111:554:96//Hs.40780:AA422049
R-NT2RP2006554//ESTs//1.0e-87:460:95//Hs.47095:AA181474	R-NT2RP3000622//ESTs//2.0e-100:473:99//Hs.11387:A1127394
R-NT2RP2006565//ESTs//3.2e-24:129:100//Hs.13499:A1299886	R-NT2RP3000624//ESTs. Weakly similar to KIAA0256 [H.sapiens]//5.4
R-NT2RP2006571//ESTs//2.6e-56:306:94//Hs.98370:AA316622	e-115:545:98//Hs.4857:A1090739
R-NT2RP2006573//ESTs//2.0e-112:533:98//Hs.18685:A1393829	R-NT2RP3000628//Homo sapiens mRNA for KIAA0772 protein, complete c
R-NT2RP2006598//ESTs. Weakly similar to retinoid X receptor intera	ds//4.3e-49:397:80//Hs.15519:AB018315
cting protein [M.musculus]//4.1e-109:542:97//Hs.7889:A1337112	R-NT2RP3000632//ESTs. Moderately similar to cyclin-selective ubiq
R-NT2RP3000002//ESTs//1.3e-08:399:59//Hs.126044:A1301598	itin carrier protein [H.sapiens]//6.3e-92:434:99//Hs.152517:AA7190
R-NT2RP30000031//Homo sapiens mRNA for histone deacetylase-like pro	22
tein [JM21]//1.9e-116:560:97//Hs.6764:AJ011972	R-NT2RP3000644//ESTs//1.0e-44:306:84//Hs.155498:W27084
R-NT2RP3000046//Small inducible cytokine A5 (RANTES)//1.9e-57:312:	R-NT2RP3000661//ESTs//3.1e-95:470:97//Hs.126069:W76185
85//Hs.155464:AF088219	R-NT2RP3000665//ESTs//3.3e-95:503:94//Hs.34313:W81185
R-NT2RP3000047//EST//0.91:130:66//Hs.140208:AA702213	R-NT2RP3000685//ESTs//2.7e-99:515:94//Hs.9711:R60873
R-NT2RP3000050//ESTs. Weakly similar to putative p150 [H.sapiens]//	R-NT2RP3000690//ESTs//3.3e-88:414:99//Hs.146589:A1085578
3.1e-41:249:90//Hs.156155:A1222202	R-NT2RP3000736
R-NT2RP3000055//EST//2.4e-19:146:86//Hs.160497:A1255095	R-NT2RP3000742//ESTs. Highly similar to 1-PHOSPHATIDYLINOSITOL-4,
R-NT2RP3000072//ESTs//2.2e-82:424:96//Hs.21542:N49574	5-BISPHOSPHATE PHOSPHODIESTERASE DELTA 1 [Rattus norvegicus]//1.8
R-NT2RP3000080//ESTs//2.1e-29:186:89//Hs.153372:AA424029	e-07:114:75//Hs.136065:W21960
R-NT2RP3000085//EST//4.5e-101:482:98//Hs.47649:AA838715	R-NT2RP3000753//ESTs//3.1e-99:461:100//Hs.150901:A1310447
R-NT2RP3000109//ESTs//9.5e-97:455:99//Hs.17731:A1342241	R-NT2RP3000759//ESTs//2.0e-74:384:95//Hs.104222:AA207243
R-NT2RP3000134//EST//4.7e-106:497:99//Hs.125531:AA884000	R-NT2RP3000815//ESTs//8.5e-97:455:99//Hs.158897:A1378583
R-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cd	R-NT2RP3000825//EST//0.0089:343:59//Hs.42897:N20810
s//1.2e-116:578:96//Hs.13273:AB011164	R-NT2RP3000826//EST//3.4e-33:342:74//Hs.162236:AA551582
R-NT2RP3000149//ESTs//7.7e-62:361:90//Hs.6649:N93418	R-NT2RP3000836//ESTs//6.8e-24:181:84//Hs.134464:A1151081
R-NT2RP3000186	R-NT2RP3000841//ESTs//4.5e-93:491:93//Hs.23618:H98082
R-NT2RP3000197//ESTs//1.5e-75:436:91//Hs.140931:R51882	R-NT2RP3000845//ESTs//2.4e-88:473:93//Hs.8312:AA813022
R-NT2RP3000207//ESTs//1.3e-98:468:98//Hs.126908:AA933091	R-NT2RP3000847//ESTs//9.3e-89:460:95//Hs.154106:A1051657
R-NT2RP3000220//ESTs//2.2e-27:144:99//Hs.106861:R61306	R-NT2RP3000850
R-NT2RP3000233//EST//7.8e-77:368:99//Hs.49075:N64817	R-NT2RP3000852//Fibrillin 2//0.55:237:63//Hs.79432:U03272
R-NT2RP3000235//ESTs//0.43:82:74//Hs.132828:A1032819	R-NT2RP3000859//ESTs//1.4e-96:509:94//Hs.7187:AA576895
R-NT2RP3000247//EST//2.2e-97:459:99//Hs.127928:AA969239	R-NT2RP3000865//EST//4.8e-23:461:66//Hs.162088:AA505741
R-NT2RP3000251	R-NT2RP3000868//ESTs//5.4e-78:430:93//Hs.102796:N70837
R-NT2RP3000252//ESTs. Weakly similar to Lpg15p [S.cerevisiae]//2.0	R-NT2RP3000869//ESTs//8.5e-77:397:94//Hs.84484:A1014673
e-108:532:97//Hs.111086:A1379177	R-NT2RP3000875//Mevalonate kinase//3.8e-78:531:84//Hs.75138:W88468
R-NT2RP3000255//EST//0.67:93:67//Hs.120579:AA743073	R-NT2RP3000901//ESTs//2.1e-95:465:97//Hs.10647:AA428217
R-NT2RP3000267//ESTs//8.5e-108:542:95//Hs.24984:AA534446	R-NT2RP3000904//ESTs//1.6e-79:380:99//Hs.100850:AA479385
R-NT2RP3000299//ESTs. Weakly similar to enhancer of filamentation 1	R-NT2RP3000917//ESTs. Highly similar to mouse Dhml protein [M.musc
[H.sapiens]//3.6e-103:516:96//Hs.4894:A1191323	ulus]//9.5e-113:566:96//Hs.5900:AA035728
R-NT2RP3000312//ESTs//1.3e-100:493:97//Hs.29379:A1094117	R-NT2RP3000919
R-NT2RP3000320//ESTs//3.2e-95:538:91//Hs.118793:AA192438	R-NT2RP3000968//40S RIBOSOMAL PROTEIN S15A//1.5e-25:375:71//Hs.295
R-NT2RP3000324	3:X84407
R-NT2RP3000333//ESTs//6.0e-39:194:100//Hs.119238:AA476267	R-NT2RP3000980//ESTs//3.3e-72:364:96//Hs.9536:AA114178
R-NT2RP3000341//ESTs//0.51:251:61//Hs.94090:AA777689	R-NT2RP3000994//ESTs//3.5e-111:537:97//Hs.21146:AA683542
R-NT2RP3000348//EST//1.8e-80:389:98//Hs.145944:A1276225	R-NT2RP3001004//ESTs//9.6e-91:456:96//Hs.58974:W87405
R-NT2RP3000350//ESTs. Weakly similar to Lpg15p [S.cerevisiae]//3.1	R-NT2RP3001007//ESTs//6.7e-99:482:97//Hs.117737:A1088029
e-110:556:96//Hs.111086:A1379177	R-NT2RP3001055//ESTs//0.0012:294:60//Hs.66479:AA863044

【0923】

【表621】

R-NT2RP3001057//ESTs, Highly similar to ZINC FINGER PROTEIN HF.12 [Homo sapiens]//5.6e-102:486:99//Hs.145956:AA007349	RC8 (TRC8) mRNA, complete cds//6.8e-112:549:97//Hs.28285:AF064801
R-NT2RP3001081//Retinal pigment epithelium-specific protein (65kD) //0.0012:447:58//Hs.2133:U18991	R-NT2RP3001527//ESTs//4.4e-105:543:95//Hs.158761:AA631047
R-NT2RP3001084//ESTs//4.3e-102:528:96//Hs.25277:W87874	R-NT2RP3001529//Homo sapiens tapasin (NCS-17) mRNA, complete cds//7.9e-59:427:83//Hs.5247:AF029750
R-NT2RP3001096//ESTs//1.1e-110:540:96//Hs.42824:AA873182	R-NT2RP3001538//ESTs//1.6e-94:521:92//Hs.6846:AA209463
R-NT2RP3001107//ESTs//7.6e-100:478:98//Hs.99669:AA287832	R-NT2RP3001554//ESTs, Moderately similar to NEURAXIN [Rattus norvegicus]//2.8e-76:392:95//Hs.66048:AA524416
R-NT2RP3001109//DNA polymerase gamma//0.0014:50:100//Hs.80961:U60325	R-NT2RP3001580//ESTs//3.7e-82:398:98//Hs.23490:W49477
R-NT2RP3001111//ESTs, Weakly similar to Trf-proximal protein [D. melanogaster]//3.2e-104:543:95//Hs.93796:C06063	R-NT2RP3001587//Homo sapiens mRNA for HRHFB2115, partial cds//1.8e-09:86:88//Hs.4311:AB015337
R-NT2RP3001113//ESTs//3.3e-100:467:99//Hs.97757:AA401575	R-NT2RP3001589//ESTs//0.0029:243:62//Hs.158924:AA605194
R-NT2RP3001115//Oxytocin receptor//7.9e-30:505:67//Hs.2820:X64878	R-NT2RP3001607//EST//0.00096:76:78//Hs.140319:AA748328
R-NT2RP3001116//ESTs//4.6e-41:229:96//Hs.58412:W74779	R-NT2RP3001608//ESTs//3.8e-105:525:96//Hs.144655:AI279798
R-NT2RP3001119//ESTs//6.9e-88:478:92//Hs.19469:AA203180	R-NT2RP3001621//ESTs//3.3e-108:535:97//Hs.47378:AI193598
R-NT2RP3001120//ESTs//3.1e-82:430:93//Hs.110956:AI190166	R-NT2RP3001629
R-NT2RP3001126//ESTs//4.4e-52:264:96//Hs.25264:R78188	R-NT2RP3001634//Homo sapiens TRIAD1 type I mRNA, complete cds//2.7e-109:541:96//Hs.9899:AF099149
R-NT2RP3001133//ESTs//4.7e-105:541:94//Hs.73239:AA573761	R-NT2RP3001642//ESTs//6.0e-105:525:96//Hs.3376:AA915989
R-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds//2.6e-115:549:97//Hs.5378:AB018305	R-NT2RP3001646//ESTs//4.8e-95:523:92//Hs.64036:AA127709
R-NT2RP3001147//ESTs, Highly similar to GTPASE ACTIVATING PROTEIN ROTUND [Drosophila melanogaster]//9.6e-113:552:97//Hs.23900:U82984	R-NT2RP3001671//ESTs//0.0013:367:60//Hs.106090:AA457030
R-NT2RP3001150//ESTs//2.9e-90:444:97//Hs.99601:AA760717	R-NT2RP3001672//ESTs//3.4e-37:191:98//Hs.57475:AI382189
R-NT2RP3001155//Homo sapiens mRNA for AND-1 protein//9.4e-118:563:98//Hs.72160:AJ006266	R-NT2RP3001676//ESTs//1.5e-81:408:97//Hs.142547:N67648
R-NT2RP3001176//ESTs//1.8e-110:534:98//Hs.58650:AI074460	R-NT2RP3001678//ESTs//4.3e-85:405:99//Hs.121915:AI268225
R-NT2RP3001214//ESTs//1.7e-109:545:96//Hs.24481:AA573139	R-NT2RP3001679//ESTs//3.4e-100:545:93//Hs.5943:AI222558
R-NT2RP3001216//EST//0.00098:128:66//Hs.160493:AI254963	R-NT2RP3001688//Human mRNA for KIAA0392 gene, partial cds//8.6e-46:301:87//Hs.40100:AB002390
R-NT2RP3001221//EST//0.010:106:66//Hs.147774:AI221196	R-NT2RP3001690//ESTs//3.3e-111:542:97//Hs.86149:AI341312
R-NT2RP3001232//ESTs//1.5e-101:518:94//Hs.21630:AA778399	R-NT2RP3001708//ESTs//1.4e-96:349:95//Hs.17975:AA868618
R-NT2RP3001236//ESTs, Highly similar to KIAA0377 [H. sapiens]//2.8e-89:462:95//Hs.116793:AA779588	R-NT2RP3001712//ESTs//9.3e-14:102:92//Hs.78041:N29669
R-NT2RP3001239//ESTs, Moderately similar to NEURAXIN [Rattus norvegicus]//5.2e-82:466:91//Hs.66048:AA524416	R-NT2RP3001716//ESTs, Highly similar to BONE MORPHOGENETIC PROTEIN 1 PRECURSOR [Mus musculus]//4.1e-80:444:91//Hs.6823:W18181
R-NT2RP3001245//EST//0.53:237:62//Hs.161131:AI417631	R-NT2RP3001724//ESTs//1.8e-109:547:96//Hs.14570:AI422009
R-NT2RP3001253//ESTs//1.7e-105:535:96//Hs.42315:AI222997	R-NT2RP3001730//ESTs//4.1e-98:528:92//Hs.155115:AA669923
R-NT2RP3001260//EST//0.16:144:62//Hs.126856:AA932135	R-NT2RP3001739//ESTs//4.4e-87:444:94//Hs.27239:W27810
R-NT2RP3001268//Human Aac11 (aac11) mRNA, complete cds//0.12:494:59//Hs.151031:U83857	R-NT2RP3001752//ESTs//6.1e-93:490:94//Hs.4210:AA740440
R-NT2RP3001272//ESTs//1.4e-92:436:99//Hs.149831:AI383965	R-NT2RP3001753//ESTs//2.5e-82:395:99//Hs.126435:AA912968
R-NT2RP3001274//ESTs//3.9e-81:424:95//Hs.113184:N25651	R-NT2RP3001764//ESTs, Weakly similar to protein-tyrosine phosphatase [H. sapiens]//1.2e-87:450:96//Hs.20281:N92517
R-NT2RP3001281//EST//3.1e-60:298:98//Hs.149230:AI247332	R-NT2RP3001777//ESTs//1.1e-86:360:97//Hs.100530:H06725
R-NT2RP3001307//EST//0.42:215:62//Hs.126165:AA868691	R-NT2RP3001782//Homo sapiens mRNA for KIAA0459 protein, partial cds//4.2e-113:549:97//Hs.28169:AB007928
R-NT2RP3001318//ESTs//4.1e-74:363:97//Hs.130832:H92571	R-NT2RP3001792//ESTs, Weakly similar to F35C12.2 [C. elegans]//1.1e-21:119:99//Hs.44268:AA455900
R-NT2RP3001325//ESTs//1.7e-106:534:96//Hs.21214:H98989	R-NT2RP3001799//OX40L RECEPTOR PRECURSOR//2.8e-45:374:79//Hs.129780:X75962
R-NT2RP3001338//Human protein tyrosine phosphatase sigma mRNA, complete cds//0.22:199:63//Hs.159534:U35234	R-NT2RP3001819//ESTs//2.6e-87:432:96//Hs.10414:AI291292
R-NT2RP3001339//Homo sapiens mRNA for KIAA0451 protein, complete cds//3.9e-114:566:96//Hs.18586:AB007920	R-NT2RP3001844//ESTs//0.024:128:67//Hs.25131:N50117
R-NT2RP3001340//ESTs//1.1e-72:411:92//Hs.21135:W81653	R-NT2RP3001854//ESTs//1.4e-92:490:92//Hs.15165:N52900
R-NT2RP3001355//ESTs//9.0e-103:521:95//Hs.99486:AA776798	R-NT2RP3001855//ESTs//1.9e-66:361:93//Hs.10043:D81792
R-NT2RP3001366//ESTs//2.7e-82:395:98//Hs.117102:AA993090	R-NT2RP3001896//ESTs//1.4e-96:343:97//Hs.24809:N73642
R-NT2RP3001383//ESTs//3.6e-10:118:78//Hs.111055:AA169778	R-NT2RP3001898//ESTs//4.1e-90:515:91//Hs.4867:AA521180
R-NT2RP3001384//ESTs, Weakly similar to A-kinase anchor protein 9 S, AKAP95 [R. norvegicus]//5.7e-92:522:90//Hs.96200:AA218942	R-NT2RP3001915//ESTs//4.4e-32:175:95//Hs.24641:AA954666
R-NT2RP3001392//ESTs//5.9e-62:296:100//Hs.125034:AA907375	R-NT2RP3001926//ESTs, Highly similar to NUCLEOLYSIN TIA-1 [Homo sapiens]//1.0e-40:202:100//Hs.24709:AI123300
R-NT2RP3001396//ESTs//3.7e-111:528:98//Hs.22612:AA152232	R-NT2RP3001929//ESTs//6.6e-84:449:94//Hs.26962:AA682781
R-NT2RP3001398//ESTs//2.6e-94:449:99//Hs.146332:AI276628	R-NT2RP3001931//ESTs//1.0e-41:214:99//Hs.32360:AA534737
R-NT2RP3001399//ESTs//2.6e-82:401:97//Hs.7932:AI041186	R-NT2RP3001938//ESTs, Highly similar to SPORULATION-SPECIFIC PROTEIN 1 [Saccharomyces cerevisiae]//1.3e-95:483:96//Hs.5771:W74591
R-NT2RP3001407//ESTs//2.2e-101:488:97//Hs.71573:AA496898	R-NT2RP3001943//ESTs//1.2e-23:169:88//Hs.103930:AA160990
R-NT2RP3001420//EST//7.4e-44:394:79//Hs.137041:AA877817	R-NT2RP3001944//ESTs//2.0e-90:439:97//Hs.103380:AI291325
R-NT2RP3001426//Homo sapiens clone 24616 mRNA sequence//3.6e-106:50:94//Hs.6957:AF052158	R-NT2RP3001969//ESTs//0.95:133:65//Hs.131669:AI025889
R-NT2RP3001427//ESTs//1.3e-87:374:97//Hs.5457:H05692	R-NT2RP3001989//ESTs, Weakly similar to C01A2.4 [C. elegans]//8.9e-64:310:99//Hs.11449:AI201540
R-NT2RP3001428//Neurotrophic tyrosine kinase, receptor, type 1//4.7e-96:533:91//Hs.85844:X66397	R-NT2RP3002002//ESTs//2.1e-95:562:89//Hs.5997:AA897088
R-NT2RP3001432//ESTs//1.9e-102:523:95//Hs.132978:AI041374	R-NT2RP3002004//H. sapiens mRNA for FAST kinase//1.6e-42:335:82//Hs.75087:X86779
R-NT2RP3001447//ESTs, Moderately similar to !!!! ALU SUBFAMILY J W ARNING ENTRY !!!! [H. sapiens]//5.1e-101:482:98//Hs.124135:AA910560	R-NT2RP3002007//ESTs//0.12:184:66//Hs.94030:AA846729
R-NT2RP3001449//ESTs//2.2e-99:502:96//Hs.7834:N45994	R-NT2RP3002014//Small inducible cytokine A5 (RANTES)//6.8e-47:291:89//Hs.155464:AF088219
R-NT2RP3001453//Small inducible cytokine A5 (RANTES)//8.1e-45:295:85//Hs.155464:AF088219	R-NT2RP3002033
R-NT2RP3001457//ESTs//1.5e-52:256:99//Hs.117982:AA644658	R-NT2RP3002045//ESTs//1.0e-92:555:88//Hs.106411:W29081
R-NT2RP3001459//ESTs//3.4e-62:299:99//Hs.146098:AA167280	R-NT2RP3002054//EST//0.45:155:63//Hs.5656:D20426
R-NT2RP3001472//ESTs//4.8e-108:540:96//Hs.69594:N37009	R-NT2RP3002056//ESTs//1.4e-95:504:93//Hs.17428:AI365221
R-NT2RP3001490//ESTs//3.5e-91:549:88//Hs.6606:AA211783	R-NT2RP3002057//Human mRNA for KIAA0152 gene, complete cds//0.69:127:66//Hs.90438:D63486
R-NT2RP3001495//Human oxidoreductase (HMCMA56) mRNA, complete cds//1.4e-61:338:93//Hs.519:U13395	R-NT2RP3002062
R-NT2RP3001497//Homo sapiens multiple membrane spanning receptor T	R-NT2RP3002063//ESTs//2.1e-113:552:97//Hs.9591:AA069657
	R-NT2RP3002081//ESTs//5.5e-43:212:100//Hs.124852:AA969139
	R-NT2RP3002097//EST//2.3e-10:80:91//Hs.102717:N59148
	R-NT2RP3002102

【0924】

【表622】

R-NT2RP3002108	0143
R-NT2RP3002146//ESTs//5.5e-58:296:97//Hs.65328:AA625385	R-NT2RP3002972//ESTs//1.7e-97:502:96//Hs.7274:AA476850
R-NT2RP3002147//EST//2.5e-53:387:81//Hs.147928:A1249703	R-NT2RP3002978//ESTs//8.6e-104:498:98//Hs.118923:AA252116
R-NT2RP3002151//ESTs, Highly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (Homo sapiens)//6.2e-107:534:96//Hs.59523:AA602837	R-NT2RP3002988//EST//1.2e-59:315:94//Hs.157743:A1360553
R-NT2RP3002163//ESTs//2.7e-106:520:97//Hs.21258:AA412293	R-NT2RP3003008//ESTs//1.4e-97:515:94//Hs.6544:AA524423
R-NT2RP3002165//ESTs//7.4e-93:479:95//Hs.27299:A1074024	R-NT2RP3003032//ESTs, Weakly similar to RETROVIRUS-RELATED POL POL YPROTEIN [Mus musculus]//3.0e-100:528:94//Hs.90353:N98551
R-NT2RP3002166//ESTs//1.0e-261:59//Hs.132817:AA593713	R-NT2RP3003059//ESTs//1.7e-76:398:95//Hs.102971:W05355
R-NT2RP3002173//ESTs//2.7e-93:512:92//Hs.23648:H07120	R-NT2RP3003061//ESTs//4.9e-82:414:96//Hs.99603:A1141912
R-NT2RP3002181//ESTs//1.0e-84:435:96//Hs.47378:A1193598	R-NT2RP3003068//ESTs, Weakly similar to M18.3 [C. elegans]//5.9e-83:392:99//Hs.101364:AA534439
R-NT2RP3002244//ESTs//2.7e-11:97:89//Hs.9412:W72446	R-NT2RP3003071//ESTs//6.3e-85:399:99//Hs.109755:AA180809
R-NT2RP3002248//ESTs//4.3e-90:459:95//Hs.9848:AA130588	R-NT2RP3003078//ESTs//1.0e-98:471:99//Hs.7995:A1359466
R-NT2RP3002255//ESTs//1.3e-45:289:88//Hs.9100:AA431672	R-NT2RP3003101//EST//0.032:235:60//Hs.147920:A1202441
R-NT2RP3002273//ESTs//2.3e-100:489:97//Hs.8258:AA744743	R-NT2RP3003121//ESTs//3.0e-47:238:97//Hs.43559:A1003520
R-NT2RP3002276//ESTs//1.2e-50:306:91//Hs.16160:AA778171	R-NT2RP3003133//EST//1.5e-77:395:96//Hs.142150:AA223982
R-NT2RP3002303//ESTs//1.1e-67:323:99//Hs.129761:AA836898	R-NT2RP3003138//ESTs, Highly similar to KINESIN-LIKE PROTEIN KIF4 [Mus musculus]//3.3e-107:535:96//Hs.27437:AA004208
R-NT2RP3002304//ESTs//2.8e-86:405:99//Hs.29643:AA418500	R-NT2RP3003139//ESTs//2.5e-106:504:98//Hs.106795:A1271632
R-NT2RP3002330//ESTs, Weakly similar to G1 TO S PHASE TRANSITION PROTEIN 1 HOMOLOG (H. sapiens)//1.8e-19:136:87//Hs.106928:A1041737	R-NT2RP3003150//ESTs//1.6e-99:539:91//Hs.46500:AA129774
R-NT2RP3002343//ESTs//1.0e-42:260:93//Hs.7797:W25667	R-NT2RP3003157//ESTs//1.5e-114:563:97//Hs.58608:AA081007
R-NT2RP3002351//Homo sapiens 9G8 splicing factor mRNA, complete cds//0.0048:221:64//Hs.556:L41887	R-NT2RP3003185//ESTs//3.9e-93:443:98//Hs.9741:A1131226
R-NT2RP3002355//Homo sapiens mRNA for protein encoded by cxorf5 (71-7A) gene//5.8e-105:516:94//Hs.6483:Y16355	R-NT2RP3003193//ESTs//2.0e-37:428:71//Hs.33354:AA179944
R-NT2RP3002455//Homo sapiens mRNA for KIAA0678 protein, partial cds//1.5e-103:524:95//Hs.12707:AB014578	R-NT2RP3003197//ESTs//5.8e-56:312:94//Hs.7016:AA215796
R-NT2RP3002484//Human APRT gene for adenine phosphoribosyltransferase//0.54:108:71//Hs.28914:Y00486	R-NT2RP3003203//EST//0.0073:212:63//Hs.161355:A142634
R-NT2RP3002501//ESTs//2.7e-96:489:95//Hs.27335:W74185	R-NT2RP3003204//ESTs//7.4e-52:253:99//Hs.120146:AA708573
R-NT2RP3002512//ESTs, Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III [C. elegans]//3.2e-90:526:90//Hs.8083:AA521436	R-NT2RP3003212//ESTs//1.8e-76:401:95//Hs.29067:W26107
R-NT2RP3002529//ESTs, Highly similar to PUTATIVE VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN C2G11.03C [Schizosaccharomyces pombe]//3.8e-101:497:96//Hs.6650:AA843246	R-NT2RP3003230//ESTs, Highly similar to CORONIN [Dictyostelium discoideum]//2.0e-40:229:93//Hs.17377:A1078151
R-NT2RP3002545//Homo sapiens mRNA for KIAA0729 protein, partial cds//1.1e-83:438:94//Hs.19542:AB018272	R-NT2RP3003242//ESTs//8.3e-97:458:99//Hs.23057:A1290343
R-NT2RP3002549//ESTs//3.8e-98:493:96//Hs.7358:AA191673	R-NT2RP3003251//ESTs//1.5e-60:320:95//Hs.36495:AA151628
R-NT2RP3002566//Homo sapiens calcium-activated potassium channel (KCNK3) mRNA, complete cds//0.14:184:63//Hs.89230:AF031815	R-NT2RP3003264//ESTs//2.1e-103:521:95//Hs.4094:AA173960
R-NT2RP3002587//Homo sapiens KIAA0420 mRNA, complete cds//2.0e-18:138:78//Hs.129843:AB007880	R-NT2RP3003278//ESTs//8.2e-109:536:96//Hs.23788:AA524061
R-NT2RP3002590//ESTs//2.9e-51:290:93//Hs.162942:A1243850	R-NT2RP3003282//Homo sapiens dynamin (DNM) mRNA, complete cds//2.4e-102:550:93//Hs.11702:L36983
R-NT2RP3002602//Homo sapiens stannin mRNA, complete cds//5.5e-06:58:100//Hs.76691:AF070673	R-NT2RP3003290//EST//4.3e-27:372:70//Hs.159131:A1384035
R-NT2RP3002603	R-NT2RP3003301//ESTs//4.4e-56:285:97//Hs.95370:AA601055
R-NT2RP3002631//ESTs//4.8e-54:367:85//Hs.13109:AA192514	R-NT2RP3003302//EST//7.2e-10:395:63//Hs.162554:AA584818
R-NT2RP3002659//ESTs//5.3e-30:229:85//Hs.152114:AA401365	R-NT2RP3003311//ESTs//4.2e-110:538:97//Hs.62180:A1341261
R-NT2RP3002660//ESTs//1.9e-88:452:95//Hs.120146:AA708573	R-NT2RP3003313//ESTs//2.1e-106:531:96//Hs.22630:C05931
R-NT2RP3002663//EST//3.2e-89:469:95//Hs.105767:AA525172	R-NT2RP3003327//ESTs//4.3e-102:518:95//Hs.120355:AA625445
R-NT2RP3002671//ESTs, Highly similar to ELONGATION FACTOR 2 [Drosophila melanogaster]//5.9e-109:537:97//Hs.19348:AA151678	R-NT2RP3003330//ESTs//8.6e-104:497:97//Hs.72071:A1125289
R-NT2RP3002682//ESTs//2.3e-98:541:91//Hs.75844:AA115502	R-NT2RP3003344//ESTs//2.5e-105:494:99//Hs.112188:AA872993
R-NT2RP3002687//ESTs//5.5e-103:498:97//Hs.72782:AA910871	R-NT2RP3003346//ESTs//1.0:123:69//Hs.116029:AA813102
R-NT2RP3002688//ESTs, Weakly similar to !!! ALU SUBFAMILY J WARM1 NC ENTRY !!! [H. sapiens]//5.0e-101:524:95//Hs.32580:A1123601	R-NT2RP3003353//EST//0.0014:162:68//Hs.149191:A1246155
R-NT2RP3002701//EST//0.07:131:63//Hs.161916:AA483169	R-NT2RP3003377//EST//4.5e-15:119:85//Hs.148129:AA885567
R-NT2RP3002713//ESTs//4.7e-106:542:95//Hs.14479:AA160945	R-NT2RP3003384//EST//0.0057:86:74//Hs.127735:AA962272
R-NT2RP3002763//ESTs//1.3e-54:290:94//Hs.142031:AA809159	R-NT2RP3003385//ESTs//0.64:347:59//Hs.5646:W72721
R-NT2RP3002770//ESTs//0.047:275:61//Hs.122984:AA526973	R-NT2RP3003403//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H. sapiens]//2.2e-24:418:67//Hs.139488:A1124095
R-NT2RP3002785//ESTs//2.4e-52:255:99//Hs.132959:A1376958	R-NT2RP3003409//ESTs//5.3e-98:479:97//Hs.155198:AA767372
R-NT2RP3002799//EST//8.2e-61:321:94//Hs.140992:R71377	R-NT2RP3003411//ESTs//4.8e-86:416:97//Hs.129059:AA126041
R-NT2RP3002810//EST//0.19:116:68//Hs.121810:AA775240	R-NT2RP3003427//ESTs//7.4e-103:510:96//Hs.25303:AA641023
R-NT2RP3002818//ESTs//1.3e-109:531:98//Hs.58924:A1348080	R-NT2RP3003433//ESTs//3.5e-85:405:99//Hs.63131:AA664156
R-NT2RP3002861//ESTs//2.5e-84:429:95//Hs.23920:AA909678	R-NT2RP3003464//Homo sapiens rab3-GAP regulatory domain mRNA, complete cds//3.6e-97:479:96//Hs.14934:AF004828
R-NT2RP3002869//EST//0.00011:116:71//Hs.161606:AA019641	R-NT2RP3003490//Homo sapiens mRNA for KIAA0725 protein, partial cds//4.1e-102:527:93//Hs.26450:AB018268
R-NT2RP3002876//ESTs//0.0024:182:63//Hs.117306:AA687262	R-NT2RP3003491//ESTs, Weakly similar to No definition line found [C. elegans]//4.0e-106:549:94//Hs.7886:A1057529
R-NT2RP3002877//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//8.1e-14:146:72//Hs.129727:AF035587	R-NT2RP3003500//Human RP3 mRNA, complete cds//0.66:401:60//Hs.75307:U02556
R-NT2RP3002909//Homo sapiens mRNA for KIAA0771 protein, partial cds//1.5e-110:570:95//Hs.6162:AB018314	R-NT2RP3003543//Human clone A9A28B87 (CAC)n/(GTG)n repeat-containing mRNA//4.1e-33:217:88//Hs.8068:U00952
R-NT2RP3002911//ESTs//3.6e-92:436:99//Hs.143917:A1206286	R-NT2RP3003552//ESTs//3.1e-106:546:94//Hs.101754:A1123430
R-NT2RP3002948//EST//1.0:102:65//Hs.144730:A1191975	R-NT2RP3003555//ESTs//3.4e-106:537:95//Hs.85550:AA187681
R-NT2RP3002953//ESTs//1.8e-107:513:98//Hs.119693:A1201698	R-NT2RP3003564
R-NT2RP3002955//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0492//0.23:563:56//Hs.127338:AB007961	R-NT2RP3003572//ESTs//1.2e-20:122:88//Hs.8253:H48721
R-NT2RP3002969//ESTs, Weakly similar to LONG-CHAIN-FATTY-ACID--COA LIGASE 1 [Saccharomyces cerevisiae]//2.0e-56:387:86//Hs.144597:W2	R-NT2RP3003576//ESTs//2.7e-71:394:94//Hs.151136:R99944

【0925】

【表623】

ds//5.6e-103:492:97//Hs.48513:AB018300
 R-NT2RP3003746//ESTs//1.9e-85:411:98//Hs.54835:A1050863
 R-NT2RP3003795//EST//6.2e-97:459:99//Hs.134769:A1089747
 R-NT2RP3003799//ESTs//2.8e-62:337:94//Hs.124023:H18913
 R-NT2RP3003800//PROTO-ONCOGENE TYROSINE-PROTEIN KINASE SRC//8.9e-108:551:95//Hs.115742:AF077754
 R-NT2RP3003805//ESTs//2.2e-103:490:99//Hs.9412:W72446
 R-NT2RP3003809//ESTs. Highly similar to SAV PROTEIN [Sulfolobus acidocaldarius]//3.4e-89:456:95//Hs.5555:A1285198
 R-NT2RP3003819//Interleukin 10//3.3e-43:173:89//Hs.2180:M57627
 R-NT2RP3003825//ESTs//1.6e-66:485:80//Hs.7405:W27761
 R-NT2RP3003828//ESTs. Weakly similar to unknown [H.sapiens]//9.6e-98:511:95//Hs.26955:A133224
 R-NT2RP3003831//ESTs//2.2e-38:317:79//Hs.142173:AA757743
 R-NT2RP3003833//Homo sapiens clones 24718 and 24825 mRNA sequence//5.2e-110:541:97//Hs.25300:AF070611
 R-NT2RP3003842//EST//9.9e-44:506:70//Hs.139093:AA166888
 R-NT2RP3003846//ESTs//4.6e-10:66:100//Hs.74924:A1332962
 R-NT2RP3003870//ESTs//3.4e-82:449:92//Hs.122691:AA152298
 R-NT2RP3003876//ESTs//1.9e-89:449:96//Hs.45046:N40170
 R-NT2RP3003914//ESTs//1.3e-99:470:98//Hs.118966:AA926726
 R-NT2RP3003918//ESTs//1.3e-79:417:94//Hs.5005:W25933
 R-NT2RP3003932//ESTs//6.0e-83:427:94//Hs.93581:H50221
 R-NT2RP3003989//ESTs//4.8e-76:403:93//Hs.127243:W80409
 R-NT2RP3003992//ESTs//2.4e-88:508:90//Hs.134200:D19593
 R-NT2RP3004013//ESTs//3.7e-111:551:97//Hs.105108:AA781142
 R-NT2RP3004016//ESTs//1.7e-81:394:98//Hs.63368:AA613714
 R-NT2RP3004041
 R-NT2RP3004051//ESTs//3.5e-69:386:93//Hs.51347:T72820
 R-NT2RP3004070//ESTs//5.5e-108:552:95//Hs.23392:A1310139
 R-NT2RP3004078//ESTs//3.3e-82:443:93//Hs.26407:W45387
 R-NT2RP3004093//ESTs//4.4e-83:426:94//Hs.140932:A1262104
 R-NT2RP3004095//ESTs//0.0013:93:78//Hs.36567:AA262045
 R-NT2RP3004110//ESTs. Weakly similar to similar to oxysterol-binding proteins: partial CDS [C.elegans]//3.5e-76:402:95//Hs.55847:W31092
 R-NT2RP3004125//ESTs//9.3e-74:363:97//Hs.32988:C01696
 R-NT2RP3004145//ESTs//2.6e-96:451:99//Hs.59584:AA587334
 R-NT2RP3004148//ESTs//1.3e-10:77:92//Hs.135890:A1183425
 R-NT2RP3004155//ESTs//1.7e-110:558:96//Hs.27003:A1279093
 R-NT2RP3004206//ESTs. Moderately similar to CROOKED NECK PROTEIN [Drosophila melanogaster]//1.8e-40:200:100//Hs.26089:AA195126
 R-NT2RP3004207//ESTs. Weakly similar to gene SEZ-6 [M.musculus]//1.1e-41:266:89//Hs.6314:AA522619
 R-NT2RP3004209//ESTs. Highly similar to PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C13A11.04C [Schizosaccharomyces pombe]//3.7e-112:547:97//Hs.99819:A1346680
 R-NT2RP3004215//ESTs//1.1e-103:541:95//Hs.124918:N64794
 R-NT2RP3004242//ESTs//4.5e-105:524:96//Hs.29724:A46252
 R-NT2RP3004246//EST//1.9e-07:67:91//Hs.125687:AA884827
 R-NT2RP3004253//EST//2.9e-88:454:94//Hs.127713:AA961628
 R-NT2RP3004258//ESTs. Weakly similar to PRE-MRNA SPLICING FACTOR SRP75 [Homo sapiens]//1.6e-89:468:95//Hs.5117:AA831530
 R-NT2RP3004262//ESTs//4.1e-86:443:96//Hs.101393:T87623
 R-NT2RP3004334//EST//0.00057:206:63//Hs.149388:A1273630
 R-NT2RP3004341//EST//0.00042:151:58//Hs.148498:A1200264
 R-NT2RP3004348//Homo sapiens LIM protein mRNA, complete cds//5.9e-61:299:85//Hs.154103:AF061258
 R-NT2RP3004349//EST//3.6e-42:175:88//Hs.161917:AA483223
 R-NT2RP3004378//ESTs//0.27:294:60//Hs.66479:AA853044
 R-NT2RP3004399//ESTs//5.8e-99:479:98//Hs.120234:AA732224
 R-NT2RP3004424//EST. Highly similar to F21C4.6 [C.elegans]//0.30:253:58//Hs.97184:AA385934
 R-NT2RP3004428//ESTs//2.8e-48:279:91//Hs.106826:W25985
 R-NT2RP3004451//ESTs//4.8e-101:509:96//Hs.29725:W74621
 R-NT2RP3004454//Homo sapiens mRNA for KIAA0448 protein, complete cds//9.3e-108:526:98//Hs.27349:AB007917
 R-NT2RP3004466//ESTs//0.25:51:90//Hs.7778:AA195616
 R-NT2RP3004470//EST//0.032:70:71//Hs.147925:A1249332
 R-NT2RP3004472//ESTs//0.0069:430:59//Hs.116651:AA993406
 R-NT2RP3004475//Homo sapiens mRNA for KIAA0456 protein, partial cds//5.0e-107:521:97//Hs.5003:AB007925
 R-NT2RP3004480
 R-NT2RP3004490//ESTs//4.7e-68:354:95//Hs.163721:M42504
 R-NT2RP3004498//ESTs. Moderately similar to ORF2: function unknown [H.sapiens]//3.4e-100:508:95//Hs.47393:AA218858
 R-NT2RP3004503//ESTs//4.6e-90:478:93//Hs.133998:AA994735
 R-NT2RP3004504//ESTs. Highly similar to cytoplasmic polyadenylation element-binding protein [M.musculus]//1.8e-83:465:92//Hs.137064:AA318257

R-NT2RP3004507//ESTs//1.5e-98:495:96//Hs.128905:A1051971
 R-NT2RP3004527//EST//1.6e-109:535:97//Hs.149481:A1279865
 R-NT2RP3004534
 R-NT2RP3004544//EST//0.035:226:60//Hs.99195:AA449232
 R-NT2RP3004566//ESTs//4.1e-86:455:95//Hs.13110:T67461
 R-NT2RP3004569//ESTs//2.9e-94:493:94//Hs.24948:AA977674
 R-NT2RP3004572//ESTs//1.1e-92:437:99//Hs.24846:A1420493
 R-NT2RP3004578//ESTs//0.98:166:64//Hs.124593:AA854456
 R-NT2RP3004594//EST//5.8e-89:426:98//Hs.134213:A1080213
 R-NT2RP3004617//ESTs//1.4e-40:226:85//Hs.15921:R71157
 R-NT2RP3004618//ESTs//1.8e-38:229:90//Hs.125153:AA453723
 R-NT2RP3004670//Homo sapiens G6ST mRNA for long form of N-acetylglucosamine-6-O-sulfotransferase (GlcNAc6ST), complete cds//7.2e-57:291:95//Hs.8786:AB014680
 R-NT2RP4000008//ESTs//8.9e-119:561:98//Hs.25035:A1123335
 R-NT2RP4000023//EST//1.2e-34:271:80//Hs.98300:AA18560
 R-NT2RP4000035//Small inducible cytokine A5 (RANTES)//2.1e-68:320:82//Hs.155464:AF088219
 R-NT2RP4000049//Homo sapiens TRAIL receptor 2 mRNA, complete cds//6.7e-60:289:82//Hs.51233:AF016266
 R-NT2RP4000051//ESTs. Weakly similar to protein B [H.sapiens]//8.3e-98:462:99//Hs.10114:A1345945
 R-NT2RP4000078//ESTs//0.00068:367:60//Hs.106090:AA457030
 R-NT2RP4000102//ESTs//9.7e-50:256:97//Hs.24266:R28287
 R-NT2RP4000109//Homo sapiens mRNA for MEGF5, partial cds//1.1e-107:536:96//Hs.57929:AB011538
 R-NT2RP4000129//Homo sapiens mRNA for KIAA0483 protein, partial cds//3.5e-112:554:97//Hs.64691:AB007952
 R-NT2RP4000147//ESTs//3.9e-11:122:80//Hs.25584:AA632014
 R-NT2RP4000150//EST//4.4e-84:510:88//Hs.144238:W52294
 R-NT2RP4000151//ESTs. Weakly similar to HYPOTHETICAL 31.0 KD PROTEIN R107.2 IN CHROMOSOME III [C.elegans]//5.7e-93:515:92//Hs.8083:AA521436
 R-NT2RP4000159//ESTs//0.0019:209:65//Hs.161816:AA400295
 R-NT2RP4000167//ESTs//2.1e-113:549:97//Hs.109441:N66569
 R-NT2RP4000185//ESTs//0.65:232:59//Hs.144445:AA807257
 R-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds//1.5e-100:505:96//Hs.13999:AB014600
 R-NT2RP4000212//ESTs//8.5e-14:169:75//Hs.8520:AA081788
 R-NT2RP4000214//Human mRNA for KIAA0392 gene, partial cds//6.2e-43:272:90//Hs.40100:AB002390
 R-NT2RP4000218//ESTs//6.1e-10:335:64//Hs.105658:AA978185
 R-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP)//2.9e-70:354:96//Hs.155481:AJ006470
 R-NT2RP4000246//ESTs//7.1e-26:154:94//Hs.14838:AA502757
 R-NT2RP4000259//Homo sapiens clone 683 unknown mRNA, complete sequence//9.3e-79:379:99//Hs.43728:AF091092
 R-NT2RP4000263
 R-NT2RP4000290//ESTs. Weakly similar to similar to Achlya ambisexualis antheridiol steroid receptor [C.elegans]//4.7e-104:525:96//Hs.152069:AA548972
 R-NT2RP4000312//ESTs//8.2e-66:319:99//Hs.35091:A1271631
 R-NT2RP4000321//Homo sapiens clone 24453 mRNA sequence//1.3e-109:513:99//Hs.13410:AF070524
 R-NT2RP4000323//ESTs//7.7e-109:534:97//Hs.34790:AA192760
 R-NT2RP4000355//ESTs//3.1e-44:320:83//Hs.141323:N80390
 R-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds//7.6e-111:520:99//Hs.107479:AB018281
 R-NT2RP4000367//Homo sapiens I kappa B kinase complex associated protein (IKAP) mRNA, complete cds//2.8e-110:527:98//Hs.31323:AF044195
 R-NT2RP4000370//ESTs//8.9e-32:166:98//Hs.70488:A1301130
 R-NT2RP4000376//ESTs//6.8e-99:465:99//Hs.27182:AA604498
 R-NT2RP4000381//ESTs//3.0e-50:280:93//Hs.8395:W27376
 R-NT2RP4000415//ESTs. Weakly similar to coded for by C. elegans CDNA yk30b.5 [C.elegans]//3.9e-87:499:91//Hs.26156:AA630975
 R-NT2RP4000417//ESTs. Moderately similar to HYPOTHETICAL 91.2 KD PROTEIN IN RPSTA-SCH9 INTERGENIC REGION [Saccharomyces cerevisiae]//8.9e-95:468:96//Hs.93871:A1191318
 R-NT2RP4000424//ESTs//3.7e-98:473:98//Hs.24945:A1189011
 R-NT2RP4000448//ESTs//2.6e-79:446:91//Hs.25159:R60955
 R-NT2RP4000449//ESTs//3.6e-98:468:98//Hs.31176:A1037953
 R-NT2RP4000455//Homo sapiens N-methyl-D-aspartate receptor 2D subunit precursor (NMDAR2D) mRNA, complete cds//0.35:153:63//Hs.113286:U77783
 R-NT2RP4000457//ESTs//4.5e-89:455:96//Hs.62638:AA127740
 R-NT2RP4000480//ESTs//4.9e-92:431:99//Hs.121072:A1204167
 R-NT2RP4000481
 R-NT2RP4000500//ESTs. Weakly similar to HYPOTHETICAL 83.6 KD PROTEIN R0503.2 IN CHROMOSOME III [C.elegans]//1.2e-40:125:97//Hs.56124:A1424792

【表625】

R-NT2RP4001838//ESTs//4.2e-58:344:90//Hs.48723:N66663
 R-NT2RP4001849//EST//0.24:105:71//Hs.136747:AA749210
 R-NT2RP4001889//Human mRNA for KIAA0118 gene, partial cds//3.4e-3
 4:212:88//Hs.154326:D42087
 R-NT2RP4001893//ESTs//3.0e-58:321:95//Hs.158787:W79502
 R-NT2RP4001896//EST//3.8e-15:108:92//Hs.160835:A1345528
 R-NT2RP4001901//ESTs//1.2e-110:536:97//Hs.31443:A1018606
 R-NT2RP4001927//ESTs//2.1e-105:546:93//Hs.73291:A1417099
 R-NT2RP4001938//ESTs//2.8e-40:235:78//Hs.163641:R61848
 R-NT2RP4001946//ESTs//1.3e-29:175:93//Hs.43703:AA088436
 R-NT2RP4001950//ESTs//4.6e-95:458:98//Hs.150890:A1341793
 R-NT2RP4001953//Clathrin, light polypeptide (Lcb)//2.3e-62:310:82//
 Hs.73919:X81637
 R-NT2RP4001966//ESTs, Weakly similar to tenascin-like protein [D.m
 elanogaster]//8.3e-87:457:94//Hs.41793:AA775879
 R-NT2RP4001975//ESTs//1.9e-52:281:94//Hs.7704:W58252
 R-NT2RP4002018
 R-NT2RP4002047//ESTs, Highly similar to GTP-BINDING PROTEIN LEPA
 [Pseudomonas fluorescens]//4.7e-09:90:86//Hs.41127:AA555184
 R-NT2RP4002052//ESTs//0.054:353:60//Hs.117510:AA903738
 R-NT2RP4002058//EST//7.8e-26:151:94//Hs.124617:AA855106
 R-NT2RP4002071//ESTs//6.9e-99:475:98//Hs.29216:AA916679
 R-NT2RP4002075//ESTs//0.67:121:65//Hs.153939:A1284198
 R-NT2RP4002078//ESTs, Highly similar to ZINC FINGER PROTEIN 35 [H
 omo sapiens]//1.6e-61:464:82//Hs.144228:N99507
 R-NT2RP4002081//ESTs, Weakly similar to HYPOTHETICAL 139.1 KD PROT
 EIN COB811.3 IN CHROMOSOME II [C.elegans]//2.3e-56:271:100//Hs.618
 5:AA428565
 R-NT2RP4002083//ESTs//2.0e-108:548:96//Hs.6120:W80407
 R-NT2RP4002408//ESTs//2.6e-77:391:96//Hs.14014:AA745592
 R-NT2RP4002791//ESTs//7.9e-101:527:93//Hs.22394:N32555
 R-NT2RP4002888//ESTs, Highly similar to ENV POLYPROTEIN [Avian sp
 leen necrosis virus]//1.9e-65:373:92//Hs.31532:H18272
 R-NT2RP4002905//ESTs//1.5e-107:517:98//Hs.40460:N36090
 R-OVARC1000001//Homo sapiens mRNA for KIAA0465 protein, partial cd
 s//2.8e-115:605:94//Hs.108258:AB007934
 R-OVARC1000004
 R-OVARC1000006//ESTs//1.5e-19:139:89//Hs.143034:A1126929
 R-OVARC1000013//ESTs//5.9e-98:531:93//Hs.16470:AA121635
 R-OVARC1000014//ESTs//0.24:243:60//Hs.19569:AA464273
 R-OVARC1000017
 R-OVARC1000035//ESTs//0.035:252:63//Hs.134123:A1078286
 R-OVARC1000058//H.sapiens mRNA for translin associated protein X//
 3.8e-46:331:83//Hs.96247:X95073
 R-OVARC1000060//EST//2.8e-28:348:71//Hs.141728:W73041
 R-OVARC1000068//ESTs//3.0e-83:491:90//Hs.29397:N51367
 R-OVARC1000071//ESTs//2.5e-60:321:96//Hs.25010:R67871
 R-OVARC1000085//Proteasome component C5//8.6e-67:366:92//Hs.75748:
 AL031259
 R-OVARC1000087//ESTs//1.0e-111:526:98//Hs.129020:A1380703
 R-OVARC1000091//ESTs, Weakly similar to HOST CELL FACTOR C1 [H.sap
 iens]//3.9e-112:596:94//Hs.20597:W58370
 R-OVARC1000092//ESTs//5.1e-18:144:82//Hs.109140:A1289942
 R-OVARC1000106
 R-OVARC1000113//Homo sapiens okadaic acid-inducible phosphoprotein
 (OA48-18) mRNA, complete cds//8.3e-102:495:97//Hs.3688:AF069250
 R-OVARC1000114//H.sapiens mRNA for phosphoinositide 3-kinase//1.7
 e-45:489:74//Hs.101238:Y11312
 R-OVARC1000133//EST//0.00028:284:61//Hs.30547:H05482
 R-OVARC1000145//EST//3.9e-40:201:99//Hs.156148:A133214
 R-OVARC1000148//EST//0.79:150:62//Hs.100078:T05090
 R-OVARC1000151
 R-OVARC1000168//EST//1.7e-19:142:90//Hs.38441:H66023
 R-OVARC1000191//EST//0.0072:292:63//Hs.132492:AA922629
 R-OVARC1000198//Homo sapiens LIM protein mRNA, complete cds//6.1e-
 44:339:81//Hs.154103:AF061258
 R-OVARC1000209//ESTs, Moderately similar to ZINC FINGER PROTEIN 93
 [H.sapiens]//1.1e-32:196:92//Hs.64322:AA142864
 R-OVARC1000212//EST//0.20:178:61//Hs.133031:A1049874
 R-OVARC1000240//ESTs//9.0e-64:314:98//Hs.42300:AA204958
 R-OVARC1000241//EST//0.00018:115:68//Hs.150728:A1213130
 R-OVARC1000288//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROT
 EIN IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]//3.
 3e-74:403:93//Hs.108117:A1097079
 R-OVARC1000302//EST//4.0e-14:102:90//Hs.136617:AA630476
 R-OVARC1000304//ESTs, Highly similar to PUTATIVE GTP-BINDING PROT
 EIN MOV10 [Mus musculus]//2.9e-37:191:98//Hs.20725:A1027777
 R-OVARC1000309//ESTs//3.6e-66:348:94//Hs.9547:AA532449
 R-OVARC1000321//ESTs//3.6e-87:454:95//Hs.110445:AA044743
 R-OVARC1000326//ESTs, Moderately similar to lamina associated poly

peptide 1C [R.norvegicus]//1.3e-98:488:96//Hs.125749:A1377682
 R-OVARC1000335//ESTs//3.0e-115:565:97//Hs.54835:A1050863
 R-OVARC1000347//EST//0.0018:145:65//Hs.136945:AA765672
 R-OVARC1000384//ESTs//2.8e-38:253:89//Hs.15093:AA203423
 R-OVARC1000408//ESTs//2.6e-98:515:94//Hs.119808:C05928
 R-OVARC1000411//ESTs//3.2e-82:395:98//Hs.104747:AA406219
 R-OVARC1000414//Landsteiner-Wiener blood group glycoprotein//1.5e-
 27:211:79//Hs.108287:L27670
 R-OVARC1000420//EST//2.8e-38:255:74//Hs.138525:R99237
 R-OVARC1000427//EST//2.6e-58:302:96//Hs.122914:AA767034
 R-OVARC1000431//ESTs//4.9e-108:551:96//Hs.11668:A1123426
 R-OVARC1000437
 R-OVARC1000440//ESTs//2.9e-91:456:96//Hs.93701:A1018671
 R-OVARC1000442//Human high-affinity copper uptake protein (hCTR1)
 mRNA, complete cds//4.3e-45:320:84//Hs.73614:U83460
 R-OVARC1000443//Homo sapiens mRNA for KIAA0683 protein, complete c
 ds//3.6e-79:418:94//Hs.12334:AB014583
 R-OVARC1000461//ESTs//3.1e-62:342:93//Hs.23241:R46582
 R-OVARC1000465//ESTs//1.7e-67:349:95//Hs.127238:AA477576
 R-OVARC1000466//ESTs//1.9e-66:337:95//Hs.5212:A1421211
 R-OVARC1000473//ESTs//5.4e-89:320:99//Hs.29173:AA134926
 R-OVARC1000479//ESTs, Highly similar to TIP120 [R.norvegicus]//1.1
 e-102:514:96//Hs.11833:A1299947
 R-OVARC1000486//ESTs//3.9e-78:405:95//Hs.98312:AA424983
 R-OVARC1000496
 R-OVARC1000520//ESTs//1.2e-20:145:88//Hs.87456:AA434484
 R-OVARC1000526//Small inducible cytokine A5 (RANTES)//8.9e-47:217:
 87//Hs.155464:AF088219
 R-OVARC1000533//ESTs, Moderately similar to integrase [H.sapiens]/
 /8.5e-48:264:92//Hs.49860:AA702248
 R-OVARC1000543//ESTs//5.7e-74:410:94//Hs.62817:AA047021
 R-OVARC1000556//H.sapiens mRNA for ribosomal S6 kinase//9.5e-27:20
 2:85//Hs.90859:X85106
 R-OVARC1000557//EST//2.8e-18:169:79//Hs.149101:A1244285
 R-OVARC1000564//EST//2.3e-34:199:92//Hs.146637:A1141587
 R-OVARC1000573//Interleukin 10//4.7e-42:300:83//Hs.2180:M57627
 R-OVARC1000578//Small inducible cytokine A5 (RANTES)//5.2e-58:392:
 84//Hs.155464:AF088219
 R-OVARC1000588//EST//1.8e-41:174:85//Hs.163333:AA879053
 R-OVARC1000605
 R-OVARC1000622//Homo sapiens mRNA, chromosome 1 specific transcrip
 t KIAA0501//6.4e-47:417:77//Hs.158897:AB007970
 R-OVARC1000640//H.sapiens mRNA for translin associated protein X//
 1.9e-28:366:72//Hs.96247:X95073
 R-OVARC1000661//Homo sapiens mRNA for KIAA0590 protein, complete c
 ds//5.1e-31:162:100//Hs.111862:AB011162
 R-OVARC1000678//EST//0.92:199:60//Hs.122025:AA778480
 R-OVARC1000679//ESTs//0.94:416:59//Hs.130754:AA279522
 R-OVARC1000681//EST//9.2e-21:179:80//Hs.132635:A1032875
 R-OVARC1000689//Homo sapiens ataxin-7 (SCA7) mRNA, complete cds//
 0.053:160:64//Hs.108447:AJ000517
 R-OVARC1000700//Homo sapiens KIAA0441 mRNA, complete cds//7.1e-09:
 141:73//Hs.32511:AB007901
 R-OVARC1000703//ESTs//1.7e-46:298:87//Hs.138856:H47461
 R-OVARC1000730//ESTs, Weakly similar to C27F2.7 gene product [C.el
 egans]//1.7e-17:137:85//Hs.7049:A1141736
 R-OVARC1000746//ESTs//0.16:366:60//Hs.136969:AA830918
 R-OVARC1000769//ESTs, Weakly similar to eukaryotic initiation fact
 or eIF-2 alpha kinase [D.melanogaster]//4.6e-28:430:69//Hs.42457:A
 A523306
 R-OVARC1000771//ESTs//1.3e-87:461:94//Hs.22399:AA531016
 R-OVARC1000781//ESTs//8.3e-119:572:97//Hs.41972:AA626793
 R-OVARC1000787//ESTs//7.4e-18:115:93//Hs.164036:AA845659
 R-OVARC1000800//MITOCHONDRIAL STRESS-70 PROTEIN PRECURSOR//4.9e-1
 9:119:95//Hs.3069:L11066
 R-OVARC1000802//ESTs//2.2e-41:383:78//Hs.161228:A1419764
 R-OVARC1000834//Homo sapiens mRNA for atopy related autoantigen CA
 LC//1.1e-106:536:95//Hs.61628:Y17711
 R-OVARC1000846//Clathrin, light polypeptide (Lcb)//1.6e-66:282:87/
 Hs.73919:X81637
 R-OVARC1000850//Homo sapiens PB39 mRNA, complete cds//1.2e-115:57
 9:96//Hs.18910:AF045584
 R-OVARC1000862//EST//4.3e-14:129:81//Hs.150663:AA923096
 R-OVARC1000876//ESTs//1.0e-115:573:96//Hs.87287:A1150674
 R-OVARC1000883//ESTs//3.5e-109:523:98//Hs.28423:A1336292
 R-OVARC1000885//ESTs, Highly similar to HYPOTHETICAL OXIDOREDUCTA
 SE IN ROCC-PTA INTERGENIC REGION [Bacillus subtilis]//7.9e-98:525:
 93//Hs.10366:W21953
 R-OVARC1000886//ESTs//8.2e-79:417:94//Hs.7729:AA830777
 R-OVARC1000891//ESTs//6.8e-75:401:94//Hs.5833:H15401

【0928】

【表626】

R-OVARC1000897//ESTs//3.5e-91:440:98//Hs.125264:AA873350	R-OVARC1001342//40S RIBOSOMAL PROTEIN S8//4.9e-110:568:95//Hs.118690:X67247
R-OVARC1000912	R-OVARC1001344//EST//3.6e-44:341:81//Hs.162197:AA535216
R-OVARC1000915//ESTs//1.0e-45:328:82//Hs.163980:AA715814	R-OVARC1001357//TUMOR-ASSOCIATED ANTIGEN L6//9.8e-44:250:93//Hs.3337:M90657
R-OVARC1000924//ESTs//1.0e-100:501:96//Hs.30204:AA497127	R-OVARC1001360//ESTs//5.2e-110:534:98//Hs.24743:AA843844
R-OVARC1000936//EST//3.0e-74:367:98//Hs.145098:AA421696	R-OVARC1001369//ESTs//1.7e-98:478:97//Hs.7729:AA830777
R-OVARC1000937//EST//1.1e-53:290:95//Hs.162846:AA631215	R-OVARC1001372//ESTs//2.6e-97:456:99//Hs.153648:AI341415
R-OVARC1000945//ESTs//4.9e-51:301:89//Hs.20100:W25794	R-OVARC1001376//Homo sapiens mRNA for KIAA0575 protein, complete cds//1.1e-53:344:72//Hs.153468:AB011147
R-OVARC1000948//ESTs//3.7e-67:332:98//Hs.112570:AA621971	R-OVARC1001381//ESTs//5.1e-19:200:66//Hs.114031:AA700958
R-OVARC1000959//Small inducible cytokine A5 (RANTES)//7.2e-44:283:86//Hs.155464:AF088219	R-OVARC1001391
R-OVARC1000960//Homo sapiens KIAA0395 mRNA, partial cds//1.1e-41:348:80//Hs.43681:AL022394	R-OVARC1001399//ESTs//0.0039:48:95//Hs.117964:M20913
R-OVARC1000971//EST//6.2e-05:126:70//Hs.160491:AI254909	R-OVARC1001417//Homo sapiens EXLM1 mRNA, complete cds//3.2e-111:561:95//Hs.21586:AB006651
R-OVARC1000984//ESTs, Weakly similar to No definition line found [C. elegans]//3.5e-68:346:96//Hs.25544:AA532784	R-OVARC1001419
R-OVARC1000996//EST//0.12:92:71//Hs.117141:AA678811	R-OVARC1001425//EST//5.7e-20:395:66//Hs.159707:AI393136
R-OVARC1000999//Homo sapiens KIAA0414 mRNA, partial cds//1.5e-44:513:73//Hs.127649:AB007874	R-OVARC1001436//ESTs//9.6e-90:427:99//Hs.6982:AA622427
R-OVARC1001000//ESTs//1.8e-22:198:80//Hs.140608:M53448	R-OVARC1001442//ESTs//1.1e-66:317:100//Hs.18437:AI206345
R-OVARC1001004//Human kpni repeat mRNA (cdna clone pcd-kpni-4), 3' end//1.7e-28:181:77//Hs.139107:K00629	R-OVARC1001453//ESTs//2.0e-20:163:84//Hs.133503:AA628592
R-OVARC1001010//EST//2.1e-09:92:85//Hs.147893:AI223270	R-OVARC1001476//EST//0.23:125:66//Hs.71444:AA131700
R-OVARC1001011//EST//2.4e-14:200:75//Hs.149290:AI248117	R-OVARC1001480//ESTs//3.1e-56:181:97//Hs.40109:AA928694
R-OVARC1001032//EST//2.7e-29:304:73//Hs.141733:W80630	R-OVARC1001489//ESTs//1.0:297:58//Hs.86723:AA393089
R-OVARC1001034//Homo sapiens apoptotic protease activating factor 1 (Apa1-1) mRNA, complete cds//2.1e-09:137:74//Hs.77579:AF013263	R-OVARC1001496//Homo sapiens C-terminal binding protein 2 mRNA, complete cds//3.0e-117:585:96//Hs.6534:AF016507
R-OVARC1001038//Homo sapiens TRIAD1 type 1 mRNA, complete cds//4.1e-101:501:96//Hs.9899:AF099149	R-OVARC1001506//Small inducible cytokine A5 (RANTES)//1.8e-48:283:90//Hs.155464:AF088219
R-OVARC1001040//ESTs//2.9e-87:415:99//Hs.132812:AI032046	R-OVARC1001525//EST//0.80:170:60//Hs.157398:AI364539
R-OVARC1001044//ESTs//1.1e-83:432:96//Hs.55043:M94384	R-OVARC1001542//Homo sapiens h1TB mRNA, complete cds//1.6e-111:566:95//Hs.6396:AB016492
R-OVARC1001051//60S RIBOSOMAL PROTEIN L41//1.2e-16:124:88//Hs.108124:Z12962	R-OVARC1001547//ESTs//5.7e-105:564:93//Hs.68835:AA088388
R-OVARC1001055//ESTs//2.4e-23:238:76//Hs.141421:M99231	R-OVARC1001577//Homo sapiens SRp46 splicing factor retropseudogene mRNA//4.4e-20:150:89//Hs.155160:AF031166
R-OVARC1001062//ESTs//3.4e-92:469:96//Hs.34658:M98652	R-OVARC1001600//Human mRNA for KIAA0118 gene, partial cds//8.6e-21:282:72//Hs.154326:D42087
R-OVARC1001068//Homo sapiens Era GTPase A protein (HERA-A) mRNA, partial cds//7.3e-97:463:98//Hs.3426:AF082657	R-OVARC1001610//ESTs//4.6e-108:555:95//Hs.44295:M32019
R-OVARC1001072//ESTs//1.3e-34:227:89//Hs.126704:W95844	R-OVARC1001611//ESTs//0.0021:117:71//Hs.135568:AA927965
R-OVARC1001074	R-OVARC1001615//Homo sapiens KIAA0409 mRNA, partial cds//9.2e-19:114:78//Hs.5158:AB007869
R-OVARC1001085//Human T-cell leukemia virus enhancer factor//1.0:94:69//Hs.103126:U57029	R-OVARC1001668//ESTs//1.0:127:69//Hs.153290:AI022659
R-OVARC1001092//Homo sapiens mRNA for JMS protein, complete CDS (clone IMAGE 53337, LLNLcl01F05707 (RZPD Berlin) and LLNLcl10C0913Q7 (RZPD Berlin))//1.4e-96:325:98//Hs.21753:AJ005897	R-OVARC1001702//ESTs//4.8e-44:225:97//Hs.96855:AA346854
R-OVARC1001113//Homo sapiens diaphanous 1 (HDIA1) mRNA, complete cds//3.3e-75:386:95//Hs.26584:AF051782	R-OVARC1001703//ESTs//2.3e-89:426:99//Hs.27099:M60080
R-OVARC1001117//Human G protein-coupled receptor (STRL22) mRNA, complete cds//3.9e-37:283:84//Hs.46468:U45984	R-OVARC1001711//ESTs//1.9e-57:251:99//Hs.9732:AA527784
R-OVARC1001118//ESTs//5.3e-99:485:97//Hs.130815:AA936548	R-OVARC1001726//ESTs, Highly similar to APICAL PROTEIN [Xenopus laevis]//1.2e-27:236:81//Hs.15485:AA046954
R-OVARC1001129//ESTs//9.8e-66:351:95//Hs.18616:T99312	R-OVARC1001731//Tropomyosin 4 (fibroblast)//7.9e-74:422:90//Hs.102824:X05276
R-OVARC1001161//ESTs, Moderately similar to !!!! ALU SUBFAMILY SX WARNING ENTRY !!!! [H. sapiens]//2.2e-66:346:95//Hs.53263:AA173226	R-OVARC1001745//Human mRNA for tryptophan hydroxylase (EC 1.14.16.4)//1.7e-62:300:83//Hs.144563:AF057280
R-OVARC1001162//EST//1.5e-44:376:80//Hs.161917:AA483223	R-OVARC1001762//ESTs, Weakly similar to N-TERMINAL ACETYLTRANSFERASE 1 [S. cerevisiae]//6.8e-100:540:92//Hs.117741:AA903456
R-OVARC1001167//ESTs//4.7e-110:548:96//Hs.35254:AI133727	R-OVARC1001766//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//1.1e-109:567:94//Hs.155377:U97670
R-OVARC1001169//ESTs//0.22:152:68//Hs.149424:AI274200	R-OVARC1001767//Homo sapiens mRNA for KIAA0675 protein, complete cds//2.0e-109:529:97//Hs.15869:AB014575
R-OVARC1001170//Small inducible cytokine A5 (RANTES)//1.8e-42:305:84//Hs.155464:AF088219	R-OVARC1001768//ESTs//3.5e-59:327:94//Hs.107923:H66127
R-OVARC1001173//EST//2.5e-35:182:84//Hs.161917:AA483223	R-OVARC1001791//ESTs//1.3e-111:565:96//Hs.6107:AA160604
R-OVARC1001180//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//6.6e-64:247:80//Hs.97203:U83171	R-OVARC1001795//ESTs//2.8e-97:526:93//Hs.72158:AA156978
R-OVARC1001188//ESTs//4.1e-18:296:69//Hs.139197:AA228343	R-OVARC1001802//Homo sapiens DEC-205 mRNA, complete cds//4.8e-36:276:81//Hs.153563:AF011333
R-OVARC1001200//ESTs//2.0e-28:207:85//Hs.35121:AA877826	R-OVARC1001805//ESTs//4.1e-78:375:98//Hs.126902:AI374688
R-OVARC1001232//ESTs//3.2e-61:358:91//Hs.6449:W95025	R-OVARC1001812//EST//4.8e-45:349:80//Hs.162677:AA604831
R-OVARC1001240//ESTs//6.7e-45:316:85//Hs.121675:AA629668	R-OVARC1001813//Homo sapiens mRNA for KIAA0538 protein, partial cds//2.1e-15:519:63//Hs.25639:AB011110
R-OVARC1001243//ESTs//2.3e-86:409:99//Hs.163091:AA742361	R-OVARC1001820//ESTs//9.5e-50:314:80//Hs.140491:M52705
R-OVARC1001261//ESTs//0.63:125:64//Hs.155743:AI344166	R-OVARC1001828//ESTs//0.11:186:63//Hs.29055:AI374621
R-OVARC1001268//ESTs//8.1e-20:113:98//Hs.109477:AA477929	R-OVARC1001846//ESTs//0.34:134:66//Hs.152992:AI242160
R-OVARC1001270//ESTs//1.5e-107:530:97//Hs.62905:AA460708	R-OVARC1001861//ESTs//2.3e-19:120:92//Hs.42225:M31809
R-OVARC1001271//ESTs//4.5e-36:401:72//Hs.20190:AA525532	R-OVARC1001873//Homo sapiens clones 24718 and 24825 mRNA sequence//1.9e-105:571:91//Hs.25300:AF070611
R-OVARC1001282//EST//4.0e-91:428:99//Hs.145599:AI263113	R-OVARC1001879//EST//1.3e-24:185:85//Hs.136617:AA630476
R-OVARC1001296//ESTs//2.6e-63:301:100//Hs.125753:AA740885	R-OVARC1001880//Homo sapiens mRNA for KIAA0575 protein, complete cds//2.2e-49:302:90//Hs.153468:AB011147
R-OVARC1001306//Homo sapiens mRNA for KIAA0518 protein, partial cds//3.8e-70:334:100//Hs.23763:AB011090	R-OVARC1001883//ESTs//1.0e-51:295:93//Hs.164059:AA447310
R-OVARC1001329//Clathrin, light polypeptide (Lcb1)//1.3e-68:304:83//Hs.73919:X81637	R-OVARC1001900//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds//1.6e-87:346:90//Hs.6216:AF061749
R-OVARC1001330//Proline arginine-rich and leucine-rich repeat protein//1.0:147:63//Hs.76494:U41344	R-OVARC1001901//ESTs//6.8e-24:132:98//Hs.130797:AA904435
R-OVARC1001339//Small inducible cytokine A5 (RANTES)//5.0e-48:452:76//Hs.155464:AF088219	R-OVARC1001911//ESTs//1.1e-88:491:92//Hs.32343:W73855
R-OVARC1001341//ESTs, Moderately similar to !!!! ALU SUBFAMILY SQ WARNING ENTRY !!!! [H. sapiens]//6.9e-85:464:93//Hs.23651:AA650356	

【0929】

【表627】

R-OVARC1001916//ESTs//7.9e-97:491:95//Hs.24989:H97842
 R-OVARC1001928
 R-OVARC1001942//ESTs. Weakly similar to N-TERMINAL ACETYLTRANSFERASE 1 [S.cerevisiae]//2.5e-39:253:88//Hs.117741:AA903456
 R-OVARC1001943//ESTs//9.3e-13:78:100//Hs.143680:W38637
 R-OVARC1001949//ESTs. Highly similar to ZINC FINGER PROTEIN 8 [Homo sapiens]//8.3e-96:498:94//Hs.22744:A1379892
 R-OVARC1001950//EST//1.3e-35:236:81//Hs.132635:A1032875
 R-OVARC1001987//ESTs//5.6e-94:514:92//Hs.21148:A1183729
 R-OVARC1001989//ESTs//9.7e-46:228:99//Hs.127046:AA935887
 R-OVARC1002044//ESTs//3.4e-45:303:85//Hs.132722:AA618531
 R-OVARC1002050//Homo sapiens mRNA for KIAA0465 protein, partial cds//4.4e-109:542:96//Hs.108258:AB007934
 R-OVARC1002066//ESTs//7.8e-97:455:96//Hs.135477:A1088556
 R-OVARC1002082//Homo sapiens mRNA for KIAA0772 protein, complete cds//8.1e-47:340:82//Hs.15519:AB018315
 R-OVARC1002107//ESTs//5.9e-103:498:98//Hs.157207:AA629860
 R-OVARC1002127//ESTs//3.0e-87:419:98//Hs.127833:A1347130
 R-OVARC1002138//ESTs. Weakly similar to HYPOTHETICAL 54.7 KD PROTEIN COT49.1 IN CHROMOSOME III [Caenorhabditis elegans]//1.7e-102:48:5:98//Hs.137516:AA805691
 R-OVARC1002143//ESTs//1.3e-79:428:92//Hs.158126:W26825
 R-OVARC1002156//ESTs//1.6e-38:198:98//Hs.22957:AA478923
 R-OVARC1002158//ESTs//7.3e-81:412:96//Hs.12211:AA908631
 R-OVARC1002165//ESTs//1.8e-09:154:72//Hs.49354:AA424160
 R-OVARC1002182//ESTs//4.3e-80:465:91//Hs.77067:AA040478
 R-PLACE1000004//ESTs. Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//7.5e-32:164:99//Hs.144194:AA706337
 R-PLACE1000005//EST//0.37:212:60//Hs.127020:AA934920
 R-PLACE1000007//Homo sapiens clone 24422 mRNA sequence//3.8e-16:10:0:97//Hs.109268:AF070557
 R-PLACE1000014//EST//9.6e-44:344:77//Hs.161917:AA483223
 R-PLACE1000031//ESTs//2.2e-32:374:70//Hs.117969:H94870
 R-PLACE1000040//ESTs//0.00017:316:59//Hs.23342:A1310440
 R-PLACE1000048//Human Line-1 repeat mRNA with 2 open reading frame s//4.8e-79:519:86//Hs.23094:M19503
 R-PLACE1000050//ESTs//9.7e-90:453:96//Hs.27410:N25612
 R-PLACE1000061//Ribosomal protein L37a//5.5e-22:126:97//Hs.1946:LO 6499
 R-PLACE1000066//ESTs. Weakly similar to coded for by C. elegans C0 NA yk10c10.3 [C.elegans]//1.4e-61:331:94//Hs.30026:A1356771
 R-PLACE1000078//ESTs//2.6e-30:212:85//Hs.89312:AA167659
 R-PLACE1000081
 R-PLACE1000094
 R-PLACE1000133//ESTs//4.4e-87:448:94//Hs.93748:AA884505
 R-PLACE1000142//ESTs. Weakly similar to enoyl-CoA hydratase [H.sapiens]//5.5e-103:538:94//Hs.9670:AA632135
 R-PLACE1000184//Homo sapiens estrogen-related receptor gamma mRNA, complete cds//4.1e-114:594:94//Hs.151017:AF058291
 R-PLACE1000185//ESTs. Weakly similar to No definition line found [C.elegans]//2.0e-19:114:95//Hs.7036:W22072
 R-PLACE1000213//ESTs//9.4e-99:494:96//Hs.24398:A1262946
 R-PLACE1000214//ESTs//5.3e-98:466:98//Hs.28661:AA805916
 R-PLACE1000236//Human BENE mRNA, partial cds//1.7e-19:162:84//Hs.8 5889:U17077
 R-PLACE1000246//EST//0.026:134:66//Hs.135611:Z21545
 R-PLACE1000297//EST//2.5e-80:418:96//Hs.138233:N57912
 R-PLACE1000332//EST//1.7e-82:422:96//Hs.118637:T61940
 R-PLACE1000341//ESTs//8.5e-36:180:100//Hs.6377:AA632424
 R-PLACE1000374//ESTs//2.8e-90:434:98//Hs.161785:A1423126
 R-PLACE1000380//ESTs//1.0e-81:399:97//Hs.47105:A1334994
 R-PLACE1000383//ESTs//3.7e-75:405:94//Hs.23200:AA203708
 R-PLACE1000401//ESTs//1.4e-16:212:72//Hs.151665:AA020959
 R-PLACE1000406//ESTs//2.1e-51:259:97//Hs.129651:M53089
 R-PLACE1000420//ESTs//7.7e-92:471:95//Hs.144407:AA737799
 R-PLACE1000421//ESTs//2.9e-14:282:67//Hs.142068:AA176125
 R-PLACE1000424//EST//2.9e-35:453:70//Hs.162404:AA573131
 R-PLACE1000435//Homo sapiens protein phosphatase with EF-hands-2 l ong form (PPEF-2) mRNA, complete cds//1.6e-47:472:77//Hs.113259:AF 023456
 R-PLACE1000444//ESTs. Moderately similar to platelet glycoprotein 1b precursor [H.sapiens]//2.0e-58:410:81//Hs.97579:AA398118
 R-PLACE1000453//ESTs//2.3e-85:442:95//Hs.9725:AA039793
 R-PLACE1000481//ESTs. Weakly similar to Ndr protein kinase [H.sapiens]//3.2e-109:549:95//Hs.13074:U69566
 R-PLACE1000492//ESTs. Highly similar to vacuolar protein sorting h omolog r-vps33b [R.norvegicus]//3.5e-83:435:94//Hs.26510:AA700425
 R-PLACE1000540//ESTs//3.2e-58:281:99//Hs.118270:AA844729
 R-PLACE1000547//Homo sapiens mRNA for KIAA0640 protein, partial cd s//2.2e-32:208:88//Hs.153026:AB014540

R-PLACE1000562//ESTs. Weakly similar to HYPOTHETICAL 23.0 KD PROTE IN IN IXR1-TFA1 INTERGENIC REGION [Saccharomyces cerevisiae]//1.9 e-26:220:81//Hs.163791:W25348
 R-PLACE1000564//ESTs//1.1e-54:302:92//Hs.158520:A1380485
 R-PLACE1000583//Human mRNA for KIAA0355 gene, complete cds//5.5e-4 3:404:75//Hs.153014:AB002353
 R-PLACE1000588//Guanylate binding protein 1, interferon-inducible, 67kd//6.1e-79:542:82//Hs.62661:W55542
 R-PLACE1000596//ESTs//0.0028:364:59//Hs.106090:AA457030
 R-PLACE1000599//Human mRNA for KIAA0118 gene, partial cds//4.3e-4 9:295:90//Hs.154326:D42087
 R-PLACE1000610//ESTs//0.0010:104:74//Hs.17413:N45301
 R-PLACE1000636//ESTs//1.8e-64:340:95//Hs.100895:AA479308
 R-PLACE1000653//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds//5.3e-101:506:96//Hs.5819:AF102265
 R-PLACE1000656//Homo sapiens mRNA for JMA protein, complete CDS (c lone IMAGE 546750 and LLNLC10F1857Q7 (RZPD Berlin))//1.4e-102:55 9:92//Hs.29595:AJ005896
 R-PLACE1000706//Homo sapiens transcription intermediary factor 1 (TIF1) mRNA, complete cds//2.8e-10:281:64//Hs.128763:AF009353
 R-PLACE1000712//ESTs//7.8e-60:317:95//Hs.8245:AA115485
 R-PLACE1000716
 R-PLACE1000748//ESTs//8.9e-87:466:93//Hs.25245:AA176701
 R-PLACE1000749//EST//0.019:186:61//Hs.135443:A1077396
 R-PLACE1000755//ESTs. Weakly similar to HYPOTHETICAL HELICASE K12H 4.8 IN CHROMOSOME III [C.elegans]//3.9e-40:224:94//Hs.87889:AA2620 08
 R-PLACE1000769//Homo sapiens clone 24566 mRNA sequence//6.5e-27:53 1:66//Hs.133342:AF070536
 R-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cd s//8.5e-103:513:96//Hs.31921:AB014548
 R-PLACE1000786//ESTs//5.2e-93:449:97//Hs.58389:W74482
 R-PLACE1000793//H.sapiens mRNA for chemokine HCC-1//0.88:201:60//H s.20144:AF088219
 R-PLACE1000798//ESTs//1.1e-97:508:94//Hs.139119:N32189
 R-PLACE1000841//ESTs. Highly similar to guanine nucleotide regulat ory protein [H.sapiens]//7.7e-31:220:86//Hs.117576:R31335
 R-PLACE1000849//ESTs//1.8e-87:459:94//Hs.43100:AA186588
 R-PLACE1000856//ESTs//0.0084:224:59//Hs.145906:A1275039
 R-PLACE1000863//ESTs. Highly similar to PUTATIVE 40S RIBOSOMAL PR OTEIN YHR148W [Saccharomyces cerevisiae]//2.2e-92:467:95//Hs.6118: A1141558
 R-PLACE1000909//ESTs//4.7e-89:435:97//Hs.95744:A1392846
 R-PLACE1000931//EST//1.9e-28:261:73//Hs.135545:A1097091
 R-PLACE1000948//ESTs//0.034:329:58//Hs.114851:AA608697
 R-PLACE1000972//EST//3.3e-24:264:74//Hs.130321:A1002941
 R-PLACE1000977//EST//0.085:153:65//Hs.131646:A1025689
 R-PLACE1000979
 R-PLACE1001000//ESTs//4.7e-56:284:96//Hs.117978:AA810725
 R-PLACE1001007//ESTs. Moderately similar to MNK1 [H.sapiens]//5.2 e-63:343:93//Hs.5662:AA868361
 R-PLACE1001010//EST//0.96:53:71//Hs.96973:AA351146
 R-PLACE1001015//Oxytocin receptor//2.8e-25:308:71//Hs.2820:X64878
 R-PLACE1001024//ESTs//5.0e-12:79:96//Hs.97910:AA404736
 R-PLACE1001036//ESTs//4.0e-15:301:65//Hs.137947:A1025762
 R-PLACE1001062//ESTs//5.2e-15:199:73//Hs.138982:AA056120
 R-PLACE1001076//ESTs//3.9e-84:406:98//Hs.115455:AA678124
 R-PLACE1001088//ESTs//3.0e-106:518:97//Hs.158964:AA639580
 R-PLACE1001092//Homo sapiens SEC63 (SEC63) mRNA, complete cds//0.0 35:259:59//Hs.31575:AF100141
 R-PLACE1001104//ESTs//6.1e-115:582:95//Hs.10972:AA164268
 R-PLACE1001118//ESTs//6.9e-81:440:93//Hs.5383:AA913610
 R-PLACE1001136//ESTs//7.4e-41:168:83//Hs.95115:AA206594
 R-PLACE1001168//ESTs//3.9e-21:116:99//Hs.5897:AA148834
 R-PLACE1001171//ESTs. Highly similar to CYTOCHROME B-245 LIGHT CHA IN [H.sapiens]//0.91:77:71//Hs.115211:AA287527
 R-PLACE1001185//ESTs//1.5e-65:330:96//Hs.26368:AA789297
 R-PLACE1001238//ESTs. Moderately similar to RNA polymerase I assoc iated factor [M.musculus]//1.9e-99:512:94//Hs.24884:AA176812
 R-PLACE1001241//ESTs//1.1e-81:446:93//Hs.42278:A1073464
 R-PLACE1001257//EST//6.4e-46:298:87//Hs.162404:AA573131
 R-PLACE1001272//ESTs//0.31:158:61//Hs.42960:N95371
 R-PLACE1001279//ESTs//1.8e-77:376:97//Hs.29276:AA427780
 R-PLACE1001280//ESTs//1.1e-30:134:89//Hs.163492:A1334460
 R-PLACE1001294//ESTs. Moderately similar to GAMETOGENESIS EXPRESSE D PROTEIN CEC-154 [M.musculus]//2.7e-22:181:84//Hs.48320:AA149548
 R-PLACE1001304//ESTs. Weakly similar to ZINC FINGER PROTEIN 135 [H.sapiens]//4.2e-34:195:92//Hs.86276:W27601
 R-PLACE1001311//ESTs//9.1e-91:438:97//Hs.41055:A1339056
 R-PLACE1001323//Human transmembrane 4 superfamily protein (SAS) mR

【0930】

【表628】

MA, complete cds//5.5e-44:215:86//Hs.50984:U01160	R-PLACE1002115//ESTs//4.6e-34:233:88//Hs.163443:R23311
R-PLACE1001351//ESTs//2.4e-101:494:97//Hs.23944:A1097077	R-PLACE1002119//ESTs//1.2e-88:444:96//Hs.15725:AA521293
R-PLACE1001366//Small inducible cytokine A5 (RANTES)//8.7e-43:284:85//Hs.155464:AF088219	R-PLACE1002140//ESTs//6.6e-22:118:100//Hs.22793:W91937
R-PLACE1001377//Homo sapiens ADAM10 (ADAM10) mRNA, complete cds//2.3e-81:431:93//Hs.152005:AF009615	R-PLACE1002150//ESTs//4.0e-96:465:98//Hs.7312:A1167614
R-PLACE1001383//Homo sapiens clone 24538 mRNA sequence//1.0e-36:192:97//Hs.12342:AF055030	R-PLACE1002157//EST, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//3.6e-39:400:76//Hs.162172:AA534189
R-PLACE1001384//Homo sapiens multi PDZ domain protein MUPP1 (MUPP1) mRNA, complete cds//1.0e-86:456:94//Hs.21301:AF093419	R-PLACE1002163//ESTs//3.2e-83:428:95//Hs.137011:A1185965
R-PLACE1001387//ESTs//6.0e-74:383:94//Hs.55016:A1298280	R-PLACE1002171//ESTs//5.3e-68:392:90//Hs.62273:AA143745
R-PLACE1001395//ESTs//2.3e-94:473:95//Hs.22394:N32555	R-PLACE1002205//ESTs//1.5e-39:211:95//Hs.28338:N48793
R-PLACE1001399//ESTs//2.6e-41:204:100//Hs.24462:N36348	R-PLACE1002213//ESTs//5.1e-38:290:83//Hs.146811:AA410788
R-PLACE1001412//Homo sapiens clone 643 unknown mRNA, complete sequence//2.6e-45:242:95//Hs.110404:AF091087	R-PLACE1002227//EST//1.3e-14:214:72//Hs.46979:N49892
R-PLACE1001414//ESTs//0.0013:77:75//Hs.144614:AA291800	R-PLACE1002256//ESTs//2.4e-100:484:98//Hs.9343:A1004257
R-PLACE1001440	R-PLACE1002259//Human Line-1 repeat mRNA with 2 open reading frame s//5.8e-67:501:81//Hs.23094:M19503
R-PLACE1001456//EST//0.76:120:62//Hs.34011:H48115	R-PLACE1002319//ESTs//1.4e-28:178:92//Hs.7353:AA209308
R-PLACE1001468//ESTs//4.0e-80:403:96//Hs.131832:A1017547	R-PLACE1002342//Homo sapiens mRNA for KIAA0728 protein, partial cds//1.6e-95:501:93//Hs.18277:AB018271
R-PLACE1001484//ESTs//3.0e-16:201:72//Hs.153413:A1248625	R-PLACE1002395//ESTs//3.6e-25:248:77//Hs.3853:AA034291
R-PLACE1001502//ESTs//8.1e-31:161:99//Hs.126264:AA455617	R-PLACE1002399//ESTs//1.5e-27:238:78//Hs.13014:W26381
R-PLACE1001503//ESTs//2.4e-37:176:81//Hs.141581:AA315361	R-PLACE1002433//ESTs//4.3e-108:511:98//Hs.98324:AA621959
R-PLACE1001517//Homo sapiens HGAA1 mRNA, complete cds//2.1e-57:339:90//Hs.4742:AB006969	R-PLACE1002437//EST//1.2e-06:158:61//Hs.159833:T24110
R-PLACE1001534//ESTs//3.6e-61:304:97//Hs.45207:A1042153	R-PLACE1002438//Sjogren syndrome antigen B (autoantigen La)//0.93:176:60//Hs.83715:X69804
R-PLACE1001545//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.6e-22:170:85//Hs.155456:AA707265	R-PLACE1002450//ESTs//1.5e-89:432:98//Hs.47371:AA136333
R-PLACE1001551//ESTs//1.5e-39:202:98//Hs.139269:AA894431	R-PLACE1002465//ESTs//1.6e-92:488:93//Hs.78110:AA741320
R-PLACE1001570//EST//1.1e-70:495:82//Hs.144234:W52249	R-PLACE1002474//Human matrilin-2 precursor mRNA, partial cds//4.9e-23:166:85//Hs.19368:U69263
R-PLACE1001602//EST//0.33:297:57//Hs.149839:A1287601	R-PLACE1002477//ESTs//2.5e-62:305:98//Hs.88605:AA421132
R-PLACE1001603//ESTs//2.0e-17:181:76//Hs.155334:AA827904	R-PLACE1002493//Homo sapiens signal transducing adaptor molecule 2 A (STAM2) mRNA, complete cds//3.6e-55:307:91//Hs.17200:AF042273
R-PLACE1001610//EST//1.1e-86:442:95//Hs.112580:AA608683	R-PLACE1002499//ESTs//7.4e-72:373:96//Hs.128221:AA972429
R-PLACE1001611//Homo sapiens histone macroH2A1.2 mRNA, complete cds//1.1e-42:217:97//Hs.75258:AF054174	R-PLACE1002500//Homo sapiens KIAA0409 mRNA, partial cds//1.2e-40:296:83//Hs.5158:AB007869
R-PLACE1001632//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]//1.5e-78:458:91//Hs.114547:AA167095	R-PLACE1002514//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB1 WARNING ENTRY !!!! [H.sapiens]//6.4e-14:217:69//Hs.152230:A1140609
R-PLACE1001634//ESTs//0.0035:40:97//Hs.101577:A1168526	R-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds//5.1e-88:582:85//Hs.88756:AB018256
R-PLACE1001640//ESTs//0.0028:377:57//Hs.131044:D61640	R-PLACE1002532//Homo sapiens BAC clone RG300E22 from Tq21-q31.1//2.7e-19:116:93//Hs.99348:AC004774
R-PLACE1001672//ESTs, Moderately similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//0.98:141:62//Hs.153060:AA195804	R-PLACE1002537//ESTs//4.8e-93:440:99//Hs.164005:AA766491
R-PLACE1001691//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//4.7e-113:545:97//Hs.3688:AF069250	R-PLACE1002571//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosophila melanogaster]//1.3e-108:555:95//Hs.23259:AA532437
R-PLACE1001692//EST//3.0e-43:430:75//Hs.162975:AA679124	R-PLACE1002578//EST//1.9e-40:337:81//Hs.162404:AA573131
R-PLACE1001705//ESTs//3.0e-81:418:94//Hs.22646:A1374903	R-PLACE1002583//EST//1.2e-07:264:65//Hs.156414:A1339738
R-PLACE1001716//EST//0.76:150:62//Hs.128906:AA983687	R-PLACE1002591//ESTs//2.3e-67:372:94//Hs.143046:N73778
R-PLACE1001720//ESTs//2.4e-64:385:90//Hs.60455:AA010993	R-PLACE1002598//ESTs, Highly similar to PROTEIN HI1715 [Haemophilus influenzae]//1.2e-44:228:97//Hs.7527:AA843208
R-PLACE1001729//ESTs//2.9e-84:418:96//Hs.134740:AA282171	R-PLACE1002604//ESTs//3.3e-106:532:96//Hs.86828:AA632147
R-PLACE1001739//ESTs, Weakly similar to P68 PROTEIN [H.sapiens]//9.1e-32:206:89//Hs.6366:AA614113	R-PLACE1002625//EST//3.8e-13:173:74//Hs.138597:H77749
R-PLACE1001740//EST//6.5e-05:113:68//Hs.139949:AA644266	R-PLACE1002665//Small inducible cytokine A4 (homologous to mouse Mip-1b)//1.0:189:58//Hs.75703:J04130
R-PLACE1001745//ESTs//3.3e-92:473:95//Hs.104270:AA236479	R-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds//3.8e-79:390:97//Hs.124903:AF068180
R-PLACE1001746//ESTs//8.8e-93:443:98//Hs.112198:A1423937	R-PLACE1002714//ESTs//8.2e-63:340:93//Hs.7973:HI9830
R-PLACE1001748//Homo sapiens metalloprotease 1 (MPI) mRNA, complete cds//4.1e-93:540:89//Hs.4812:AF061243	R-PLACE1002722//ESTs, Weakly similar to putative G-protein-coupled receptor [H.sapiens]//6.8e-75:445:90//Hs.29202:R71586
R-PLACE1001756//ESTs//0.17:157:66//Hs.141565:N64662	R-PLACE1002768//ESTs//1.2e-70:359:95//Hs.132600:HI2865
R-PLACE1001761	R-PLACE1002772//ESTs//8.1e-49:362:82//Hs.141254:A1334099
R-PLACE1001771//ESTs//0.92:165:62//Hs.47387:N51980	R-PLACE1002782//ESTs//2.4e-58:284:98//Hs.143545:A1149014
R-PLACE1001781//ESTs//5.7e-84:437:95//Hs.23363:AA081236	R-PLACE1002794//ESTs//5.4e-21:114:100//Hs.77365:W93593
R-PLACE1001799//EST//0.00039:126:65//Hs.123267:AA807352	R-PLACE1002811//ESTs//6.7e-68:329:98//Hs.78026:AA456955
R-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds//1.3e-93:463:95//Hs.40820:AF058953	R-PLACE1002815//ESTs//6.8e-103:537:93//Hs.5459:A1304392
R-PLACE1001821//Small inducible cytokine A5 (RANTES)//2.7e-35:328:75//Hs.155464:AF088219	R-PLACE1002816//ESTs//3.9e-05:118:68//Hs.98641:AA429916
R-PLACE1001845	R-PLACE1002834//ESTs, Highly similar to ZINC FINGER PROTEIN 91 [Homo sapiens]//2.1e-42:233:94//Hs.61518:AA167094
R-PLACE1001859//EST//1.0:207:62//Hs.137298:W32868	R-PLACE1002839//ESTs//1.7e-10:292:64//Hs.93012:R96142
R-PLACE1001897//ESTs//2.4e-23:219:80//Hs.7503:H50009	R-PLACE1002851//ESTs//1.7e-73:381:95//Hs.135021:A1096756
R-PLACE1001912//ESTs//1.5e-32:162:78//Hs.136810:AA789098	R-PLACE1002853//ESTs//1.2e-89:453:96//Hs.23630:N57539
R-PLACE1001920//Homo sapiens TNF-induced protein GG2-1 mRNA, complete cds//3.9e-74:363:97//Hs.17839:AF099936	R-PLACE1002881//ESTs//1.1e-71:360:96//Hs.34392:A1066762
R-PLACE1001928//Homo sapiens mRNA for KIAA0623 protein, complete cds//0.85:130:66//Hs.151405:AB014523	R-PLACE1002908//EST//2.7e-31:177:94//Hs.147925:A1249332
R-PLACE1001983//ESTs//2.8e-66:334:96//Hs.110155:AA007313	R-PLACE1002941//ESTs//4.0e-96:519:92//Hs.125139:AA523995
R-PLACE1001989//ESTs//1.3e-88:453:95//Hs.132717:AA171941	R-PLACE1002962
R-PLACE1002046	R-PLACE1002968//ESTs//4.7e-31:420:69//Hs.116518:AA653202
R-PLACE1002052//ESTs//1.7e-79:428:94//Hs.6737:N32595	R-PLACE1002991//ESTs//9.0e-81:418:95//Hs.132717:AA171941
R-PLACE1002066//ESTs//2.8e-82:427:94//Hs.132972:AA543094	R-PLACE1002993//ESTs, Weakly similar to !!!! ALU SUBFAMILY SB WARNING ENTRY !!!! [H.sapiens]//1.3e-86:502:89//Hs.32232:AA604268
R-PLACE1002072//ESTs//0.27:108:66//Hs.123163:AA809619	R-PLACE1002996//ESTs//1.9e-44:218:100//Hs.63657:A1144268
R-PLACE1002073//EST//5.5e-70:369:95//Hs.132339:A1028552	R-PLACE1003025//ESTs//8.4e-104:517:96//Hs.10711:A1151499
R-PLACE1002090//ESTs//6.3e-73:361:98//Hs.134469:AA731632	R-PLACE1003027//Human mRNA for KIAA0238 gene, partial cds//0.97:15

【0931】

【表629】

6:60//Hs.82042:D87075
 R-PLACE1003044//Human onconeural ventral antigen-1 (Nova-1) mRNA, complete cds//1.0:200:63//Hs.214:U04840
 R-PLACE1003092//ESTs//0.0046:267:60//Hs.133095:AA927777
 R-PLACE1003100//ESTs, Highly similar to MODULATION PROTEIN G [Rhizobium meliloti]//9.5e-94:491:93//Hs.6318:AI131178
 R-PLACE1003108//ESTs//0.00065:184:66//Hs.154366:AA527359
 R-PLACE1003136//Signal recognition particle 54 kD protein//0.057:317:59//Hs.49346:U51920
 R-PLACE1003145//ESTs//1.9e-98:534:92//Hs.61929:AA044757
 R-PLACE1003153//ESTs//5.8e-76:367:98//Hs.105196:AA483467
 R-PLACE1003174//ESTs//1.7e-44:226:98//Hs.59688:AA453924
 R-PLACE1003176
 R-PLACE1003190//ESTs//1.6e-74:356:99//Hs.121282:AI091453
 R-PLACE1003200//ESTs//4.6e-93:461:96//Hs.24321:AA971017
 R-PLACE1003205//ESTs//0.037:171:61//Hs.157077:HA4802
 R-PLACE1003238//ESTs, Weakly similar to KIAA0001 [H.sapiens]//2.5e-82:436:94//Hs.58561:W9123
 R-PLACE1003249//Human high-affinity copper uptake protein (hCTR1) mRNA, complete cds//7.9e-46:284:80//Hs.73614:U83460
 R-PLACE1003256//ESTs//9.6e-46:284:80//Hs.162404:AA573131
 R-PLACE1003258//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//8.3e-102:551:92//Hs.52431:AA625326
 R-PLACE1003296//ESTs//1.9e-88:451:96//Hs.57749:W92986
 R-PLACE1003302//ESTs, Highly similar to ZINC FINGER PROTEIN 43 [Homo sapiens]//8.2e-93:458:96//Hs.29147:AA883993
 R-PLACE1003334//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//3.3e-94:463:97//Hs.155050:AA908765
 R-PLACE1003342//ESTs//6.0e-88:447:96//Hs.107527:R66438
 R-PLACE1003343//EST//0.0087:412:58//Hs.159963:AA977701
 R-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds//1.1e-99:469:98//Hs.6564:U92715
 R-PLACE1003361//ESTs//3.5e-64:332:95//Hs.163861:AI199636
 R-PLACE1003366//ESTs//1.0e-87:492:92//Hs.72222:AA158234
 R-PLACE1003369//ESTs, Weakly similar to ZK1058.4 [C.elegans]//3.5e-18:109:95//Hs.27670:AI051591
 R-PLACE1003373//Homo sapiens mRNA for KIAA0472 protein, partial cds//2.6e-54:279:80//Hs.6874:AB007941
 R-PLACE1003375//ESTs//1.7e-88:431:97//Hs.41327:AI039909
 R-PLACE1003383//ESTs//0.00084:177:64//Hs.120695:AI377755
 R-PLACE1003401//ESTs//1.1e-16:147:80//Hs.132187:AI039020
 R-PLACE1003420//ESTs//1.4e-93:481:94//Hs.122565:AI126840
 R-PLACE1003454//ESTs//4.0e-57:310:93//Hs.121688:AA743697
 R-PLACE1003478//EST//1.0:162:63//Hs.147003:AI184671
 R-PLACE1003493//ESTs//1.2e-73:383:95//Hs.28852:R64270
 R-PLACE1003516//ESTs//3.2e-23:206:80//Hs.138632:H97952
 R-PLACE1003519//H.sapiens hnRNP-E1 mRNA//1.7e-22:236:79//Hs.2853:Z29505
 R-PLACE1003521//ESTs//5.8e-74:371:96//Hs.30818:AA194980
 R-PLACE1003528//ESTs//1.1e-40:219:82//Hs.138856:HA7461
 R-PLACE1003537//ESTs, Weakly similar to multispanning membrane protein [H.sapiens]//7.4e-69:338:98//Hs.110439:H93209
 R-PLACE1003553//ESTs//2.2e-87:438:97//Hs.132022:AI040321
 R-PLACE1003566//ESTs//1.2e-62:298:92//Hs.30799:AI052591
 R-PLACE1003575//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.4e-22:145:80//Hs.92381:AB007956
 R-PLACE1003583//ESTs, Weakly similar to hypothetical L1 protein [H.sapiens]//1.5e-14:264:65//Hs.158253:R86178
 R-PLACE1003584
 R-PLACE1003592//ESTs//1.3e-15:213:69//Hs.139507:T77542
 R-PLACE1003593//ESTs, Highly similar to FRG1 gene product [H.sapiens]//5.8e-75:459:89//Hs.23884:AI377106
 R-PLACE1003596//ESTs//0.011:273:61//Hs.71719:AA142875
 R-PLACE1003602//Homo sapiens mRNA expressed in placenta//7.8e-97:576:88//Hs.56851:D83200
 R-PLACE1003605//ESTs//3.7e-86:407:99//Hs.136057:AA988299
 R-PLACE1003611//ESTs//1.0:78:71//Hs.101248:T26446
 R-PLACE1003618//ESTs//6.8e-30:281:79//Hs.114455:AA411943
 R-PLACE1003625//ESTs//7.2e-78:377:98//Hs.102708:AA292285
 R-PLACE1003638//ESTs//6.7e-38:274:82//Hs.138852:AA284247
 R-PLACE1003669//ESTs//9.7e-83:418:95//Hs.4842:AI342607
 R-PLACE1003704//ESTs//3.0e-13:99:89//Hs.81648:W26521
 R-PLACE1003709//ESTs//0.019:178:60//Hs.32100:N59866
 R-PLACE1003711//ESTs//0.99:126:63//Hs.47005:N98639
 R-PLACE1003723//ESTs//1.7e-89:448:96//Hs.157222:AA766987
 R-PLACE1003738//ESTs//2.5e-36:182:100//Hs.122162:AI057087
 R-PLACE1003760//Human globin gene//1.9e-98:538:91//Hs.100090:W69023
 R-PLACE1003762//EST//2.9e-15:125:85//Hs.162083:AA487512
 R-PLACE1003768//Human PO42 gene, complete cds//3.1e-18:300:69//Hs.158302:U88965
 R-PLACE1003771//ESTs//1.2e-09:64:100//Hs.23799:AI003798
 R-PLACE1003783//ESTs, Weakly similar to D2085.5 [C.elegans]//3.8e-38:199:97//Hs.115197:AA215757
 R-PLACE1003784//ESTs//3.7e-87:428:97//Hs.157985:AI366909
 R-PLACE1003795//Homo sapiens mRNA for KIAA0575 protein, complete cds//3.2e-36:236:88//Hs.153468:AB011147
 R-PLACE1003833//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//8.5e-62:313:96//Hs.121020:AA526092
 R-PLACE1003850//ESTs//4.0e-67:351:96//Hs.159303:T91059
 R-PLACE1003858//ESTs//0.96:87:66//Hs.107112:AA679058
 R-PLACE1003864
 R-PLACE1003870//EST//2.9e-34:281:79//Hs.160895:AI365871
 R-PLACE1003885
 R-PLACE1003886//ESTs//6.7e-85:410:97//Hs.25129:W93595
 R-PLACE1003888//ESTs//0.0085:165:64//Hs.96739:AA441915
 R-PLACE1003900//EST//2.4e-05:129:69//Hs.127931:AA969259
 R-PLACE1003903//ESTs, Highly similar to CTP SYNTHASE [Homo sapiens]//1.5e-54:282:96//Hs.58553:AA100804
 R-PLACE1003915//EST//0.87:55:76//Hs.145930:AI275760
 R-PLACE1003923//ESTs//1.7e-89:456:95//Hs.14125:AA156236
 R-PLACE1003932//ESTs//3.0e-50:340:84//Hs.151208:AI126110
 R-PLACE1003936//EST//1.8e-08:208:65//Hs.162656:AA603567
 R-PLACE1003968//ESTs//7.4e-49:301:90//Hs.93850:AA115330
 R-PLACE1004104//ESTs//1.9e-46:254:94//Hs.96802:AA443231
 R-PLACE1004114//ESTs//1.2e-64:322:97//Hs.28928:AI052052
 R-PLACE1004118//ESTs//1.0e-83:404:98//Hs.112764:AA609770
 R-PLACE1004128//ESTs//5.3e-80:415:95//Hs.11835:AA040244
 R-PLACE1004149//ESTs//7.2e-25:331:72//Hs.141084:HI1714
 R-PLACE1004156//Homo sapiens PYRIN (MEFV) mRNA, complete cds//2.0e-56:491:76//Hs.113283:AF018080
 R-PLACE1004161//ESTs//2.0e-59:355:88//Hs.13830:AA918601
 R-PLACE1004183//Homo sapiens cytochrome c-oxidase assembly protein COX11 (COX11) mRNA, complete cds//4.7e-78:434:91//Hs.153504:AF044321
 R-PLACE1004197
 R-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds//1.5e-105:501:98//Hs.24640:AF069493
 R-PLACE1004242//ESTs//1.0e-71:364:87//Hs.138632:H97952
 R-PLACE1004256//EST//0.0011:347:61//Hs.131385:AI022630
 R-PLACE1004257//EST//0.027:99:71//Hs.97587:AA398209
 R-PLACE1004258//KERATIN, TYPE I CYTOSKELETAL 14//0.72:180:63//Hs.17729:J00124
 R-PLACE1004270//ESTs//0.011:264:59//Hs.110044:AA181800
 R-PLACE1004274//Human retinoic acid receptor-beta associated open reading frame, complete sequence//0.28:121:66//Hs.1938:S82362
 R-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, complete cds//1.4e-107:581:91//Hs.127007:AF084830
 R-PLACE1004284//ESTs//5.0e-22:187:82//Hs.23141:W92114
 R-PLACE1004289//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.9e-28:279:77//Hs.38687:AA744496
 R-PLACE1004302//ESTs, Weakly similar to SOF1 PROTEIN [Saccharomyces cerevisiae]//8.2e-61:313:95//Hs.71435:AI253099
 R-PLACE1004316//H.sapiens mRNA for apoptosis specific protein//6.0e-115:590:94//Hs.111171:Y11588
 R-PLACE1004336//Cytochrome P450, subfamily I (aromatic compound-inducible), polypeptide 2//6.7e-69:572:77//Hs.1361:M55053
 R-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds//7.7e-72:379:93//Hs.16232:AF100153
 R-PLACE1004376//ESTs//0.49:362:59//Hs.138086:AI056309
 R-PLACE1004384//EST//1.0:47:76//Hs.128546:AA905556
 R-PLACE1004388//ESTs, Weakly similar to contains similarity to ATP/GTP-binding site motif [C.elegans]//1.3e-98:572:90//Hs.14202:N46000
 R-PLACE1004405//ESTs//3.4e-99:507:95//Hs.28792:AI343467
 R-PLACE1004425//ESTs//2.7e-85:442:95//Hs.12544:N53665
 R-PLACE1004428//ESTs//1.0e-07:114:78//Hs.140225:AA704101
 R-PLACE1004437//Human NAD+-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds//9.4e-90:516:88//Hs.155410:U49283
 R-PLACE1004451
 R-PLACE1004460//ESTs//5.4e-14:338:64//Hs.97464:AA662980
 R-PLACE1004467//ESTs//3.3e-85:467:92//Hs.9527:W52721
 R-PLACE1004471//ESTs//3.0e-73:389:94//Hs.23240:R46578
 R-PLACE1004473//ESTs, Weakly similar to F20D1.2 [C.elegans]//3.8e-101:510:95//Hs.16986:W89194
 R-PLACE1004491//Human mitochondrial l.25-dihydroxyvitamin D3 24-hydroxylase mRNA, complete cds//0.23:278:61//Hs.89663:L13286
 R-PLACE1004506//ESTs//2.5e-98:559:90//Hs.19447:AI057117

【表630】

R-PLACE1004510//ESTs//1.5e-91:436:98//Hs.24846:A120493	R-PLACE1005102//ESTs//7.2e-68:493:84//Hs.10593:A1201336
R-PLACE1004516//EST//1.7e-66:344:96//Hs.99303:AA453164	R-PLACE1005108//Human DNA fragmentation factor-45 mRNA, complete cds//9.2e-40:232:82//Hs.155344:U91985
R-PLACE1004518//ESTs//5.2e-79:410:94//Hs.27091:AA436553	R-PLACE1005111//EST//8.1e-10:189:68//Hs.136356:AA493225
R-PLACE1004548//Homo sapiens mRNA for small GTP-binding protein, complete cds//1.8e-40:332:72//Hs.115325:D84488	R-PLACE1005128//ESTs//1.4e-78:501:87//Hs.15093:AA203423
R-PLACE1004550	R-PLACE1005146//ESTs//4.8e-93:460:97//Hs.37896:AA777349
R-PLACE1004564//ESTs//5.5e-76:367:98//Hs.49683:AA564742	R-PLACE1005162//ESTs//7.5e-51:277:95//Hs.28838:A1089013
R-PLACE1004629//ESTs. Weakly similar to OS-9 precursor [H.sapiens]//8.1e-40:272:87//Hs.7100:W07181	R-PLACE1005176//ESTs//5.4e-75:366:97//Hs.48119:AA454227
R-PLACE1004645//ESTs//6.3e-14:83:100//Hs.17270:AA701903	R-PLACE1005181//EST//0.012:172:66//Hs.147107:A1190589
R-PLACE1004646//ESTs//3.7e-22:231:76//Hs.141250:N29734	R-PLACE1005187//ESTs//5.6e-72:363:95//Hs.16577:A1022830
R-PLACE1004658//ESTs//2.0e-12:109:84//Hs.23508:AA101113	R-PLACE1005206//ESTs//5.3e-48:203:88//Hs.31792:H45211
R-PLACE1004664//Homo sapiens mRNA for KIAA0714 protein, partial cds//7.8e-23:129:99//Hs.123129:AB018257	R-PLACE1005232//ESTs//5.1e-41:287:84//Hs.138552:R99532
R-PLACE1004672//ESTs//2.0e-50:256:98//Hs.136367:A114254	R-PLACE1005243//ESTs//1.1e-48:348:83//Hs.113310:R16767
R-PLACE1004674//Homo sapiens calcium binding protein (ALG-2) mRNA, complete cds//1.8e-90:510:91//Hs.80019:AF035606	R-PLACE1005261//ESTs//0.19:175:62//Hs.124337:AA829524
R-PLACE1004681//EST//2.1e-08:283:62//Hs.99543:AA461482	R-PLACE1005266//ESTs//1.9e-22:388:66//Hs.124146:AA699633
R-PLACE1004686	R-PLACE1005277//ESTs//1.5e-29:314:72//Hs.163710:AA024516
R-PLACE1004691//EST//7.3e-42:305:82//Hs.141833:AA021552	R-PLACE1005287//ESTs//3.6e-95:456:98//Hs.49282:AA970322
R-PLACE1004693//ESTs//0.014:135:64//Hs.145333:A1251374	R-PLACE1005305//ESTs//9.9e-71:428:88//Hs.144855:A1197937
R-PLACE1004716//ESTs. Weakly similar to No definition line found [C.elegans]//3.4e-80:413:94//Hs.23528:A1279571	R-PLACE1005308//ESTs//3.8e-32:173:96//Hs.58239:AA215797
R-PLACE1004722//EST//0.14:165:63//Hs.18213:T97997	R-PLACE1005313//ESTs//5.2e-74:409:93//Hs.33368:AA206614
R-PLACE1004736//ESTs//1.0e-72:385:94//Hs.10657:N63911	R-PLACE1005327//Chromosome 1 specific transcript KIAA0491//1.7e-10:4:537:94//Hs.136309:AB007960
R-PLACE1004740//ESTs//1.0:267:58//Hs.101661:AA416619	R-PLACE1005331//ESTs//2.1e-91:487:93//Hs.9291:A1189343
R-PLACE1004743//EST//0.45:94:69//Hs.147174:A1192195	R-PLACE1005335//ESTs. Weakly similar to F23B2.4 [C.elegans]//3.8e-90:442:97//Hs.70202:AA732975
R-PLACE1004751//EST//9.8e-32:174:83//Hs.147901:A1223374	R-PLACE1005373//ESTs//8.0e-93:526:91//Hs.98541:N38901
R-PLACE1004773//Homo sapiens invasin protein mRNA, complete cds//2.7e-89:437:96//Hs.104715:AF084367	R-PLACE1005374//Homo sapiens KIAA0395 mRNA, partial cds//3.3e-44:3:44:80//Hs.43681:AL022394
R-PLACE1004777//ESTs//7.4e-68:351:94//Hs.23395:AA398548	R-PLACE1005409//EST//0.43:174:59//Hs.162077:AA479978
R-PLACE1004793//ESTs//1.3e-53:290:78//Hs.142375:AA398619	R-PLACE1005453//EST//7.9e-57:330:90//Hs.162306:AA555304
R-PLACE1004804//Homo sapiens mRNA for KIAA0606 protein, partial cds//1.9e-99:580:88//Hs.38176:AB011178	R-PLACE1005467//ESTs//2.2e-42:294:84//Hs.142257:AA188423
R-PLACE1004813//ESTs//7.6e-86:433:96//Hs.85640:AA535856	R-PLACE1005471//Human Line-1 repeat mRNA with 2 open reading frame s//2.3e-88:561:86//Hs.23094:M19503
R-PLACE1004814//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//1.1e-108:358:99//Hs.3688:AF069250	R-PLACE1005477//Human methionine aminopeptidase mRNA, complete cds//6.9e-80:549:83//Hs.78935:U29607
R-PLACE1004815//EST//4.7e-50:333:84//Hs.142196:AA258356	R-PLACE1005480//EST//0.99:39:82//Hs.157275:A1364046
R-PLACE1004824//Protein kinase, interferon-inducible double stranded RNA dependent//4.8e-46:450:76//Hs.73821:M35663	R-PLACE1005481//EST//1.5e-31:281:79//Hs.132635:A1032875
R-PLACE1004827//ESTs//2.3e-48:250:96//Hs.138766:AA342185	R-PLACE1005494//Homo sapiens mRNA for semaphorin E, complete cds//0.036:319:59//Hs.62705:AB000220
R-PLACE1004836//ESTs//2.7e-39:222:94//Hs.78661:AA195299	R-PLACE1005502//Homo sapiens formin binding protein 21 mRNA, complete cds//5.4e-57:277:98//Hs.28307:AF071185
R-PLACE1004838//EST//0.056:198:60//Hs.129589:AA995901	R-PLACE1005526//ESTs//2.5e-30:233:83//Hs.119304:AA443325
R-PLACE1004840//ESTs. Highly similar to TRANSCRIPTIONAL ACTIVATOR GCN5 [Saccharomyces cerevisiae]//6.5e-71:381:93//Hs.8383:AA013272	R-PLACE1005528//Homo sapiens mRNA for cartilage-associated protein (CASP)//8.9e-20:321:69//Hs.155481:AJ006470
R-PLACE1004868//ESTs//4.9e-70:367:94//Hs.100895:AA479308	R-PLACE1005530//ESTs//3.7e-81:438:92//Hs.103380:A1291325
R-PLACE1004885//Homo sapiens protein phosphatase with EF-hands-2 1 long form (PPEF-2) mRNA, complete cds//1.8e-37:330:78//Hs.113259:AF023456	R-PLACE1005550//ESTs. Highly similar to HYPOTHETICAL 40.2 KD PROT E1N K12H4.3 IN CHROMOSOME III [Caenorhabditis elegans]//5.2e-95:45:8:98//Hs.38114:N62927
R-PLACE1004900//EST//1.2e-46:306:86//Hs.149580:A1281881	R-PLACE1005554//ESTs//8.8e-36:267:86//Hs.98288:AA203555
R-PLACE1004902//Sucrase-isomaltase//0.87:254:61//Hs.2996:X63597	R-PLACE1005557//ESTs. Highly similar to MITOCHONDRIAL 60S RIBOSOMAL PROTEIN L2 PRECURSOR [Saccharomyces cerevisiae]//2.2e-64:345:94//Hs.7736:W81261
R-PLACE1004913//ESTs//4.5e-75:375:96//Hs.91115:A1221563	R-PLACE1005574//ESTs//2.3e-27:231:83//Hs.117771:R99835
R-PLACE1004918//ESTs//2.6e-103:519:95//Hs.143607:A1424948	R-PLACE1005584//ESTs//1.6e-36:188:98//Hs.152050:AA724612
R-PLACE1004930//Homo sapiens TNF-induced protein G2-1 mRNA, complete cds//6.6e-102:532:93//Hs.17839:AF099936	R-PLACE1005595//ESTs//1.6e-91:453:96//Hs.85079:A1276023
R-PLACE1004934//EST//0.035:156:67//Hs.162071:AA478980	R-PLACE1005603//ESTs//0.2e-99:533:93//Hs.96357:A1026927
R-PLACE1004937//ESTs. Weakly similar to F55B12.3 [C.elegans]//6.4e-80:409:95//Hs.31945:AA702166	R-PLACE1005611//ESTs//5.2e-28:183:89//Hs.24941:AA261857
R-PLACE1004969//ESTs//9.8e-18:101:99//Hs.112837:N78013	R-PLACE1005623//ESTs//1.4e-102:505:96//Hs.58382:AA808964
R-PLACE1004972//ESTs//1.3e-65:337:95//Hs.75798:H29106	R-PLACE1005630
R-PLACE1004979//EST//1.2e-96:475:96//Hs.120158:AA708789	R-PLACE1005639//ESTs//1.4e-51:256:98//Hs.1975:W72452
R-PLACE1004982//ESTs//1.0e-98:471:98//Hs.106496:A1291776	R-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds//1.0e-111:585:93//Hs.8765:AF083255
R-PLACE1004985//ESTs//2.1e-88:456:93//Hs.135050:A1420335	R-PLACE1005656//ESTs//2.7e-88:469:92//Hs.164054:AA528169
R-PLACE1005026	R-PLACE1005666//Homo sapiens X-ray repair cross-complementing protein 2 (XRCC2) mRNA, complete cds//3.3e-24:401:66//Hs.129727:AF035587
R-PLACE1005027//ESTs. Weakly similar to N-methyl-D-aspartate receptor glutamate-binding chain [R.norvegicus]//0.72:145:66//Hs.11215:N56719	R-PLACE1005698//ESTs//0.00013:82:79//Hs.116331:AA629355
R-PLACE1005046//Homo sapiens mRNA for KIAA0575 protein, complete cds//5.3e-66:297:88//Hs.153468:AB011147	R-PLACE1005727//EST//0.15:206:63//Hs.105002:AA449332
R-PLACE1005052//ESTs. Weakly similar to weak similarity to rat cytosolic acyl coenzyme A thioester hydrolase [C.elegans]//1.2e-106:543:95//Hs.18625:A1074605	R-PLACE1005730//EST//0.0014:129:70//Hs.127931:AA969259
R-PLACE1005066//ESTs//3.9e-92:459:96//Hs.62684:AA806103	R-PLACE1005739//ESTs. Moderately similar to unknown intracellular protein [M.musculus]//1.3e-42:236:94//Hs.23889:A1341137
R-PLACE1005077//Human triadin mRNA, complete cds//1.8e-05:121:69//Hs.68731:U18985	R-PLACE1005755//ESTs//2.8e-32:308:80//Hs.159821:AA524070
R-PLACE1005085//Homo sapiens PYRIN (MEFV) mRNA, complete cds//6.6e-49:314:74//Hs.113283:AF018080	R-PLACE1005763//Human mRNA for KIAA0118 gene, partial cds//3.3e-47:268:87//Hs.154326:D42087
R-PLACE1005086//ESTs//1.2e-73:379:94//Hs.110128:AA584364	R-PLACE1005799//ESTs. Highly similar to HYPOTHETICAL 68.7 KD PROT E1N ZK757.1 IN CHROMOSOME III [Caenorhabditis elegans]//7.7e-15:8:8:98//Hs.109857:AA088385
R-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds//8.0e-99:531:92//Hs.75437:L40401	R-PLACE1005802//ESTs//2.8e-19:208:76//Hs.9271:W30941
	R-PLACE1005803//ESTs//2.6e-75:417:92//Hs.71414:AA131327
	R-PLACE1005804//EST//6.5e-20:182:70//Hs.149844:A1287693

【0933】

【表631】

R-PLACE1005828//ESTs//3.0e-15:194:77//Hs.106236:N50058	R-PLACE1006371//ESTs//7.7e-74:442:88//Hs.143671:W61053
R-PLACE1005834//Retinoblastoma 1 (including osteosarcoma)//0.040:435:58//Hs.75770:L41870	R-PLACE1006382
R-PLACE1005845//EST//5.0e-61:294:99//Hs.133202:A1050965	R-PLACE1006385//ESTs//5.3e-06:346:61//Hs.163706:AA515748
R-PLACE1005850//ESTs//3.4e-82:425:96//Hs.7966:A1203471	R-PLACE1006412//EST//7.7e-46:306:86//Hs.149580:A1281881
R-PLACE1005851//ESTs//2.9e-21:165:84//Hs.23607:N98305	R-PLACE1006414//Homo sapiens LIM protein mRNA, complete cds//4.1e-43:551:69//Hs.154103:AF061258
R-PLACE1005876//ESTs//0.4e:296:57//Hs.39140:A1041842	R-PLACE1006438//ESTs//1.1e-77:284:86//Hs.24545:A1278629
R-PLACE1005884//ESTs//0.0027:177:66//Hs.150295:AA570558	R-PLACE1006445//ESTs//4.4e-53:259:99//Hs.24481:AA573139
R-PLACE1005898//ESTs//1.7e-98:467:98//Hs.159475:A1339981	R-PLACE1006469//ESTs//9.4e-102:482:98//Hs.7218:AA936951
R-PLACE1005921//ESTs//5.8e-96:480:95//Hs.30822:AA885501	R-PLACE1006470//ESTs//1.0:271:57//Hs.144517:AA938297
R-PLACE1005923//ESTs//1.8e-66:333:96//Hs.150890:A1341793	R-PLACE1006482//ESTs//4.0e-61:354:92//Hs.51305:T47418
R-PLACE1005925//Human Line-1 repeat mRNA with 2 open reading frame s//2.8e-27:382:70//Hs.23094:M19503	R-PLACE1006492//EST//1.8e-09:48:91//Hs.144451:AA827722
R-PLACE1005932//ESTs, Moderately similar to MNK1 [H.sapiens]//1.1e-70:377:93//Hs.5662:AA868361	R-PLACE1006506//ESTs//0.012:161:61//Hs.145333:A1251374
R-PLACE1005934//ESTs//1.0e-42:251:91//Hs.25092:AA922142	R-PLACE1006521//Human mRNA for KIAA0013 gene, complete cds//2.1e-15:415:63//Hs.48824:D87717
R-PLACE1005936//ESTs//1.2e-88:461:94//Hs.94125:M62913	R-PLACE1006531//ESTs//5.6e-31:213:87//Hs.125153:AA453723
R-PLACE1005951//ESTs//1.4e-83:533:86//Hs.21148:A1183729	R-PLACE1006534//ESTs//6.5e-101:512:95//Hs.27763:W46368
R-PLACE1005953	R-PLACE1006540//ESTs//7.3e-40:320:79//Hs.121659:MD2532
R-PLACE1005955//ESTs, Highly similar to HYPOTHETICAL 54.2 KD PROT EIN IN CDC12-ORC6 INTERGENIC REGION [Saccharomyces cerevisiae]//2.2e-83:494:88//Hs.108117:A1097079	R-PLACE1006552//EST//0.38:418:56//Hs.140470:AA765214
R-PLACE1005966//ESTs//1.1e-95:465:97//Hs.98510:A1016239	R-PLACE1006598//ESTs//4.0e-80:409:95//Hs.142868:A1128443
R-PLACE1005968//EST//0.26:103:66//Hs.161300:A1420897	R-PLACE1006615//Homo sapiens eukaryotic translation initiation factor eIF3, p35 subunit mRNA, complete cds//9.3e-118:590:95//Hs.155377:U97670
R-PLACE1005990	R-PLACE1006617//ESTs//8.1e-31:246:83//Hs.139128:AA205322
R-PLACE1006002//Human mRNA for KIAA0355 gene, complete cds//2.0e-45:481:74//Hs.153014:AB002353	R-PLACE1006626//ESTs//0.90:98:68//Hs.96322:AA541615
R-PLACE1006003//ESTs, Highly similar to HYPOTHETICAL 30.3 KD PROT EIN IN APE1/LAP4-CWP1 INTERGENIC REGION [Saccharomyces cerevisiae]//3.1e-112:593:93//Hs.111449:A1192946	R-PLACE1006629//Human mRNA for KIAA0386 gene, complete cds//5.3e-33:315:78//Hs.101359:AB002384
R-PLACE1006011//ESTs, Moderately similar to MAD(+) ADP-RIBOSYLTRANSFERASE [D. melanogaster]//5.7e-100:596:88//Hs.24284:AA595596	R-PLACE1006640//ESTs//3.7e-26:137:100//Hs.32672:W16522
R-PLACE1006017//ESTs//4.2e-18:296:68//Hs.133350:A1056276	R-PLACE1006673//Interleukin 10//8.4e-47:330:83//Hs.2180:M57627
R-PLACE1006037//ESTs, Weakly similar to T23D8.3 [C. elegans]//4.1e-102:491:98//Hs.61164:A1096332	R-PLACE1006678//ESTs//1.1e-13:87:98//Hs.34035:O87736
R-PLACE1006040//ESTs//1.2e-92:443:98//Hs.111680:N93765	R-PLACE1006704//ESTs//2.6e-65:394:89//Hs.30582:D12214
R-PLACE1006076//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//2.0e-26:213:77//Hs.139007:H74314	R-PLACE1006731//Homo sapiens clone 23923 mRNA sequence//1.9e-102:486:98//Hs.12472:AF038172
R-PLACE1006119//ESTs//0.14:257:61//Hs.113149:AA908904	R-PLACE1006754//EST//1.0e-61:381:89//Hs.14727:T83861
R-PLACE1006129//ESTs//3.8e-54:285:97//Hs.18827:W68002	R-PLACE1006760//Homo sapiens clone 24800 mRNA sequence//3.8e-73:394:93//Hs.7252:AF070622
R-PLACE1006139//ESTs, Highly similar to HYPOTHETICAL 52.9 KD PROT EIN IN SAP155-YMR31 INTERGENIC REGION [Saccharomyces cerevisiae]//2.6e-99:560:91//Hs.5249:U55977	R-PLACE1006779//ESTs//1.4e-69:405:90//Hs.136235:AA262658
R-PLACE1006143//Amylo-1,6-glucosidase, 4-alpha-glucanotransferase (glycogen debranching enzyme, glycogen storage disease type III)//0.038:463:58//Hs.904:U84010	R-PLACE1006782//EST//1.8e-25:197:86//Hs.137257:N33234
R-PLACE1006157//ESTs//0.014:341:58//Hs.121773:A1357886	R-PLACE1006792//ESTs//1.8e-43:317:84//Hs.139190:N55515
R-PLACE1006159//EST//0.00036:247:61//Hs.140054:AA668925	R-PLACE1006795//ESTs//6.4e-68:350:95//Hs.11092:AA916335
R-PLACE1006164//ESTs//2.6e-31:362:73//Hs.141024:H07128	R-PLACE1006800//ESTs//1.9e-55:268:100//Hs.126695:AA917989
R-PLACE1006167//Homo sapiens chromosome 19, cosmid F23149//5.8e-54:286:94//Hs.152894:AC005239	R-PLACE1006805//ESTs//6.6e-91:484:93//Hs.94262:AA768847
R-PLACE1006170//ESTs, Highly similar to ALPHA-ADAPTIN [Rattus norvegicus]//2.7e-79:393:96//Hs.19121:A1125280	R-PLACE1006815//ESTs//2.1e-49:364:83//Hs.142031:AA809159
R-PLACE1006187//Homo sapiens cyclin E2 mRNA, complete cds//5.1e-118:597:95//Hs.30464:AF091433	R-PLACE1006819//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPT ASE HOMOLOG [Homo sapiens]//1.0e-87:481:92//Hs.141263:H64113
R-PLACE1006195//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//6.8e-94:532:91//Hs.105216:A1361807	R-PLACE1006829//ESTs//5.7e-43:332:83//Hs.19906:AA456933
R-PLACE1006196//ESTs//3.2e-66:382:90//Hs.18665:T99507	R-PLACE1006860//ESTs//0.96:138:63//Hs.136649:AA828359
R-PLACE1006205//EST//1.7e-89:448:96//Hs.116665:AA669114	R-PLACE1006867//ESTs//1.4e-98:478:97//Hs.10299:W35008
R-PLACE1006223//Human RNase P protein p38 (RPP38) mRNA, complete cds//0.90:304:58//Hs.94986:U77664	R-PLACE1006878//EST//8.4e-48:243:97//Hs.54970:N93536
R-PLACE1006225//ESTs//7.2e-96:474:97//Hs.91165:A1079555	R-PLACE1006883//EST//3.1e-46:300:88//Hs.162404:AA573131
R-PLACE1006236//ESTs//8.8e-105:535:95//Hs.7919:A1341472	R-PLACE1006901//ESTs//3.0e-95:496:94//Hs.47546:AA181348
R-PLACE1006239//Homo sapiens BAC clone RG118D07 from 7q31//3.2e-99:497:95//Hs.3781:AC004142	R-PLACE1006904//ESTs//5.8e-18:304:68//Hs.125816:AA806089
R-PLACE1006246//ESTs, Weakly similar to CMP-sialic acid transporter [M. musculus]//1.3e-104:532:95//Hs.41151:A1301961	R-PLACE1006917//Endothelin receptor type B//0.00012:451:60//Hs.82002:D13168
R-PLACE1006248//Homo sapiens mRNA for KIAA0648 protein, partial cds//3.0e-97:499:95//Hs.31921:AB014548	R-PLACE1006932//ESTs//4.6e-56:285:96//Hs.114727:A1379514
R-PLACE1006262//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//1.6e-07:321:62//Hs.53057:W67839	R-PLACE1006935//ESTs//3.6e-12:157:73//Hs.161714:AA229078
R-PLACE1006288//Voltage-dependent anion channel 1//3.8e-100:605:88//Hs.2060:L06132	R-PLACE1006958//Human mRNA for KIAA0201 gene, complete cds//3.2e-25:494:63//Hs.36927:O86956
R-PLACE1006318//ESTs//2.4e-102:536:94//Hs.8109:AA005265	R-PLACE1006961//Tyrosine aminotransferase//2.5e-46:471:74//Hs.2999:U52520
R-PLACE1006325//ESTs//5.2e-105:518:96//Hs.102319:A1246503	R-PLACE1006962//ESTs, Moderately similar to plakophilin 2b [H.sapiens]//9.0e-29:324:68//Hs.154257:A1275982
R-PLACE1006335//ESTs//5.1e-45:254:93//Hs.153585:R70900	R-PLACE1006966//ESTs//4.5e-99:470:99//Hs.46913:A1017636
R-PLACE1006351//EST//6.5e-09:309:62//Hs.132493:AA923168	R-PLACE1006989//ESTs//2.2e-68:353:97//Hs.14394:R61257
R-PLACE1006360//Human mRNA for KIAA0090 gene, partial cds//0.0097:381:58//Hs.154797:D42044	R-PLACE1007014//ESTs//3.4e-86:457:94//Hs.129819:AA838366
R-PLACE1006368//ESTs//7.9e-85:412:97//Hs.150587:A1079284	R-PLACE1007021//ESTs//1.6e-93:539:90//Hs.7111:U55971
	R-PLACE1007045//Human Line-1 repeat mRNA with 2 open reading frame s//6.6e-83:584:82//Hs.23094:M19503
	R-PLACE1007053//ESTs//4.2e-85:550:88//Hs.7984:A1202575
	R-PLACE1007097//ESTs//6.4e-78:493:86//Hs.56406:W91027
	R-PLACE1007105//ESTs//5.3e-70:381:91//Hs.22605:W74202
	R-PLACE1007111//ESTs//8.6e-75:358:99//Hs.145629:AA398646
	R-PLACE1007112//ESTs//6.9e-69:371:94//Hs.71922:AA148417
	R-PLACE1007132//ESTs//1.2e-36:373:69//Hs.10762:W28948
	R-PLACE1007140//ESTs//1.7e-70:360:96//Hs.56179:W56794
	R-PLACE1007178//EST//0.68:85:65//Hs.147010:A1184765
	R-PLACE1007226//ESTs//3.1e-78:452:90//Hs.8033:N94998
	R-PLACE1007238//ESTs//5.2e-70:362:95//Hs.85636:AA740619
	R-PLACE1007239//Human mRNA for transcription elongation factor S-1 l, hS-II-T1, complete cds//6.3e-93:534:89//Hs.80598:D50495

【0934】

【表632】

R-PLACE1007242//ESTs//1.2e-80:390:98//Hs.117325:AA699450
 R-PLACE1007243//ESTs, Weakly similar to transporter protein [H.sapiens]//3.7e-73:357:98//Hs.18272:N78499
 R-PLACE1007257//Homo sapiens mRNA for dia-156 protein//4.3e-85:487:91//Hs.121556:Y15909
 R-PLACE1007274//ESTs//4.3e-79:430:93//Hs.146023:A1275071
 R-PLACE1007276//ESTs//1.5e-33:338:74//Hs.142850:R38419
 R-PLACE1007282//ESTs//4.8e-98:532:93//Hs.10071:AI100812
 R-PLACE1007286//Human mRNA for KIAA0118 gene, partial cds//2.9e-50:518:74//Hs.154326:D42087
 R-PLACE1007301
 R-PLACE1007317
 R-PLACE1007342
 R-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBP) mRNA, complete cds//1.2e-66:367:91//Hs.76596:AF096870
 R-PLACE1007367//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//2.2e-98:488:96//Hs.24359:AA699594
 R-PLACE1007375//ESTs//2.3e-67:375:92//Hs.33368:AA206614
 R-PLACE1007386//ESTs//0.020:242:62//Hs.42768:AI129945
 R-PLACE1007402//ESTs//1.6e-91:441:97//Hs.26243:AA455877
 R-PLACE1007409//Homo sapiens mitoxanthrone resistance protein I mRNA, partial sequence//2.4e-113:590:94//Hs.14387:AF093771
 R-PLACE1007416//ESTs, Weakly similar to DIPEPTIDYL PEPTIDASE IV [H.sapiens]//3.8e-115:579:95//Hs.72165:AI243857
 R-PLACE1007450//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//2.7e-38:311:80//Hs.97203:U83171
 R-PLACE1007452//EST//2.5e-42:386:77//Hs.140562:AA826514
 R-PLACE1007460//ESTs//4.9e-87:434:95//Hs.28472:AI028230
 R-PLACE1007478
 R-PLACE1007484//ESTs//6.8e-08:64:92//Hs.100251:AA535975
 R-PLACE1007488//Dystrophin (muscular dystrophy, Duchenne and Becker types), includes DXS142, DXS164, DXS206, DXS230, DXS239, DXS268, DXS269, DXS270, DXS272//0.26:411:60//Hs.79012:M18533
 R-PLACE1007507//ESTs//2.2e-11:136:76//Hs.128815:AA678072
 R-PLACE1007511//ESTs, Highly similar to KERATIN, TYPE I CYTOSKELETAL 14 [Homo sapiens]//1.5e-41:261:89//Hs.9029:W57657
 R-PLACE1007524//ESTs//5.8e-45:297:87//Hs.154923:AA491377
 R-PLACE1007525//Human mRNA for KIAA0118 gene, partial cds//1.9e-44:422:75//Hs.154326:D42087
 R-PLACE1007544//ESTs//8.4e-59:327:93//Hs.27410:N25612
 R-PLACE1007547//EST//0.00010:107:71//Hs.146867:AI161404
 R-PLACE1007557//ESTs//1.6e-43:356:79//Hs.44702:AI148840
 R-PLACE1007583//ESTs//1.7e-41:214:97//Hs.155071:AA584257
 R-PLACE1007598//Homo sapiens clone 23939 mRNA sequence//4.8e-104:54:93//Hs.21838:AF038179
 R-PLACE1007618//Lymphocyte cytosolic protein 1 (L-plastin)//0.54:161:65//Hs.76506:J02923
 R-PLACE1007621//Homo sapiens clone 23859 mRNA sequence//4.8e-105:537:94//Hs.151046:AF038176
 R-PLACE1007632
 R-PLACE1007645//ESTs//0.99:187:62//Hs.163453:AI344106
 R-PLACE1007649//ESTs//2.2e-108:561:94//Hs.24398:AI262946
 R-PLACE1007677//ESTs, Moderately similar to !!!! ALU SUBFAMILY SB2 WARNING ENTRY !!!! [H.sapiens]//9.0e-37:190:97//Hs.23437:AA707331
 R-PLACE1007688//ESTs//7.5e-79:409:95//Hs.6166:AI376944
 R-PLACE1007690//ESTs, Weakly similar to NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 5 [Ascaris suum]//3.4e-61:384:89//Hs.92918:AA133274
 R-PLACE1007697//ESTs, Highly similar to GCN20 PROTEIN [Saccharomyces cerevisiae]//1.8e-84:501:88//Hs.91251:U66685
 R-PLACE1007705//Human mRNA for apolipoprotein E receptor 2, complete cds//0.43:307:59//Hs.54481:D86407
 R-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds//5.7e-75:374:96//Hs.4812:AF061243
 R-PLACE1007725//ESTs, Weakly similar to No definition line found [C.elegans]//3.1e-39:253:88//Hs.108797:AA476815
 R-PLACE1007729//ESTs//2.7e-44:392:79//Hs.142375:AA398619
 R-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds//6.7e-94:556:89//Hs.153121:AB014585
 R-PLACE1007737//ESTs//1.1e-41:345:80//Hs.114671:N39322
 R-PLACE1007743//ESTs//2.8e-17:98:100//Hs.124258:AA976778
 R-PLACE1007746//ESTs//5.3e-69:413:90//Hs.5297:AA156903
 R-PLACE1007791//ESTs, Weakly similar to TEICHOCIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//8.6e-27:143:98//Hs.144194:AA706337
 R-PLACE1007807//Human Line-1 repeat mRNA with 2 open reading frame s//9.9e-45:428:76//Hs.23094:M19503
 R-PLACE1007810//ESTs//5.9e-15:143:82//Hs.126257:AI279044
 R-PLACE1007829//ESTs//2.2e-22:190:84//Hs.142707:W24050
 R-PLACE1007843//ESTs//5.3e-110:556:95//Hs.107287:AI308839
 R-PLACE1007846//Human Line-1 repeat mRNA with 2 open reading frame s//1.7e-95:525:91//Hs.23094:M19503

R-PLACE1007852//ESTs//4.5e-14:174:75//Hs.153419:N52017
 R-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds//2.1e-111:574:94//Hs.28020:AB018309
 R-PLACE1007866//EST//1.8e-48:262:96//Hs.141009:H01178
 R-PLACE1007877//ESTs//1.2e-94:478:96//Hs.5999:AI207832
 R-PLACE1007897//ESTs//2.3e-92:437:99//Hs.122843:AI189060
 R-PLACE1007908//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//2.8e-89:460:95//Hs.92381:AB007956
 R-PLACE1007946//ESTs//2.8e-28:172:78//Hs.126784:AA521510
 R-PLACE1007954//ESTs//6.1e-72:366:95//Hs.27842:AI217966
 R-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA, complete cds//3.9e-103:509:96//Hs.5671:AF084530
 R-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//7.2e-89:465:93//Hs.78106:AF079529
 R-PLACE1007969//ESTs, Weakly similar to F35C12.2 [C.elegans]//1.4e-113:534:98//Hs.44268:AA455900
 R-PLACE1007990//ESTs, Highly similar to DOSAGE COMPENSATION REGULATORY [Drosophila melanogaster]//3.8e-97:493:95//Hs.6141:U69564
 R-PLACE1008000//ESTs//0.00013:241:65//Hs.44369:AI206835
 R-PLACE1008002//ESTs//2.2e-83:397:98//Hs.28780:AI263612
 R-PLACE1008044//ESTs, Moderately similar to NUCLEAR PORE COMPLEX PROTEIN NUP107 [R.norvegicus]//2.0e-115:575:95//Hs.92395:AA779854
 R-PLACE1008045//EST//2.6e-89:465:94//Hs.47374:N51935
 R-PLACE1008080//EST//0.27:118:65//Hs.144110:AI054269
 R-PLACE1008095//ESTs//5.5e-23:268:73//Hs.152525:AA516469
 R-PLACE1008111//ESTs, Weakly similar to oxidoreductase [H.sapiens]//4.4e-108:537:96//Hs.28877:AI309334
 R-PLACE1008122//ESTs//6.5e-103:531:94//Hs.34737:AI028617
 R-PLACE1008129//ESTs//0.76:96:66//Hs.65373:AA883511
 R-PLACE1008132//ESTs//5.9e-05:113:72//Hs.13014:W26381
 R-PLACE1008177//ESTs//7.2e-107:557:93//Hs.132851:AI028266
 R-PLACE1008181//ESTs//5.3e-97:473:97//Hs.57483:AA776267
 R-PLACE1008198//ESTs//3.9e-16:120:85//Hs.9142:AA662107
 R-PLACE1008201//Homo sapiens mRNA for KIAA0530 protein, partial cds//1.6e-104:551:93//Hs.10801:AB011102
 R-PLACE1008209//ESTs//1.2e-72:366:96//Hs.92308:AI052701
 R-PLACE1008231//ESTs//1.2e-70:363:94//Hs.25094:R00871
 R-PLACE1008244//ESTs//1.3e-98:543:92//Hs.25130:AA218990
 R-PLACE1008273//ESTs//6.1e-16:153:79//Hs.115987:AA483808
 R-PLACE1008275
 R-PLACE1008280//ESTs//1.3e-66:353:94//Hs.156376:AI338705
 R-PLACE1008309//ESTs//2.8e-100:511:95//Hs.45080:N49852
 R-PLACE1008329//V-myc avian myelocytomatosis viral oncogene homolog//0.53:206:62//Hs.79070:K02276
 R-PLACE1008330//ESTs, Weakly similar to EOSINOPHIL LYSOPHOSPHOLIPASE [H.sapiens]//8.6e-79:297:91//Hs.146477:AI128445
 R-PLACE1008331//ESTs//0.98:156:62//Hs.108548:AA081656
 R-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds//2.1e-99:556:90//Hs.5734:AB014579
 R-PLACE1008368//EST//0.0027:198:63//Hs.160868:AI359052
 R-PLACE1008369//ESTs//5.4e-28:167:92//Hs.19530:AA480009
 R-PLACE1008392//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//2.0e-41:448:72//Hs.139007:HT4314
 R-PLACE1008398//ESTs, Highly similar to Mig-6//1.4e-103:529:94//Hs.11169:AA156242
 R-PLACE1008401//ESTs, Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//1.2e-81:536:87//Hs.7570:W31010
 R-PLACE1008402//Homo sapiens mRNA for p115, complete cds//5.1e-103:521:95//Hs.7763:D86326
 R-PLACE1008405//ESTs//1.2e-89:485:92//Hs.138241:AA767440
 R-PLACE1008424//ESTs//6.7e-97:508:93//Hs.6709:AI379778
 R-PLACE1008426//ESTs//5.5e-30:174:92//Hs.7946:AA651577
 R-PLACE1008429//ESTs//2.1e-12:188:71//Hs.140769:AA931562
 R-PLACE1008437//ESTs//7.1e-54:266:98//Hs.13068:AA001928
 R-PLACE1008455//ESTs//4.7e-69:471:85//Hs.28337:AA210761
 R-PLACE1008457//EST//8.6e-14:202:71//Hs.149887:AI289387
 R-PLACE1008465//ESTs//3.8e-80:426:93//Hs.153146:AI299636
 R-PLACE1008488//ESTs//7.9e-73:388:94//Hs.97268:AA292180
 R-PLACE1008524//ESTs//7.4e-107:545:95//Hs.10441:N62816
 R-PLACE1008531//ESTs//3.8e-68:427:87//Hs.56607:H23560
 R-PLACE1008532
 R-PLACE1008533//ESTs//2.5e-52:318:88//Hs.7274:AA476850
 R-PLACE1008568//ESTs//3.2e-99:486:97//Hs.84414:AI423223
 R-PLACE1008584//EST//2.2e-18:154:68//Hs.141498:N50064
 R-PLACE1008621//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]//8.6e-67:483:82//Hs.140416:AA778649
 R-PLACE1008625
 R-PLACE1008626//ESTs//4.7e-73:372:95//Hs.23491:AA642454
 R-PLACE1008627//ESTs//1.6e-90:475:93//Hs.102401:AI004972
 R-PLACE1008629//ESTs//8.0e-93:492:93//Hs.20843:AA699512

【0935】

【表633】

R-PLACE1008630//ESTs//1.0e-94:453:98//Hs.34840:A1279612	R-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//6.6e-85:479:90//Hs.76987:AF012872
R-PLACE1008643//Human mRNA for KIAA0355 gene, complete cds//2.8e-49:422:79//Hs.153014:AB002353	R-PLACE1009459//ESTs//9.3e-86:437:95//Hs.104871:A1161427
R-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds//7.9e-90:434:97//Hs.147967:AF044333	R-PLACE1009476//Homo sapiens Chromosome 16 BAC clone C17987SK-A-67 A1//1.3e-42:266:89//Hs.155049:AC004531
R-PLACE1008693//SLET AMYLOID POLYPEPTIDE PRECURSOR//1.8e-41:505:71//Hs.51048:X68830	R-PLACE1009477//ESTs//2.0e-50:367:82//Hs.152788:AA630925
R-PLACE1008696//Cytochrome P450, subfamily 1 (aromatic compound-inducible), polypeptide 2//1.7e-51:316:76//Hs.1361:M55053	R-PLACE1009493//ESTs//4.5e-14:150:78//Hs.143918:AA699596
R-PLACE1008715//ESTs//0.63:114:64//Hs.121353:AA758600	R-PLACE1009524//ESTs//2.9e-97:454:99//Hs.7189:AA767688
R-PLACE1008748//ESTs, Weakly similar to !!!! ALU CLASS B WARNING ENTRY !!!! [H.sapiens]//2.3e-40:281:83//Hs.142209:AA873303	R-PLACE1009539//ESTs//9.1e-94:454:97//Hs.154706:A1262131
R-PLACE1008757//ESTs//1.4e-45:226:99//Hs.22822:H06408	R-PLACE1009542//Homo sapiens apoptotic protease activating factor 1 (Apaf-1) mRNA, complete cds//1.4e-10:289:63//Hs.77579:AF013263
R-PLACE1008790//ESTs//0.035:67:76//Hs.153554:A1286313	R-PLACE1009571//ESTs//2.1e-23:125:100//Hs.41767:AA732326
R-PLACE1008798//ESTs//4.9e-59:285:99//Hs.49018:N79930	R-PLACE1009581//ESTs, Weakly similar to FIBRINOGEN ALPHA AND ALPHA-E CHAIN PRECURSORS [H.sapiens]//0.0012:56:91//Hs.12151:AA001818
R-PLACE1008807//ESTs//1.7e-82:413:96//Hs.130745:AA573217	R-PLACE1009595//Homo sapiens mRNA for KIAA0635 protein, complete cds//6.0e-42:547:70//Hs.69157:AB014535
R-PLACE1008808//Homo sapiens putative checkpoint control protein H RAD1 mRNA, complete cds//1.1e-98:499:95//Hs.7179:AF011905	R-PLACE1009596//ESTs//1.9e-102:588:90//Hs.142395:A1374735
R-PLACE1008813//ESTs, Weakly similar to coded for by C. elegans CD NA cat0e3 [C.elegans]//4.2e-92:490:93//Hs.110454:H11810	R-PLACE1009607//ESTs//0.093:107:70//Hs.70932:AA126482
R-PLACE1008851//ESTs//2.4e-84:421:95//Hs.158893:A1378428	R-PLACE1009613//ESTs//7.5e-101:488:97//Hs.5905:AA946680
R-PLACE1008854	R-PLACE1009621//EST//0.99:261:60//Hs.149030:A1243338
R-PLACE1008867//ESTs//1.1e-77:400:95//Hs.44198:A1093502	R-PLACE1009622//ESTs//8.0e-93:508:92//Hs.20967:A1422858
R-PLACE1008887//Oxytocin receptor//1.1e-43:601:67//Hs.2820:X64878	R-PLACE1009637//EST//8.7e-90:442:97//Hs.121372:AA758701
R-PLACE1008902//ESTs//0.023:208:61//Hs.154164:A1246893	R-PLACE1009639//EST//8.5e-49:279:93//Hs.117447:R27213
R-PLACE1008920//Homo sapiens mRNA for KIAA0765 protein, partial cds//2.6e-56:344:89//Hs.62318:AB018308	R-PLACE1009659//Homo sapiens mRNA for KIAA0587 protein, complete cds//3.3e-109:589:92//Hs.21862:AB011159
R-PLACE1008925//ESTs//0.17:294:57//Hs.105113:AA457018	R-PLACE1009665//ESTs, Weakly similar to line-1 protein ORF1 [H.sapiens]//9.9e-62:483:79//Hs.140416:AA778649
R-PLACE1008934//ESTs//2.0e-61:339:92//Hs.100448:AA622653	R-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds//6.6e-63:310:97//Hs.109590:AF062534
R-PLACE1008941//ESTs, Moderately similar to ATP-BINDING CASSETTE TRANSPORTER 2 [Mus musculus]//1.3e-19:488:63//Hs.15780:U66680	R-PLACE1009708//ESTs//3.0e-94:471:96//Hs.40091:N48582
R-PLACE1008947//ESTs//1.3e-81:385:99//Hs.71574:A1376573	R-PLACE1009721//ESTs, Weakly similar to MSF1 PROTEIN [S.cerevisiae]//4.2e-98:529:92//Hs.3945:AA004210
R-PLACE1009020//ESTs//2.9e-79:419:94//Hs.121816:AA775419	R-PLACE1009731//ESTs, Weakly similar to immune associated protein 38 [M.musculus]//6.8e-85:489:89//Hs.26194:AA033989
R-PLACE1009027//Homo sapiens mRNA for doublecortin//3.1e-82:434:94//Hs.34780:AJ003112	R-PLACE1009763//Homo sapiens UBA3 (UBA3) mRNA, complete cds//2.0e-117:598:95//Hs.154320:AF046024
R-PLACE1009039//ESTs//2.8e-83:448:92//Hs.129179:AA988520	R-PLACE1009794//ESTs//7.9e-102:529:95//Hs.42927:N20989
R-PLACE1009045//ESTs//1.6e-64:318:97//Hs.103423:AA814195	R-PLACE1009798//Human DNA sequence from clone 1189B24 on chromosome Xq25-26.3. Contains NADH-Ubiquinone Oxidoreductase MLRQ subunit (EC 1.6.5.3, EC 1.6.9.3, C1-MLRQ), Tubulin Beta and Proto-oncogene Tyrosine-protein Kinase FER (EC 2.7.1.112, P94-FER, C-FER, TYK3) pseudogenes, and part of a novel gene similar to hypothetical proteins S. pombe C22F3.14C and C. elegans C16A3.8. Contains ESTs and GSSs//1.1e-113:549:97//Hs.16411:AL030996
R-PLACE1009099//ESTs, Highly similar to MKR2 PROTEIN [Mus musculus]//0.037:63:84//Hs.39943:AA203136	R-PLACE1009845//ESTs//9.5e-106:560:93//Hs.117751:A1056868
R-PLACE1009110//ESTs//5.8e-17:307:65//Hs.117264:AA682549	R-PLACE1009879//ESTs//1.8e-61:399:86//Hs.141012:R68748
R-PLACE1009111//ESTs//1.9e-57:349:90//Hs.11260:N98983	R-PLACE1009886//EST//0.54:153:64//Hs.144281:AA081328
R-PLACE1009130//ESTs, Weakly similar to hypothetical protein 2 [H.sapiens]//6.5e-97:501:94//Hs.11123:AA703945	R-PLACE1009888//ESTs//2.7e-105:520:97//Hs.108646:AA613031
R-PLACE1009150//LAMIN B1//0.064:393:60//Hs.89497:L37747	R-PLACE1009908//ESTs, Weakly similar to similar to mouse MMR1 [C.elegans]//1.6e-114:594:94//Hs.67466:A1219740
R-PLACE1009155//ESTs, Moderately similar to ovarian-specific protein [R.norvegicus]//2.5e-36:163:82//Hs.93332:AA811920	R-PLACE1009921//ESTs//7.6e-05:291:60//Hs.124786:AA825563
R-PLACE1009158//ESTs//0.30:149:65//Hs.155798:R80005	R-PLACE1009924//EST//1.2e-42:216:98//Hs.31742:H20276
R-PLACE1009166//ESTs//3.3e-34:292:77//Hs.140255:AA708322	R-PLACE1009925//ESTs//5.4e-30:154:100//Hs.114605:A1304317
R-PLACE1009172//ESTs//8.9e-21:364:67//Hs.142557:AA464948	R-PLACE1009935//ESTs//1.4e-83:417:97//Hs.131755:AA496543
R-PLACE1009174//ESTs//2.9e-18:274:70//Hs.139241:AA283707	R-PLACE1009947//Keratin 9//1.0:273:61//Hs.2783:Z29074
R-PLACE1009183//ESTs//2.3e-44:297:87//Hs.136839:H93717	R-PLACE1009971//ESTs//1.5e-87:424:98//Hs.13781:A1160540
R-PLACE1009186//ESTs, Weakly similar to No definition line found [C.elegans]//1.5e-109:572:94//Hs.54943:Z78396	R-PLACE1009992//ESTs//1.3e-87:531:87//Hs.55044:AA460698
R-PLACE1009190//ESTs//2.6e-53:318:90//Hs.25245:AA176701	R-PLACE1009995//ESTs//1.3e-103:575:91//Hs.71218:C75347
R-PLACE1009200//H.sapiens mRNA for sortilin//3.2e-33:195:92//Hs.104247:X98248	R-PLACE1009997//Small inducible cytokine A5 (RANTES)//1.1e-42:286:86//Hs.155464:AF088219
R-PLACE1009230//ESTs//3.0e-31:153:92//Hs.124116:AA772680	R-PLACE1010023//ESTs, Weakly similar to C27F2.7 gene product [C.elegans]//1.7e-17:137:86//Hs.7049:A1141736
R-PLACE1009246//ESTs//2.7e-90:488:92//Hs.10706:AA909018	R-PLACE1010031//ESTs//0.22:191:62//Hs.127787:AA832204
R-PLACE1009308//ESTs//0.022:46:97//Hs.36545:AA075423	R-PLACE1010053//ESTs, Moderately similar to spermatid perinuclear RNA-binding protein Spnr [M.musculus]//7.6e-104:546:94//Hs.8215:AA521150
R-PLACE1009319//ESTs//7.7e-99:533:92//Hs.109654:N91279	R-PLACE1010069//ESTs//0.99:173:59//Hs.21415:A1150905
R-PLACE1009328//Human Line-1 repeat mRNA with 2 open reading frame s//7.3e-82:578:82//Hs.23094:M19503	R-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds//1.5e-88:543:88//Hs.11183:AF065482
R-PLACE1009335//EST//1.3e-64:311:99//Hs.130558:A1004397	R-PLACE1010076//ESTs//3.4e-106:530:95//Hs.28005:AA604375
R-PLACE1009338//ESTs//6.0e-70:386:93//Hs.3542:A1015782	R-PLACE1010083//ESTs//4.1e-65:395:88//Hs.6103:AA496424
R-PLACE1009368//ESTs//1.4e-18:107:98//Hs.133303:W04760	R-PLACE1010089//ESTs//1.6e-70:348:97//Hs.9011:AA418615
R-PLACE1009375//ESTs//8.9e-36:313:76//Hs.24608:AA161260	R-PLACE1010096//ESTs, Highly similar to hypothetical protein, 100K [R.norvegicus]//2.8e-104:565:92//Hs.11469:U69567
R-PLACE1009388//EST//4.4e-11:101:83//Hs.147074:A1188883	R-PLACE1010102//ESTs//7.7e-50:311:89//Hs.5518:A1052015
R-PLACE1009398//ESTs//5.7e-63:335:93//Hs.149003:A1243186	R-PLACE1010105//ESTs//6.0e-94:483:94//Hs.62684:AA806103
R-PLACE1009404//ESTs//3.6e-94:452:98//Hs.103177:W72798	R-PLACE1010106//ESTs, Weakly similar to putative p150 [H.sapiens]//1.6e-107:575:93//Hs.48301:AA122270
R-PLACE1009410//ESTs//2.2e-112:553:96//Hs.61779:AA195255	R-PLACE1010134//EST//8.5e-59:314:94//Hs.135005:A1095130
R-PLACE1009434//EST//3.4e-15:109:74//Hs.103742:U48632	R-PLACE1010148//A-KINASE ANCHOR PROTEIN 79//0.52:351:56//Hs.48714:
R-PLACE1009443//EST//7.5e-61:302:98//Hs.157787:A1361269	

【0936】

【表634】

M90359	cds//8.9e-82:441:93//Hs.66392:AF064244
R-PLACE1010152//ESTs//1.9e-40:240:90//Hs.17054:A1139897	R-PLACE1010944
R-PLACE1010181//ESTs//3.6e-64:307:99//Hs.154163:AJ003313	R-PLACE1010947//ESTs//6.7e-15:102:91//Hs.116808:AA211519
R-PLACE1010194//ESTs//2.7e-70:366:96//Hs.5301:T58466	R-PLACE1010954//Small inducible cytokine A5 (RANTES)//8.8e-51:278:93//Hs.155464:AF088219
R-PLACE1010202//ESTs//0.57:120:67//Hs.58873:W95037	R-PLACE1010960//ESTs, Highly similar to ACTIN-LIKE PROTEIN 13E [Drosophila melanogaster]//1.0e-103:565:92//Hs.23259:AA532437
R-PLACE1010231	R-PLACE1010965//EST//6.3e-80:447:91//Hs.139529:AA219580
R-PLACE1010261//EST//6.9e-50:251:98//Hs.148208:AA897478	R-PLACE1011026//ESTs//4.6e-99:463:99//Hs.149732:A1199846
R-PLACE1010270//ESTs//1.9e-87:430:96//Hs.25252:A1079545	R-PLACE1011032//ESTs//6.3e-56:295:94//Hs.143576:A1147867
R-PLACE1010274//ESTs//1.9e-57:439:81//Hs.30078:H04535	R-PLACE1011041//ESTs//5.3e-27:168:91//Hs.7936:AA932349
R-PLACE1010293//ESTs//8.1e-41:310:81//Hs.146811:AA410788	R-PLACE1011046//Homo sapiens mRNA for KIAA0581 protein, partial cds//9.4e-102:563:91//Hs.41143:AB011153
R-PLACE1010321//ESTs//5.7e-50:246:99//Hs.151445:AA351081	R-PLACE1011054//EST//1.1e-15:245:69//Hs.112648:AA609135
R-PLACE1010324//ESTs//0.00025:377:60//Hs.97430:AA398568	R-PLACE1011056//Small inducible cytokine A5 (RANTES)//3.5e-38:285:82//Hs.155464:AF088219
R-PLACE1010329//Small inducible cytokine A5 (RANTES)//2.4e-40:300:82//Hs.155464:AF088219	R-PLACE1011057//ESTs//3.5e-81:410:96//Hs.96499:AA252537
R-PLACE1010341//EST, Moderately similar to !!!! ALU SUBFAMILY SQ W ARNING ENTRY !!!! [H.sapiens]//9.9e-32:190:77//Hs.152369:AA504818	R-PLACE1011090//ESTs, Weakly similar to !!!! ALU SUBFAMILY J W ARNING ENTRY !!!! [H.sapiens]//1.6e-54:398:84//Hs.108740:W20094
R-PLACE1010362//ESTs//8.2e-86:404:99//Hs.25625:AA669327	R-PLACE1011109//EST//1.3e-48:321:85//Hs.146794:A1149478
R-PLACE1010364//ESTs//1.5e-105:556:93//Hs.12229:AA149594	R-PLACE1011114//ESTs//5.4e-90:475:94//Hs.69331:AA099587
R-PLACE1010383//Homo sapiens mRNA for putative liponic acid synthetase, partial//4.9e-35:166:86//Hs.53531:AJ224162	R-PLACE1011133//ESTs, Highly similar to 40 KD PROTEIN [Borna disease virus]//3.0e-105:552:83//Hs.31257:AA875998
R-PLACE1010401//ESTs//2.3e-85:450:93//Hs.23193:AA418152	R-PLACE1011143//ESTs//0.40:127:65//Hs.118701:AA420795
R-PLACE1010481//ESTs//0.012:280:59//Hs.5579:A1392816	R-PLACE1011160//Homo sapiens mRNA for HRHFB2038, partial cds//7.7e-97:534:91//Hs.28719:AB015333
R-PLACE1010491//Homo sapiens Cre binding protein-like 2 mRNA, complete cds//2.4e-89:438:96//Hs.13313:AF039081	R-PLACE1011165//ESTs//1.0:135:69//Hs.32163:A1374673
R-PLACE1010492	R-PLACE1011185//ESTs, Weakly similar to !!!! ALU CLASS B W ARNING ENTRY !!!! [H.sapiens]//3.4e-85:442:95//Hs.136910:AA810782
R-PLACE1010522//EST//0.43:82:68//Hs.89303:AA284031	R-PLACE1011203//EST//0.0047:268:60//Hs.68832:AA084838
R-PLACE1010547//ESTs//4.8e-36:228:89//Hs.128724:AA215455	R-PLACE1011219//ESTs//7.6e-96:504:93//Hs.124834:A1138671
R-PLACE1010562//ESTs//4.8e-68:408:90//Hs.17244:W86306	R-PLACE1011221//ESTs//5.2e-23:241:78//Hs.26761:AA203299
R-PLACE1010579//EST//0.015:193:63//Hs.67093:C14033	R-PLACE1011229//ESTs//1.9e-90:461:95//Hs.132288:A1027693
R-PLACE1010580//ESTs//2.4e-93:445:98//Hs.127325:AA234116	R-PLACE1011263//ESTs//6.6e-56:321:93//Hs.158787:W79602
R-PLACE1010599	R-PLACE1011273//ESTs//0.016:131:65//Hs.140466:AA766772
R-PLACE1010616//ESTs//2.9e-101:497:97//Hs.142197:AA573418	R-PLACE1011291//EST//8.7e-47:267:91//Hs.158806:A1376913
R-PLACE1010622//ESTs//1.1e-23:157:91//Hs.159877:W57895	R-PLACE1011296//EST//2.7e-38:225:92//Hs.160934:A1376849
R-PLACE1010624//ESTs//1.4e-89:428:98//Hs.116561:AA658475	R-PLACE1011310//ESTs//9.1e-37:196:96//Hs.39328:H71807
R-PLACE1010628//ESTs, Weakly similar to !!!! ALU SUBFAMILY J W ARNING ENTRY !!!! [H.sapiens]//6.4e-74:391:95//Hs.163495:W57637	R-PLACE1011325//Human clone 23721 mRNA sequence//0.0012:486:58//Hs.83572:U79291
R-PLACE1010629//ESTs//5.8e-75:359:99//Hs.123630:A1250805	R-PLACE1011332//ESTs//8.4e-44:217:99//Hs.101365:R60578
R-PLACE1010630//ESTs//9.5e-101:519:94//Hs.77873:AA731719	R-PLACE1011340//ESTs, Weakly similar to TEICHOIC ACID BIOSYNTHESIS PROTEIN A [Bacillus subtilis]//3.4e-92:452:97//Hs.144194:AA706337
R-PLACE1010631//Homo sapiens mRNA for KIAA0530 protein, partial cds//8.3e-94:497:93//Hs.10801:AB011102	R-PLACE1011375//ESTs//2.2e-35:195:96//Hs.106486:H11376
R-PLACE1010661//ESTs, Highly similar to TESTIS-SPECIFIC PROTEIN P BS13 [Mus musculus]//4.8e-83:467:91//Hs.22383:R51067	R-PLACE1011399//ESTs//0.00096:224:67//Hs.151643:AA001194
R-PLACE1010662//ESTs, Weakly similar to UDP-GLUCOSE: GLYCOPROTEIN C LUCOSYLTRANSFERASE PRECURSOR [D.melanogaster]//8.3e-103:538:94//Hs.105794:AA701659	R-PLACE1011419//ESTs//4.9e-50:267:95//Hs.7045:AA167337
R-PLACE1010702//Homo sapiens DNA from chromosome 19, BAC 33152//4.8e-46:531:71//Hs.55452:AC003973	R-PLACE1011433//Homo sapiens mRNA for KIAA0530 protein, partial cds//4.8e-114:600:94//Hs.10801:AB011102
R-PLACE1010714//Human organic anion transporting polypeptide (OATP) mRNA, complete cds//0.0074:351:60//Hs.46440:U21943	R-PLACE1011452//Homo sapiens mRNA for KIAA0707 protein, partial cds//3.7e-32:310:76//Hs.138488:AB014607
R-PLACE1010720//Homo sapiens chromosome-associated protein-C (hCAP-C) mRNA, partial cds//1.2e-56:300:95//Hs.50758:AF092564	R-PLACE1011465//ESTs//4.5e-86:471:93//Hs.144519:R70887
R-PLACE1010739//Homo sapiens mRNA for oligophrenin 1//2.6e-84:501:88//Hs.158122:AJ001189	R-PLACE1011472//Homo sapiens mRNA for KIAA0712 protein, complete cds//2.6e-104:515:96//Hs.111138:AB018255
R-PLACE1010743	R-PLACE1011492//ESTs//1.7e-96:488:95//Hs.116555:AA639278
R-PLACE1010761//Homo sapiens okadaic acid-inducible phosphoprotein (OA48-18) mRNA, complete cds//5.2e-94:442:96//Hs.3688:AF069250	R-PLACE1011503//Homo sapiens clone 23597 mRNA sequence//1.0:193:60//Hs.28197:AF035294
R-PLACE1010771//ESTs//3.8e-54:264:99//Hs.27299:A1074024	R-PLACE1011520//ESTs//6.8e-99:477:97//Hs.85077:AA968576
R-PLACE1010786//ESTs, Highly similar to MYOSIN HEAVY CHAIN 1B [Acanthamoeba castellanii]//7.6e-111:575:94//Hs.10260:A1126627	R-PLACE1011563//ESTs//1.4e-94:514:92//Hs.16471:AA206421
R-PLACE1010800//ESTs//1.9e-109:557:95//Hs.11460:AA057558	R-PLACE1011567//EST//2.8e-89:417:100//Hs.149770:A1285985
R-PLACE1010802//ESTs//0.00021:428:58//Hs.70258:A1091203	R-PLACE1011576//Zinc finger protein 91 (HPF7, HTF10)//4.7e-55:267:81//Hs.8597:L11672
R-PLACE1010811//ESTs//7.4e-73:394:93//Hs.48499:AA428896	R-PLACE1011586//Myosin, heavy polypeptide 11, smooth muscle//0.98:168:61//Hs.78344:AF001548
R-PLACE1010833//ESTs//9.0e-33:274:78//Hs.24391:W27472	R-PLACE1011635//ESTs//2.5e-67:332:98//Hs.108194:AA780067
R-PLACE1010856//ESTs//5.8e-41:351:81//Hs.17401:W81048	R-PLACE1011641//ESTs//2.5e-71:338:100//Hs.153085:AA993965
R-PLACE1010857//ESTs, Weakly similar to T14B4.2 gene product [C.elegans]//1.4e-71:326:92//Hs.3385:N25917	R-PLACE1011643//EST//1.9e-18:181:78//Hs.160879:A1361900
R-PLACE1010870//ESTs//5.8e-57:303:96//Hs.30503:H05090	R-PLACE1011649//Homo sapiens clone 24432 mRNA sequence//2.5e-73:414:91//Hs.78019:AF070535
R-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds//2.3e-101:501:96//Hs.118087:AB011182	R-PLACE1011650//EST//5.8e-18:118:92//Hs.124486:AA846036
R-PLACE1010891	R-PLACE1011664//Restin (Reed-Steinberg cell-expressed intermediate filament-associated protein)//0.50:178:62//Hs.31638:X64838
R-PLACE1010896//EST//0.0039:249:57//Hs.126090:AA867983	R-PLACE1011675
R-PLACE1010900//Human Xq28 mRNA, complete cds//3.3e-07:106:76//Hs.20136:U46023	R-PLACE1011682//ESTs//2.4e-90:465:94//Hs.57830:A1312025
R-PLACE1010916//Plasminogen activator inhibitor, type II (argininase-serpin)//0.25:190:61//Hs.75716:Y06630	R-PLACE1011719//Human Line-1 repeat mRNA with 2 open reading frame s//8.5e-57:410:83//Hs.23094:W19503
R-PLACE1010917//ESTs//1.3e-82:452:92//Hs.68055:AA081093	R-PLACE1011725//ESTs//2.0e-70:340:98//Hs.161725:AA251392
R-PLACE1010925//ESTs//1.1e-92:471:95//Hs.17448:A1125479	R-PLACE1011729//ESTs//7.5e-19:180:79//Hs.119516:AA443426
R-PLACE1010926//Homo sapiens mRNA for KIAA0554 protein, partial cds//1.3e-66:402:89//Hs.74750:AB011126	R-PLACE1011749//Myelin oligodendrocyte glycoprotein (alternative products)//7.3e-40:361:77//Hs.53217:Z48051
R-PLACE1010942//Homo sapiens intersectin short form mRNA, complete	R-PLACE1011762//Human kpn1 repeat mRNA (cdna clone pcd-kpn1-8), 3'

【0937】

【表635】

end//3.0e-60:319:76//Hs.103948:K00627	D38081
R-PLACE1011778//ESTs//0.0e-70:372:94//Hs.46765:AA521080	R-PLACE2000371//ESTs//3.6e-81:409:97//Hs.155138:AA158731
R-PLACE1011783//Calcium modulating ligand//8.4e-41:279:85//Hs.13572:AF068179	R-PLACE2000373//Homo sapiens mRNA for KIAA0734 protein, partial cds//0.89:186:62//Hs.101516:AB018277
R-PLACE1011858//ESTs//2.6e-69:396:91//Hs.55220:D11563	R-PLACE2000379//ESTs//3.4e-10:228:64//Hs.57842:W63781
R-PLACE1011874//Human mRNA for KIAA0033 gene, partial cds//1.2e-53:439:80//Hs.22271:D26067	R-PLACE2000394//ESTs//6.7e-41:462:74//Hs.107657:AA126814
R-PLACE1011875//ESTs//9.0e-88:420:98//Hs.70897:AA987648	R-PLACE2000398//ESTs//4.2e-33:373:74//Hs.155184:AA573189
R-PLACE1011891//ESTs//3.9e-17:97:100//Hs.84698:AA725913	R-PLACE2000399
R-PLACE1011896//ESTs//2.8e-23:176:84//Hs.121540:A1275497	R-PLACE2000404//ESTs, Highly similar to LEUCYL-TRNA SYNTHETASE, C YTOPLASMIC [Saccharomyces cerevisiae]//4.2e-109:540:96//Hs.6762:AA 088424
R-PLACE1011922//ESTs//6.6e-35:415:73//Hs.10972:AA164268	R-PLACE2000411//ESTs//1.6e-89:459:95//Hs.117589:M25941
R-PLACE1011923//Homo sapiens serum-inducible kinase mRNA, complete cds//2.3e-99:546:92//Hs.3838:AF059617	R-PLACE2000419//ESTs, Weakly similar to F25H9.6 [C.elegans]//1.6e-97:436:95//Hs.24647:W19739
R-PLACE1011962//ESTs//3.3e-49:294:90//Hs.106800:A1031969	R-PLACE2000425//Homo sapiens DEC-205 mRNA, complete cds//2.2e-44:287:88//Hs.153563:AF011333
R-PLACE1011964//ESTs, Weakly similar to LINE-1 REVERSE TRANSCRIPTASE HOMOLOG [H.sapiens]//2.6e-06:284:63//Hs.124102:AA701285	R-PLACE2000427//ESTs, Weakly similar to coded for by C. elegans CD NA CEES142F [C.elegans]//3.0e-113:543:97//Hs.16933:AA976002
R-PLACE1011982//ESTs//2.9e-51:291:93//Hs.20792:R14890	R-PLACE2000433//ESTs//1.8e-46:311:85//Hs.145032:AA343523
R-PLACE1011995//ESTs//4.5e-39:304:81//Hs.138852:AA284247	R-PLACE2000435//ESTs//2.9e-33:243:87//Hs.90964:AA393986
R-PLACE1012031//Homo sapiens mRNA for KIAA0713 protein, partial cds//8.0e-106:540:95//Hs.88756:AB018256	R-PLACE2000438//ESTs//2.8e-09:66:96//Hs.59548:A1279887
R-PLACE2000003//ESTs//2.0e-103:488:98//Hs.8341:AA490069	R-PLACE2000450//Human mRNA for KIAA0392 gene, partial cds//3.3e-39:394:74//Hs.40100:AB002390
R-PLACE2000007//ESTs//2.4e-110:564:95//Hs.65135:W89120	R-PLACE2000455//ESTs//1.2e-62:301:99//Hs.151708:AA554714
R-PLACE2000011//Homo sapiens clone 614 unknown mRNA, complete sequence//4.8e-105:524:95//Hs.21811:AF091080	R-PLACE2000458//ESTs//6.8e-92:473:96//Hs.115897:AA156638
R-PLACE2000015//ESTs//7.1e-111:543:96//Hs.32178:AA083211	R-PLACE2000465//ESTs//1.3e-45:435:76//Hs.141635:N79228
R-PLACE2000017//EST//8.2e-46:404:79//Hs.133006:A1049504	R-PLACE2000477//ESTs//2.6e-100:536:94//Hs.77822:AA532642
R-PLACE2000021//EST//4.5e-19:221:71//Hs.150830:A1302868	R-PLACE2000004//ESTs//9.1e-114:558:97//Hs.13035:AA151838
R-PLACE2000033//Human melanoma antigen recognized by T-cells (MART-1) mRNA//1.6e-43:355:79//Hs.154069:U06452	R-PLACE2000029//Homo sapiens mRNA for KIAA0575 protein, complete cds//6.3e-64:350:86//Hs.153468:AB011147
R-PLACE2000034//ESTs//2.2e-21:314:70//Hs.107697:W29013	R-PLACE2000059//EST//0.028:175:61//Hs.159873:R92763
R-PLACE2000039//H.sapiens mRNA for translin associated protein X//2.9e-45:514:72//Hs.96247:X95073	R-PLACE2000070//ESTs//3.8e-16:200:74//Hs.138771:N70979
R-PLACE2000047//Homo sapiens class-I MHC-restricted T cell associated molecule (CRTAM) mRNA, complete cds//4.1e-45:358:81//Hs.159523:AF001622	R-PLACE2000103//ISLET AMYLOID POLYPEPTIDE PRECURSOR//3.7e-48:468:75//Hs.51048:X68830
R-PLACE2000050//ESTs//4.5e-65:322:98//Hs.155820:N67652	R-PLACE2000119//ESTs//1.2e-45:330:83//Hs.35254:A1133727
R-PLACE2000061//Homo sapiens mRNA for KIAA0575 protein, complete cds//9.2e-41:429:72//Hs.153468:AB011147	R-PLACE2000124//EST//3.1e-75:391:96//Hs.161515:N71739
R-PLACE2000062//Human mRNA for KIAA0392 gene, partial cds//2.0e-43:296:86//Hs.40100:AB002390	R-PLACE2000136//ESTs//8.3e-18:152:84//Hs.10043:D81792
R-PLACE2000072//Homo sapiens ZNF202 alpha (ZNF202) mRNA, complete cds//6.2e-111:550:95//Hs.9443:AF027219	R-PLACE2000142//ESTs//0.047:183:62//Hs.43102:AA131369
R-PLACE2000097//Calcium modulating ligand//6.2e-47:372:80//Hs.13572:AF068179	R-PLACE2000147//ESTs//6.6e-53:310:90//Hs.8230:W07142
R-PLACE2000100//ESTs//8.8e-42:281:86//Hs.150727:A1292236	R-PLACE2000148//EST//1.9e-16:184:76//Hs.146570:A1139815
R-PLACE2000103//ESTs//4.7e-97:518:93//Hs.118727:W26941	R-PLACE2000155//ESTs//1.2e-19:192:79//Hs.131350:AA805223
R-PLACE2000111//Homo sapiens ubiquitin hydrolyzing enzyme 1 (UBH1) mRNA, partial cds//0.00043:127:71//Hs.42400:AF022789	R-PLACE2000156//ESTs, Highly similar to ENV POLYPROTEIN [Avian sp leen necrosis virus]//4.8e-36:262:88//Hs.31532:H18272
R-PLACE2000115//ESTs//7.8e-93:458:96//Hs.104520:AA481662	R-PLACE2000157
R-PLACE2000132//ESTs//3.8e-69:409:91//Hs.98502:AA433988	R-PLACE2000158//Small inducible cytokine A5 (RANTES)//8.2e-39:296:81//Hs.155464:AF088219
R-PLACE2000136//ESTs//6.2e-05:274:61//Hs.114067:AA701558	R-PLACE2000160
R-PLACE2000140//Homo sapiens mRNA for KIAA0562 protein, complete cds//4.7e-44:302:85//Hs.118401:AB011134	R-PLACE2000169//ESTs//1.5e-64:329:97//Hs.129864:R20798
R-PLACE2000164//ESTs//6.3e-106:506:98//Hs.16390:A1052357	R-PLACE2000194
R-PLACE2000170//Small inducible cytokine A5 (RANTES)//3.7e-42:326:79//Hs.155464:AF088219	R-PLACE2000197//ESTs//1.4e-38:197:98//Hs.146341:A1269930
R-PLACE2000172//ESTs//9.6e-43:232:94//Hs.6709:A1379778	R-PLACE2000199//ESTs, Highly similar to APOLIPOPROTEIN E PRECURSOR [Sus scrofa]//0.018:261:61//Hs.131370:AA927516
R-PLACE2000176//EST//1.6e-24:154:91//Hs.157734:A1360292	R-PLACE2000207//EST//1.3e-15:154:78//Hs.136617:AA630476
R-PLACE2000187//Human mRNA for KIAA0033 gene, partial cds//2.0e-49:292:90//Hs.22271:D26067	R-PLACE2000208//ESTs//1.6e-18:151:82//Hs.155498:W27084
R-PLACE2000216//ESTs//0.0041:166:64//Hs.159476:A1382378	R-PLACE2000218//ESTs//1.8e-85:463:93//Hs.7849:A1129964
R-PLACE2000223//ESTs//0.49:171:60//Hs.85154:AA207191	R-PLACE2000220//ESTs//6.4e-44:308:84//Hs.136839:H93717
R-PLACE2000235//ESTs//2.9e-39:264:85//Hs.136839:H93717	R-PLACE2000226//ESTs//1.3e-49:269:95//Hs.9059:A1359014
R-PLACE2000246//NAD(P)H:menadiene oxidoreductase//4.0e-44:331:82//Hs.80706:M81600	R-PLACE2000230//EST//2.3e-34:258:83//Hs.4382:T02878
R-PLACE2000264//Human mRNA for KIAA0365 gene, partial cds//4.0e-38:311:81//Hs.84123:AB002363	R-PLACE2000242//Human trophinin mRNA, complete cds//1.1e-63:546:78//Hs.76313:U04811
R-PLACE2000274//ESTs, Weakly similar to dynein-related protein [H.sapiens]//1.9e-87:422:98//Hs.9740:A1004779	R-PLACE2000244//ESTs, Highly similar to NEGATIVE REGULATOR OF MITOSIS [Emeritella nidulans]//7.5e-110:549:95//Hs.13692:AA632002
R-PLACE2000302//ESTs, Highly similar to THREONYL-TRNA SYNTHETASE, CYTOPLASMIC [Homo sapiens]//4.8e-68:380:92//Hs.107365:AA720664	R-PLACE2000254//Human mRNA for KIAA0309 gene, partial cds//2.4e-29:174:94//Hs.87908:AB002307
R-PLACE2000303//ESTs//2.6e-43:413:75//Hs.118732:A1344055	R-PLACE2000271//Human macrophage-derived chemokine precursor (MDC) mRNA, complete cds//2.3e-62:287:82//Hs.97203:U83171
R-PLACE2000311//ESTs//2.8e-92:501:92//Hs.28432:R83380	R-PLACE2000276//ESTs//7.5e-07:187:64//Hs.80720:AA031782
R-PLACE2000335//ESTs//4.3e-32:300:77//Hs.163035:AA748058	R-PLACE2000304//Human 53K isoform of Type II phosphatidylinositol-4-phosphate 5-kinase (PIPK) mRNA, complete cds//4.0e-59:456:80//Hs.108966:U48696
R-PLACE2000342//Homo sapiens ubiquitin hydrolyzing enzyme 1 (UBH1) mRNA, partial cds//0.00071:117:73//Hs.42400:AF022789	R-PLACE2000310//ISLET AMYLOID POLYPEPTIDE PRECURSOR//6.0e-45:302:86//Hs.51048:X68830
R-PLACE2000347//ESTs//1.6e-30:214:86//Hs.135272:A1347618	R-PLACE2000320//Interleukin 10//9.6e-42:288:85//Hs.2180:M57627
R-PLACE2000359//Zinc finger protein 139 (clone pHz-37)//5.5e-42:288:86//Hs.140090:U09848	R-PLACE2000322//ESTs, Highly similar to ARGININOSUCCINATE LYASE [Homo sapiens]//5.8e-34:190:95//Hs.114531:N74103
R-PLACE2000366//Thromboxane A2 receptor//6.7e-53:392:82//Hs.89887:	R-PLACE2000331//Homo sapiens mRNA for KIAA0772 protein, complete cds//3.7e-32:239:84//Hs.15519:AB018315
	R-PLACE2000339//ESTs//1.3e-109:548:96//Hs.7871:A1041837
	R-PLACE2000341//EST//1.1e-11:231:68//Hs.131328:AA922688
	R-PLACE2000350//Human mRNA for adipogenesis inhibitory factor//8.0

【0938】

【表636】

e-40:291:76//Hs.1721:X58377	R-PLACE4000548//ESTs//3.3e-86:441:96//Hs.5070:AA149527
R-PLACE3000352//EST//1.8e-72:343:100//Hs.144871:A1202380	R-PLACE4000558//Human putative monocarboxylate transporter (MCT) mRNA, complete cds//5.7e-46:425:76//Hs.23590:U59185
R-PLACE3000353//ESTs//2.0e-75:395:95//Hs.107260:W52683	R-THYR01000026//ESTs//2.6e-42:331:82//Hs.137875:AA993532
R-PLACE3000362//EST//2.8e-80:381:99//Hs.136233:AA261888	R-THYR01000034//ESTs//2.1e-43:214:100//Hs.153018:A1243524
R-PLACE3000363	R-THYR01000035//ESTs//7.6e-52:325:90//Hs.49817:AA001249
R-PLACE3000365//EST//4.8e-50:307:88//Hs.149580:A1281881	R-THYR01000040//ESTs//1.7e-94:459:98//Hs.48712:A1027889
R-PLACE3000373//ESTs//5.8e-60:422:83//Hs.142826:W87430	R-THYR01000070//ESTs//6.7e-43:283:86//Hs.37573:H59651
R-PLACE3000388//ESTs, Moderately similar to !!!! ALU SUBFAMILY J W	R-THYR01000072//ESTs//1.3e-57:313:96//Hs.127827:H13438
ARNING ENTRY !!!! [H.sapiens]//1.0e-35:427:73//Hs.138795:R98534	R-THYR01000085//ESTs//1.1e-90:439:98//Hs.150539:AA908435
R-PLACE3000399//ESTs//6.5e-05:162:66//Hs.149440:A1274570	R-THYR01000092//Human mRNA for KIAA0355 gene, complete cds//1.3e-4
R-PLACE3000400//ESTs//8.3e-05:310:63//Hs.17697:AA287528	1:344:79//Hs.153014:AB002353
R-PLACE3000401//ESTs//4.6e-60:326:80//Hs.139555:N48230	R-THYR01000107//Interleukin 10//2.8e-43:292:84//Hs.2180:W57627
R-PLACE3000402//Homo sapiens clone 24629 mRNA sequence//0.50:227:6	R-THYR01000111//ESTs, Highly similar to LINE-1 REVERSE TRANSCRIPT
2//Hs.142570:AF052160	ASE HOMOLOG [Homo sapiens]//1.0e-52:413:80//Hs.140385:AA773359
R-PLACE3000405//Human HsLim15 mRNA for HsLim15, complete cds//5.3	R-THYR01000121//EST//0.24:78:74//Hs.156632:A1345108
e-43:315:82//Hs.37181:D64108	R-THYR01000124//ESTs//2.8e-86:428:96//Hs.141634:A122764
R-PLACE3000408//Human high-affinity copper uptake protein (hCTR1)	R-THYR01000129//Homo sapiens TED protein (TED) mRNA, complete cds//
mRNA, complete cds//4.4e-47:302:87//Hs.73614:U83460	6.8e-90:449:96//Hs.87619:AF087142
R-PLACE3000413//ESTs//1.6e-116:571:97//Hs.10235:H93077	R-THYR01000132//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC
R-PLACE3000416//Small inducible cytokine A5 (RANTES)//1.8e-41:300:	ARNING ENTRY !!!! [H.sapiens]//5.2e-49:486:77//Hs.24164:N95217
85//Hs.155464:AF088219	R-THYR01000156//ESTs//6.1e-36:344:75//Hs.70279:AA757426
R-PLACE3000425//Homo sapiens 4F5S mRNA, complete cds//1.6e-46:307:	R-THYR01000163//Homo sapiens LIM protein mRNA, complete cds//4.8e-
85//Hs.32567:AF073519	38:278:84//Hs.154103:AF061258
R-PLACE3000455//ESTs//1.0:160:64//Hs.156045:AA884461	R-THYR01000173//ESTs, Highly similar to CLATHRIN COAT ASSEMBLY PR
R-PLACE3000475//Human signal transducing adaptor molecule STAM mRNA	OTEIN AP47 [Mus musculus]//1.1e-111:554:96//Hs.18894:AA910946
A, complete cds//6.1e-84:440:92//Hs.153487:U43899	R-THYR01000186//ESTs//1.0e-44:339:83//Hs.155184:AA573189
R-PLACE3000477//ESTs//2.4e-113:568:96//Hs.24557:AA142980	R-THYR01000187//Small inducible cytokine A5 (RANTES)//1.1e-41:305:
R-PLACE40000099//ESTs//1.5e-72:361:96//Hs.10119:AA700227	81//Hs.155464:AF088219
R-PLACE4000014//Homo sapiens mRNA for KIAA0809 protein, partial cd	R-THYR01000190//Small inducible cytokine A5 (RANTES)//2.3e-44:301:
s//8.8e-85:433:95//Hs.105399:AB018352	85//Hs.155464:AF088219
R-PLACE4000034//ESTs//7.0e-110:550:96//Hs.76607:AA156240	R-THYR01000197//Homo sapiens mRNA for poly(A)-specific ribonuclease
R-PLACE4000049//EST//0.028:87:75//Hs.89303:AA284031	e//3.6e-110:535:97//Hs.43445:AJ005698
R-PLACE4000052//ESTs//5.6e-116:553:98//Hs.19067:AA521292	R-THYR01000199//Homo sapiens mRNA for KIAA0652 protein, complete c
R-PLACE4000063//ESTs//5.0e-80:388:98//Hs.135028:A1096444	ds//4.3e-115:559:97//Hs.79672:AB014552
R-PLACE4000089//ESTs//2.3e-97:479:97//Hs.102425:AA807547	R-THYR01000206//ESTs//3.1e-90:507:90//Hs.32456:W29063
R-PLACE4000093//ESTs//1.5e-82:391:99//Hs.160730:A1142739	R-THYR01000221//ESTs, Weakly similar to !!!! ALU SUBFAMILY J W
R-PLACE4000100	ARNING ENTRY !!!! [H.sapiens]//1.1e-72:357:98//Hs.140002:AA635349
R-PLACE4000106//Homo sapiens mRNA for KIAA0462 protein, partial cd	R-THYR01000241//Homo sapiens mRNA for KIAA0688 protein, complete c
s//2.7e-98:419:91//Hs.129937:AB007931	ds//7.8e-69:524:82//Hs.141874:AB014588
R-PLACE4000128//ESTs, Moderately similar to !!!! ALU SUBFAMILY J W	R-THYR01000242//ESTs//4.2e-27:222:85//Hs.77554:W87927
ARNING ENTRY !!!! [H.sapiens]//3.8e-111:184:71//Hs.154278:N45985	R-THYR01000253//Sialophorin (gpL115, leukosialin, CD43)//7.3e-40:3
R-PLACE4000129//Homo sapiens mRNA, chromosome 1 specific transcrip	18:80//Hs.80738:X52075
t KIAA0500//5.2e-21:118:100//Hs.118164:AB007969	R-THYR01000270//ESTs//1.9e-99:531:94//Hs.17767:N62925
R-PLACE4000147//EST//1.6e-23:175:79//Hs.162236:AA551582	R-THYR01000279//EST//2.7e-54:266:99//Hs.149527:A1280674
R-PLACE4000156//Homo sapiens mRNA for KIAA0575 protein, complete c	R-THYR01000288//Homo sapiens mRNA for Hs Ste24p, complete cds//3.5
ds//3.0e-47:306:88//Hs.153468:AB011147	e-100:566:91//Hs.25845:AB016068
R-PLACE4000192//ESTs, Weakly similar to Human zinc fing	R-THYR01000320//POLYPOSIS LOCUS PROTEIN 1//1.0:321:58//Hs.74648:W7
er protein (ZNF142) [H.sapiens]//6.7e-31:232:82//Hs.16493:T92186	3547
R-PLACE4000222//ESTs//2.2e-53:195:85//Hs.141575:AA211734	R-THYR01000327//Autocrine motility factor receptor//9.2e-54:289:93
R-PLACE4000233//ESTs//2.9e-81:456:93//Hs.124964:R81949	//Hs.80731:W63175
R-PLACE4000247//Homo sapiens PYRIN (MEFV) mRNA, complete cds//5.5	R-THYR01000343//Homo sapiens mRNA for KIAA0790 protein, partial cd
e-72:307:85//Hs.113283:AF018080	s//3.4e-113:559:96//Hs.12002:AB018333
R-PLACE4000250//Small inducible cytokine A5 (RANTES)//7.1e-43:301:	R-THYR01000358//Human selenium-binding protein (hSBP) mRNA, comple
83//Hs.155464:AF088219	te cds//1.5e-48:317:87//Hs.7833:U29091
R-PLACE4000252//EST//1.6e-40:275:85//Hs.162197:AA535216	R-THYR01000368//ESTs//4.7e-88:430:98//Hs.146085:AA021064
R-PLACE4000261//EST//0.0063:384:58//Hs.136284:AA400442	R-THYR01000381//ESTs//1.0:253:57//Hs.128783:AA436250
R-PLACE4000269//ESTs//7.3e-67:345:97//Hs.5000:R44586	R-THYR01000387//Homo sapiens ubiquitin conjugating enzyme G2 (UBE2
R-PLACE4000270//Homo sapiens apoptotic protease activating factor	G2) mRNA, complete cds//4.6e-69:294:84//Hs.151614:AF032456
1 (Apaf-1) mRNA, complete cds//2.1e-37:352:77//Hs.77579:AF013263	R-THYR01000394//Thromboxane A2 receptor//4.1e-40:232:87//Hs.89887:
R-PLACE4000300//EST//0.26:103:68//Hs.144438:AA70782	D38081
R-PLACE4000320//EST//2.7e-44:298:85//Hs.162404:AA573131	R-THYR01000395//ESTs//3.3e-20:160:83//Hs.101570:AA505429
R-PLACE4000323//ESTs//8.8e-38:178:79//Hs.155475:AA761454	R-THYR01000401//ESTs//1.3e-109:516:99//Hs.78524:A1140601
R-PLACE4000326//ESTs//7.4e-103:516:96//Hs.55042:AA150460	R-THYR01000438//ESTs//2.1e-48:360:83//Hs.141203:H52638
R-PLACE4000344//ESTs//9.9e-94:463:96//Hs.100057:AA001414	R-THYR01000452//ESTs, Weakly similar to No definition line found
R-PLACE4000367//ESTs//0.81:102:73//Hs.107692:H38478	[C.elegans]//8.5e-40:239:90//Hs.84009:A1309761
R-PLACE4000369//ESTs//1.5e-69:390:92//Hs.13733:AA418656	R-THYR01000471//ESTs//3.3e-36:302:80//Hs.70279:AA757426
R-PLACE4000379//ESTs//1.3e-67:373:91//Hs.48569:AA905425	R-THYR01000484//Homo sapiens mRNA for KIAA0737 protein, complete c
R-PLACE4000387//EST, Moderately similar to !!!! ALU SUBFAMILY SQ W	ds//2.2e-49:479:75//Hs.17630:AB018280
ARNING ENTRY !!!! [H.sapiens]//1.9e-44:379:78//Hs.152369:AA504818	R-THYR01000488//Homo sapiens mRNA for HRIHFB2038, partial cds//4.1
R-PLACE4000392//ESTs, Weakly similar to line-1 protein ORF1 [H.sap	e-89:471:94//Hs.28719:AB015333
iens]//2.3e-70:482:83//Hs.140416:AA778649	R-THYR01000501//ESTs//1.5e-46:287:89//Hs.125300:R62360
R-PLACE4000401//ESTs//1.3e-18:151:84//Hs.150355:A1273502	R-THYR01000502//ESTs//1.7e-08:63:96//Hs.116319:A1208005
R-PLACE4000411//ESTs//1.1e-108:543:96//Hs.23901:AA169780	R-THYR01000505//ESTs, Weakly similar to KIAA0281 [H.sapiens]//3.9
R-PLACE4000445//ESTs, Weakly similar to C0509.6 gene product [C.el	e-57:286:96//Hs.105861:A1206965
egans]//2.6e-111:530:98//Hs.12003:AA643063	R-THYR01000558//ESTs//1.7e-95:454:99//Hs.125063:AA648511
R-PLACE4000465//Cytochrome P450, subfamily I (aromatic compound-in	R-THYR01000569//ESTs//3.2e-89:463:94//Hs.20555:W22193
ducible), polypeptide 2//8.5e-58:409:72//Hs.1361:W55053	R-THYR01000570//ESTs//2.8e-97:471:97//Hs.8245:AA115485
R-PLACE4000489//ESTs//5.0e-70:342:98//Hs.72865:A1380932	R-THYR01000585//Homo sapiens protein associated with Myc mRNA, com
R-PLACE4000494//ESTs//1.4e-109:525:98//Hs.22539:A1334210	plete cds//2.6e-108:533:97//Hs.151411:AF075587
R-PLACE4000522//ESTs//6.3e-88:471:93//Hs.8121:AA521290	

【0939】

【表637】

R-THYRO1000596//ESTs//3.1e-99:527:94//Hs.6084:AA045247
 R-THYRO1000602//EST//6.9e-50:381:83//Hs.161917:AA483223
 R-THYRO1000605//ESTs. Weakly similar to monocytic leukaemia zinc finger protein [H.sapiens]//1.2e-96:483:96//Hs.21907:N24415
 R-THYRO1000625//ESTs//5.6e-36:257:84//Hs.139657:AA191742
 R-THYRO1000637
 R-THYRO1000641//ESTs. Weakly similar to ERYTHROCYTE BAND 7 INTEGRAL MEMBRANE PROTEIN [H.sapiens]//4.9e-46:245:95//Hs.97398:AA398634
 R-THYRO1000658//ESTs//5.8e-48:281:90//Hs.142259:AA828840
 R-THYRO1000662//ESTs//1.5e-82:389:99//Hs.155573:AA487384
 R-THYRO1000666//ESTs//1.4e-26:179:88//Hs.98382:AA779866
 R-THYRO1000676//EST//6.4e-05:88:77//Hs.133424:A1061063
 R-THYRO1000684//ESTs//1.9e-69:374:94//Hs.144617:R77109
 R-THYRO1000699//ESTs//1.7e-58:394:86//Hs.26373:AA700713
 R-THYRO1000712
 R-THYRO1000734//EST//2.0e-06:95:73//Hs.156201:AA724287
 R-THYRO1000748//EST//4.1e-12:155:74//Hs.118694:AA148713
 R-THYRO1000756//ESTs. Weakly similar to CMP-N-ACETYLNEURAMINATE-BE TA-GALACTOSAMIDE-ALPHA-2, 3-SIALYLTRANSFERASE [H.sapiens]//8.1e-82:497:87//Hs.109672:W22624
 R-THYRO1000777
 R-THYRO1000783//EST//5.6e-100:470:99//Hs.123515:AA812932
 R-THYRO1000787//EST//8.0e-34:175:99//Hs.99607:AA463897
 R-THYRO1000793//ESTs//2.2e-106:505:99//Hs.50929:AA443144
 R-THYRO1000796//ESTs//4.3e-44:445:75//Hs.55855:AA621381
 R-THYRO1000805//EST//2.6e-32:407:67//Hs.123424:AA813594
 R-THYRO1000815//Human mRNA for KIAA0033 gene, partial cds//2.0e-56:307:87//Hs.22271:D26067
 R-THYRO1000829
 R-THYRO1000843//Interleukin 10//1.1e-44:285:87//Hs.2180:M57627
 R-THYRO1000852//EST//2.3e-20:157:85//Hs.149580:A1281881
 R-THYRO1000855//ESTs//2.6e-44:359:81//Hs.140329:AA714011
 R-THYRO1000865//Protein kinase, interferon-inducible double strand ed RNA dependent//2.8e-44:374:79//Hs.73821:M35663
 R-THYRO1000895//ESTs//1.0e-32:196:85//Hs.138630:H97871
 R-THYRO1000916//ESTs//4.6e-99:492:96//Hs.152442:AA528234
 R-THYRO1000926//Homo sapiens cAMP-specific phosphodiesterase 8B (PDE8B) mRNA, partial cds//3.1e-110:566:94//Hs.78106:AF079529
 R-THYRO1000934//ESTs//7.4e-102:535:95//Hs.58194:W72182
 R-THYRO1000951//ESTs//4.2e-11:91:89//Hs.6278:TI5859
 R-THYRO1000952//ESTs//3.9e-93:489:94//Hs.48928:AA211761
 R-THYRO1000974//Homo sapiens ribosomal protein L33-like protein mRNA, complete cds//1.1e-60:321:95//Hs.14454:AF047440
 R-THYRO1000975//EST//9.8e-49:303:89//Hs.149580:A1281881
 R-THYRO1000983//ESTs. Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD II [Arabidopsis thaliana]//1.6e-90:474:93//Hs.106616:A1027524
 R-THYRO1000984//ESTs//5.9e-97:481:96//Hs.142457:A1202777
 R-THYRO1000988//EST//3.5e-42:241:83//Hs.162404:AA573131
 R-THYRO1001003//ESTs. Weakly similar to ubiquitin-conjugating enzyme [H.sapiens]//3.0e-57:341:91//Hs.44049:AA521489
 R-THYRO1001031//ESTs//5.5e-47:322:85//Hs.136839:H93717
 R-THYRO1001033//ESTs//5.7e-89:427:98//Hs.71508:AA809070
 R-THYRO1001062//EST//1.5e-46:291:89//Hs.161917:AA483223
 R-THYRO1001093//ESTs//2.7e-80:468:90//Hs.124601:AA203497
 R-THYRO1001100
 R-THYRO1001120//ESTs. Moderately similar to fractionated X-irradiation-induced 29 thymoma [M.musculus]//6.6e-86:491:89//Hs.89135:A1138834
 R-THYRO1001121//Homo sapiens mRNA for beta-tubulin folding cofactor D//2.6e-82:429:94//Hs.12570:AJ006417
 R-THYRO1001133//ESTs//2.9e-39:242:90//Hs.152340:AA521399
 R-THYRO1001134//ESTs//1.8e-102:521:95//Hs.108408:N31922
 R-THYRO1001142//ESTs//0.26:84:69//Hs.153434:A1287853
 R-THYRO1001173//Human mRNA for KIAA0238 gene, partial cds//0.0012:305:62//Hs.82042:D87075
 R-THYRO1001177
 R-THYRO1001189//H.sapiens F11 mRNA//1.5e-59:260:83//Hs.159639:X77744
 R-THYRO1001204//ESTs. Weakly similar to THI protein [D.melanogaster]//1.0e-75:431:91//Hs.5184:AA709151
 R-THYRO1001213//ESTs//1.3e-75:409:92//Hs.140213:AA828932
 R-THYRO1001262//Human kpn1 repeat mRNA (cdna clone pcd-kpn1-4), 3' end//1.3e-48:349:83//Hs.139107:X00629
 R-THYRO1001271//PUTATIVE PROTEIN PHOSPHATASE 2C//1.0:128:64//Hs.118728:D13640
 R-THYRO1001290//ESTs//2.1e-89:424:99//Hs.118152:AA702561
 R-THYRO1001313//ESTs//3.5e-17:139:87//Hs.15827:H16269
 R-THYRO1001320//ESTs//1.4e-61:403:79//Hs.139555:AA8230
 R-THYRO1001321//Hypoxanthine phosphoribosyltransferase 1 (Lesch-Ny

han syndrome)//8.5e-05:326:60//Hs.82314:M31642
 R-THYRO1001322//ESTs//0.16:422:59//Hs.23876:AA082935
 R-THYRO1001347//ESTs. Weakly similar to C35A5.8 [C.elegans]//1.1e-106:562:94//Hs.15032:AA774250
 R-THYRO1001363//ESTs//1.4e-99:508:95//Hs.5028:D51033
 R-THYRO1001365
 R-THYRO1001374
 R-THYRO1001401//Human HsLim15 mRNA for HsLim15, complete cds//2.5e-48:467:75//Hs.37181:D64108
 R-THYRO1001403//Interleukin 10//2.1e-46:305:85//Hs.2180:M57627
 R-THYRO1001405//ESTs//4.8e-25:197:84//Hs.6907:W72733
 R-THYRO1001406//EST//0.0023:117:66//Hs.162931:AA633197
 R-THYRO1001411//ESTs//6.1e-77:421:93//Hs.22973:R40979
 R-THYRO1001426//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0508//9.1e-49:305:86//Hs.159187:AB007977
 R-THYRO1001434//ESTs//0.40:161:61//Hs.161993:AA503172
 R-THYRO1001458//ESTs. Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//1.7e-05:159:66//Hs.104239:AA488082
 R-THYRO1001480//Small inducible cytokine A5 (RANTES)//1.3e-40:331:79//Hs.155464:AF088219
 R-THYRO1001487//Homo sapiens mRNA for KIAA0563 protein, complete cds//2.1e-17:134:76//Hs.15731:AB011135
 R-THYRO1001534//ESTs//4.6e-96:447:100//Hs.135204:A1093110
 R-THYRO1001537//ESTs. Weakly similar to !!!! ALU SUBFAMILY J WARNING ENTRY !!!! [H.sapiens]//5.0e-33:304:80//Hs.108740:W20094
 R-THYRO1001541//Human peptide transporter (HPEPT1) mRNA, complete cds//9.0e-49:427:76//Hs.2217:U21936
 R-THYRO1001559//ESTs//0.99:210:62//Hs.33619:AA021594
 R-THYRO1001570//ESTs//4.9e-48:287:91//Hs.27131:AA442413
 R-THYRO1001573//ESTs//2.1e-87:446:95//Hs.143669:AA621958
 R-THYRO1001584//ESTs//1.5e-64:354:95//Hs.146222:AA397741
 R-THYRO1001595//ESTs//5.7e-39:366:78//Hs.22562:RS4247
 R-THYRO1001602//Insulin-like growth factor 1 (somatomedin C)//7.4e-12:288:67//Hs.85112:X57025
 R-THYRO1001605//Human GS2 mRNA, complete cds//6.9e-49:359:83//Hs.264:U03886
 R-THYRO1001617//Homo sapiens peroxisomal acyl-CoA:di-hydroxyacetone phosphate acyltransferase (DHAPAT) mRNA, complete cds//1.3e-82:434:93//Hs.12482:AJ002190
 R-THYRO1001637//Homo sapiens KIAA0414 mRNA, partial cds//7.1e-58:331:83//Hs.127649:AB007874
 R-THYRO1001656//ESTs//3.8e-19:209:75//Hs.92186:A1080282
 R-THYRO1001661//ESTs//1.4e-56:323:91//Hs.24984:AA534446
 R-THYRO1001671//Homo sapiens mRNA for 2'-5' oligoadenylate synthetase 59 kDa isoform//1.6e-111:562:95//Hs.118633:AJ225089
 R-THYRO1001673//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488//1.0e-17:246:73//Hs.67619:AB007957
 R-THYRO1001703//ESTs//1.1e-39:142:97//Hs.110748:A1341726
 R-THYRO1001706//ESTs//2.2e-42:214:99//Hs.112536:A1147691
 R-THYRO1001721
 R-THYRO1001738//ESTs. Weakly similar to ZK1128.6 [C.elegans]//1.7e-10:147:77//Hs.158196:R53184
 R-THYRO1001745//ELK1, member of ETS oncogene family//1.8e-12:282:65//Hs.116549:AL009172
 R-THYRO1001746//EST//0.0073:226:61//Hs.146544:A1125323
 R-THYRO1001772//ESTs//8.2e-100:495:97//Hs.144993:AA243474
 R-THYRO1001793//ESTs//2.5e-89:430:97//Hs.58127:AA534224
 R-THYRO1001809//ESTs//1.0e-41:327:80//Hs.146811:AA410788
 R-THYRO1001854//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0487//5.7e-38:242:83//Hs.92381:AB007956
 R-THYRO1001895//ESTs//1.7e-08:213:64//Hs.156056:A1352123
 R-THYRO1001907//ESTs. Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//3.7e-41:362:79//Hs.139007:H74314
 R-VESEN1000122
 R-Y79AA1000013//ESTs//0.99:233:57//Hs.132216:AA923289
 R-Y79AA1000033//EST//1.9e-62:324:95//Hs.157692:A1359321
 R-Y79AA1000037//ESTs//6.1e-47:234:98//Hs.30773:AA557178
 R-Y79AA1000059//Homo sapiens mRNA for KIAA0540 protein, partial cds//2.8e-51:330:89//Hs.153026:AB014540
 R-Y79AA1000065//ESTs//2.0e-91:497:94//Hs.37759:H59629
 R-Y79AA1000131//EST//2.3e-16:184:75//Hs.141501:N50792
 R-Y79AA1000181//ESTs. Weakly similar to No definition line found [C.elegans]//2.4e-110:553:95//Hs.23159:AA113849
 R-Y79AA1000202//Human mRNA for KIAA0169 gene, partial cds//0.094:185:62//Hs.79414:D79991
 R-Y79AA1000214//ESTs//1.7e-93:495:94//Hs.11673:W68103
 R-Y79AA1000230//ESTs//3.5e-114:553:98//Hs.47125:A1421812
 R-Y79AA1000231//ESTs//1.1e-106:526:97//Hs.82856:A1246624
 R-Y79AA1000258//ESTs//1.5e-99:490:97//Hs.6459:A1092936
 R-Y79AA1000268//Human mRNA for KIAA0365 gene, partial cds//1.3e-4

【表638】

4.320:84//Hs.84123:AB002363	R-Y79AA1001323//ESTs//1.6e-67:422:89//Hs.118559:AA887084
R-Y79AA1000313//ESTs//1.7e-105:558:93//Hs.18851:AA857826	R-Y79AA1001384//ESTs//3.1e-104:496:98//Hs.153692:AA604143
R-Y79AA1000328//ESTs//1.9e-76:448:91//Hs.16470:AA121635	R-Y79AA1001391//ESTs//2.2e-77:418:94//Hs.118608:AA101819
R-Y79AA1000342//ESTs, Weakly similar to MATRIN 3 [H.sapiens]//2.0e-37:239:88//Hs.23476:AA401210	R-Y79AA1001394//ESTs//2.1e-78:409:95//Hs.23413:AA579859
R-Y79AA1000346//ESTs//7.9e-12:139:76//Hs.115987:AA483808	R-Y79AA1001402//EST//9.3e-08:128:75//Hs.141607:N63891
R-Y79AA1000349//ESTs, Moderately similar to spermatid perinuclear RNA-binding protein Spnr [M.musculus]//4.4e-66:339:97//Hs.8215:AA521150	R-Y79AA1001493//ESTs, Highly similar to UBIQUITIN-CONJUGATING ENZYME E2-17 KD 11 [Arabidopsis thaliana]//4.4e-109:553:95//Hs.106616:AI027524
R-Y79AA1000355//ESTs, Moderately similar to !!!! ALU SUBFAMILY SC WARNING ENTRY !!!! [H.sapiens]//3.2e-44:279:88//Hs.139007:H74314	R-Y79AA1001511//ESTs//4.9e-49:271:92//Hs.109045:AA523704
R-Y79AA1000368//ESTs//3.8e-97:513:94//Hs.68090:AA641018	R-Y79AA1001533//ESTs, Moderately similar to RNA polymerase I associated factor [M.musculus]//6.2e-46:260:94//Hs.24884:AA176812
R-Y79AA1000405//ESTs//4.4e-47:267:94//Hs.125304:R51613	R-Y79AA1001541//EST//0.62:126:67//Hs.137020:AA868563
R-Y79AA1000410//ESTs//7.4e-49:359:82//Hs.158107:AA707758	R-Y79AA1001548//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA//3.5e-95:517:91//Hs.76987:AF012872
R-Y79AA1000420//EST//0.17:99:69//Hs.160859:AI352292	R-Y79AA1001555//Collagen, type XI, alpha 1//1.0:157:64//Hs.82772:J04177
R-Y79AA1000469//ESTs, Highly similar to ancient ubiquitous 46 kDa protein AUP46 precursor [M.musculus]//3.1e-60:362:88//Hs.6381:AI18509	R-Y79AA1001585//ESTs//1.9e-90:430:98//Hs.48333:AA704508
R-Y79AA1000480//ESTs//1.0e-75:433:91//Hs.78110:AA741320	R-Y79AA1001594//ESTs//9.6e-23:122:100//Hs.63795:AI126237
R-Y79AA1000538//EST//1.9e-48:307:87//Hs.149580:AI281881	R-Y79AA1001603//ESTs//1.0e-50:193:100//Hs.25635:AI336204
R-Y79AA1000539//Human kinesin-like spindle protein HKSP (HKSP) mRNA, complete cds//0.95:172:62//Hs.41723:U37426	R-Y79AA1001613//ESTs, Weakly similar to zinc finger protein [H.sapiens]//7.2e-81:400:97//Hs.13323:AA897542
R-Y79AA1000540//ESTs//1.5e-97:534:93//Hs.67991:AA147848	R-Y79AA1001647//ESTs//6.8e-92:479:95//Hs.154270:N26486
R-Y79AA1000560//ESTs, Highly similar to ALPHA-ADAPTIN [Rattus norvegicus]//8.2e-97:482:97//Hs.19121:AI125280	R-Y79AA1001665//ESTs, Weakly similar to 50S RIBOSOMAL PROTEIN L20 [E.coli]//2.5e-19:112:97//Hs.26252:AA643235
R-Y79AA1000574//ESTs, Weakly similar to MD4B2.4 [C.elegans]//1.3e-107:564:93//Hs.16361:AI147455	R-Y79AA1001679//ESTs, Highly similar to LAMBDA-CRYSTALLIN [Oryctolagus cuniculus]//9.7e-99:553:92//Hs.108896:R54040
R-Y79AA1000627//Homo sapiens zinc finger protein (ZF5128) mRNA, complete cds//3.4e-99:517:94//Hs.60580:AF060503	R-Y79AA1001692
R-Y79AA1000705//ESTs, Weakly similar to HYPOTHETICAL 128.5 KD HELI CASE IN ATSI-TPD3 INTERGENIC REGION [Saccharomyces cerevisiae]//8.1e-27:140:100//Hs.129049:H28818	R-Y79AA1001696//ESTs//1.4e-84:478:91//Hs.6606:AA211783
R-Y79AA1000734//Homo sapiens peroxisomal biogenesis factor (PEX11 b) mRNA, complete cds//8.7e-114:586:95//Hs.83023:AF093670	R-Y79AA1001705//ESTs//6.7e-107:546:95//Hs.106805:AA18490
R-Y79AA1000748//ESTs, Weakly similar to HYPOTHETICAL 61.3 KD PROTEIN F2585.5 IN CHROMOSOME III [C.elegans]//9.8e-111:563:95//Hs.19845:AI005330	R-Y79AA1001711//Human DNA sequence from clone 111909 on chromosome 20p12. Contains part of a gene for a PAK1 LIKE Serine/Threonine-P protein Kinase and part of the PLCB4 gene for Phospholipase C, beta (1-Phosphatidylinositol -4,5-Bisphosphate Phosphodiesterase Beta 4). Contains ESTs, STSs and CDSs//0.0085:251:63//Hs.21864:AL031652
R-Y79AA1000752//Homo sapiens (huc) mRNA, complete cds//0.97:235:59//Hs.1701:L26405	R-Y79AA1001781//ESTs, Weakly similar to partial CDS [C.elegans]//9.4e-87:427:97//Hs.18645:AI023798
R-Y79AA1000774//ESTs//5.9e-109:559:95//Hs.17138:M91463	R-Y79AA1001805//ESTs//1.1e-112:558:97//Hs.109755:AA180809
R-Y79AA1000782//Human mRNA for KIAA0246 gene, partial cds//1.6e-18:107:100//Hs.84753:D87433	R-Y79AA1001827//ESTs, Weakly similar to Similar to S.cerevisiae YD9335.03c protein [H.sapiens]//8.1e-95:530:91//Hs.72444:W23217
R-Y79AA1000784//EST//0.80:87:67//Hs.158558:AI368359	R-Y79AA1001846//EST//2.8e-41:312:81//Hs.162236:AA551582
R-Y79AA1000794//ESTs//2.7e-99:498:96//Hs.25441:AA580512	R-Y79AA1001848//Human adhalin (DAG2) mRNA, complete cds//0.54:221:58//Hs.99931:L34355
R-Y79AA1000800//ESTs//1.2e-97:532:93//Hs.77822:AA532642	R-Y79AA1001866//ESTs//2.2e-102:498:97//Hs.130683:AI278630
R-Y79AA1000802//Carboxypeptidase E//0.018:354:59//Hs.75360:X51405	R-Y79AA1001874//ESTs//1.9e-76:377:98//Hs.79707:AA354094
R-Y79AA1000805	R-Y79AA1001875//ESTs//0.64:152:63//Hs.156159:AI333652
R-Y79AA1000824//ESTs//0.99:276:61//Hs.153992:AA280227	R-Y79AA1001923//EST//0.19:180:58//Hs.148290:AA908404
R-Y79AA1000827//ESTs//1.2e-55:326:92//Hs.158127:AI334650	R-Y79AA1002027//ESTs//1.6e-104:497:98//Hs.21275:N73275
R-Y79AA1000850//Homo sapiens small optic lobes homolog (SOLH) mRNA, complete cds//0.016:386:59//Hs.55836:U85647	R-Y79AA1002083//Homo sapiens mRNA for KIAA0563 protein, complete cds//0.69:93:73//Hs.15731:AB01135
R-Y79AA1000962//EST//0.024:177:63//Hs.25214:R37079	R-Y79AA1002089//Homo sapiens PYRIN (MEFV) mRNA, complete cds//1.1e-46:392:80//Hs.113283:AF018080
R-Y79AA1000968	R-Y79AA1002093//Homo sapiens GT198 mRNA, complete ORF//1.2e-12:80:100//Hs.78185:L38933
R-Y79AA1000969//ESTs//2.9e-70:251:98//Hs.120858:AA417181	R-Y79AA1002103//ESTs//1.3e-52:535:76//Hs.142167:AI417785
R-Y79AA1000976//ESTs//7.8e-56:299:95//Hs.120125:M86049	R-Y79AA1002115//ESTs//4.2e-101:519:96//Hs.23977:AA115275
R-Y79AA1000985	R-Y79AA1002125//ESTs//9.8e-68:363:94//Hs.72085:AA193399
R-Y79AA1001023//ESTs//5.7e-66:379:90//Hs.64616:W22851	R-Y79AA1002139//ESTs//1.2e-100:498:96//Hs.72020:AA149858
R-Y79AA1001041//ESTs//8.6e-06:54:100//Hs.8980:AA629067	R-Y79AA1002204//ESTs//2.1e-83:434:95//Hs.22979:R43725
R-Y79AA1001048//ESTs//4.4e-97:461:99//Hs.7010:AA837407	R-Y79AA1002208//ESTs//1.7e-55:478:76//Hs.154554:AA552715
R-Y79AA1001061//ESTs//3.8e-105:493:99//Hs.128419:AI271325	R-Y79AA1002209//ESTs, Weakly similar to similar to tyrosyl-tRNA synthetase. [C.elegans]//3.5e-108:553:95//Hs.50441:AA747428
R-Y79AA1001068//Homo sapiens mRNA for KIAA0563 protein, complete cds//4.8e-53:279:83//Hs.15731:AB01135	R-Y79AA1002210//ESTs//4.2e-16:92:100//Hs.54862:AA248349
R-Y79AA1001077//ESTs//1.9e-51:339:87//Hs.11197:AA309047	R-Y79AA1002211//ESTs, Weakly similar to PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN [H.sapiens]//6.5e-86:518:90//Hs.25682:AA857843
R-Y79AA1001078//ESTs//8.3e-98:528:92//Hs.24608:AA161260	R-Y79AA1002220//EST//1.3e-68:326:100//Hs.131052:AI016274
R-Y79AA1001105//ESTs//6.0e-77:393:96//Hs.30837:H08155	R-Y79AA1002229//ESTs//1.9e-98:467:98//Hs.132002:AI039977
R-Y79AA1001145//ESTs//1.7e-13:285:64//Hs.128259:AA343015	R-Y79AA1002234//Homo sapiens mRNA for KIAA0692 protein, partial cds//2.0e-118:564:98//Hs.100729:AB014592
R-Y79AA1001167	R-Y79AA1002246//ESTs, Weakly similar to PROTEIN KINASE C, BRAIN ISOTYPE [D.melanogaster]//9.0e-102:507:96//Hs.25895:AI341537
R-Y79AA1001177//EST//1.2e-05:92:76//Hs.65277:T15884	R-Y79AA1002258//Homo sapiens mRNA for KIAA0655 protein, partial cds//2.4e-93:453:97//Hs.96731:AB014555
R-Y79AA1001185	R-Y79AA1002298//ESTs//0.022:241:62//Hs.118272:N90288
R-Y79AA1001211//ESTs//1.3e-70:344:97//Hs.49760:AA741051	R-Y79AA1002307//Homo sapiens mRNA for KIAA0634 protein, partial cds//8.1e-110:403:99//Hs.30898:AB014534
R-Y79AA1001216//ESTs//5.8e-63:416:88//Hs.8595:W60933	R-Y79AA1002311//EST//2.6e-27:214:85//Hs.144721:AI187985
R-Y79AA1001228//ESTs//9.3e-101:483:98//Hs.13916:AI025750	R-Y79AA1002351//ESTs//5.6e-100:489:97//Hs.30318:AA913371
R-Y79AA1001233//EST//0.00027:232:62//Hs.132431:AA909674	R-Y79AA1002361
R-Y79AA1001236//Homo sapiens mRNA for JM23 protein, complete coding sequence (clone IMAGE 34581 and IMAGE 45355 and LLNLc110113397 (RZPD Berlin))//1.1e-110:549:95//Hs.23170:AJ005892	R-Y79AA1002399//ESTs//0.029:149:65//Hs.43872:N26908
R-Y79AA1001281//ESTs//3.6e-98:466:99//Hs.104442:AA481271	R-Y79AA1002407//ESTs//2.8e-117:552:99//Hs.99519:AI042000
R-Y79AA1001299//Human Inil mRNA, complete cds//9.6e-25:133:100//Hs.155626:U04847	
R-Y79AA1001312//ESTs//3.4e-92:454:97//Hs.127319:AI191149	

【0941】

【表639】

R-Y79AA1002416//ESTs//2.6e-107:531:96//Hs.6716:AA502753
 R-Y79AA1002431//EST//6.6e-23:128:98//Hs.128417:AA975026
 R-Y79AA1002433//ESTs, Highly similar to CELL DIVISION CONTROL PRO
 TEIN 68 [Saccharomyces cerevisiae]//4.4e-62:390:88//Hs.143930:AI20
 7821
 R-Y79AA1002472//ESTs//1.1e-39:234:78//Hs.117969:H94870
 R-Y79AA1002482//ESTs//3.4e-45:312:85//Hs.146811:AA410788
 R-Y79AA1002487//ESTs//1.7e-80:427:94//Hs.49210:H66499

【0942】

全長塩基配列及び推定アミノ酸配列に対する相同性検索結果データ。ただし、タンパク質コード領域の推定が困難であったものや、推定アミノ酸配列が100アミノ酸残基未満であったものについてはアミノ酸配列を示していない。以下に示す検索結果には、比較配列の長さの単位にaaとbpが混在している。

各データは、配列名、ヒットデータのDefinition、P値、比較配列の長さ、相同性、ヒットデータのAccession No.の順に//で区切って記載した。

【0943】

【表640】

C-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.9E-250//554aa//85%//Q61712
 C-HEMBA1000030
 C-HEMBA1000046
 C-HEMBA1000050
 C-HEMBA1000076
 C-HEMBA1000156//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//1.9E-12//368aa//24%//P08553
 C-HEMBA1000158//HEPATOCTE NUCLEAR FACTOR 3-GAMMA (HNF-3G).//5E-16//166aa//36%//P35584
 C-HEMBA1000168//CYLICIN 1 (MULTIPLE-BAND POLYPEPTIDE 1).//2.9E-14//303aa//25%//P35662
 C-HEMBA1000185//RAS-RELATED PROTEIN RAL-A.//3.4E-12//125aa//31%//P48555
 C-HEMBA1000193
 C-HEMBA1000227
 C-HEMBA1000288
 C-HEMBA1000302
 C-HEMBA1000304
 C-HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1//5.2E-49//107aa//91%//O35594
 C-HEMBA1000369//Novel human mRNA similar to mouse gene PICK1 (TR:Q62083).//0//1950bp//98%//AL049654
 C-HEMBA1000387
 C-HEMBA1000392
 C-HEMBA1000460
 C-HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).//3.3E-45//481aa//29%//Q04652
 C-HEMBA1000491//RAS-LIKE PROTEIN 2.//2E-22//188aa//31%//P22279
 C-HEMBA1000501
 C-HEMBA1000508
 C-HEMBA1000520
 C-HEMBA1000531//HEAT SHOCK 70 KD PROTEIN COGNATE 1 (HEAT SHOCK 70 KD PROTEIN 70C) (FRAGMENTS).//2.6E-12//73aa//41%//P02826
 C-HEMBA1000534
 C-HEMBA1000555
 C-HEMBA1000568
 C-HEMBA1000588
 C-HEMBA1000608//HYPOTHETICAL PROTEIN KIAA0411 (FRAGMENT).//1.8E-55//179aa//61%//Q43295
 C-HEMBA1000636
 C-HEMBA1000682
 C-HEMBA1000686
 C-HEMBA1000719
 C-HEMBA1000727
 C-HEMBA1000752
 C-HEMBA1000817
 C-HEMBA1000851
 C-HEMBA1000867
 C-HEMBA1000869
 C-HEMBA1000872
 C-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-XP ANTIGEN).//1.6E-30//127aa//40%//P43366
 C-HEMBA1000918
 C-HEMBA1000919//HYPOTHETICAL 65.5 KD TRP-ASP REPEATS CONTAINING PROTEIN FOZEB.5 IN CHROMOSOME X.//1E-10//288aa//23%//Q19124
 C-HEMBA1000946
 C-HEMBA1000968
 C-HEMBA1000971
 C-HEMBA1000975
 C-HEMBA1001009
 C-HEMBA1001022
 C-HEMBA1001043//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NON ERYTHROID) (FRAGMENT).//1.4E-12//131aa//38%//Q01485
 C-HEMBA1001052
 C-HEMBA1001080
 C-HEMBA1001085
 C-HEMBA1001088//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//3.5E-50//176aa//57%//P48059
 C-HEMBA1001109
 C-HEMBA1001122
 C-HEMBA1001133
 C-HEMBA1001137//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN K0X3 1) (KIAA0065) (HA0946) (FRAGMENT).//1.5E-116//197aa//58%//Q06730
 C-HEMBA1001140
 C-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN S.//6.8E-79//179aa//80%//P51646
 C-HEMBA1001197//Homo sapiens mRNA for KIAA0871 protein, complete cds.//9.5E-257//1307bp//94%//AB020678
 C-HEMBA1001235
 C-HEMBA1001257//Homo sapiens mRNA 2-methylacyl-CoA racemase.//0//1672bp//99%//AJ130733
 C-HEMBA1001281
 C-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//0.0000002//198aa//29%//Q60401
 C-HEMBA1001303
 C-HEMBA1001310
 C-HEMBA1001326
 C-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VA P-33) mRNA, complete cds.//1.4E-133//614bp//99%//AF057358
 C-HEMBA1001387//GTP-BINDING PROTEIN TC10.//2.9E-64//104aa//82%//P17081
 C-HEMBA1001388
 C-HEMBA1001398
 C-HEMBA1001405
 C-HEMBA1001407
 C-HEMBA1001413
 C-HEMBA1001415
 C-HEMBA1001446
 C-HEMBA1001450
 C-HEMBA1001455
 C-HEMBA1001510//CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).//1.7E-16//63aa//61%//P18850
 C-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//4.9E-37//399aa//29%//P29166
 C-HEMBA1001533
 C-HEMBA1001579//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1662bp//99%//AB020657
 C-HEMBA1001581
 C-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//4.9E-156//348aa//83%//Q14141
 C-HEMBA1001635//TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSG A).//1.6E-10//155aa//28%//Q63679
 C-HEMBA1001661//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT P ROEIN).//4.6E-36//365aa//33%//P33450
 C-HEMBA1001702
 C-HEMBA1001714//Homo sapiens mRNA: cDNA DKFZp564G0422 (from clone DKFZp564G0422).//0//1845bp//99%//AL050386
 C-HEMBA1001731
 C-HEMBA1001744//SCY1 PROTEIN.//9.9E-32//481aa//25%//P53009
 C-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//3.8E-11//206aa//36%//P11675
 C-HEMBA1001815
 C-HEMBA1001819//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.9E-135//459aa//52%//Q99676
 C-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//7.6E-64//221aa//55%//Q07230
 C-HEMBA1001864
 C-HEMBA1001869//TRITHORAX PROTEIN.//0.000096//166aa//27%//P20659
 C-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.9.2) (ME2GLYDH).//9.3E-36//395aa//26%//Q63342
 C-HEMBA1001987
 C-HEMBA1002018
 C-HEMBA1002049
 C-HEMBA1002084
 C-HEMBA1002125
 C-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.4E-51//180aa//56%//P79293
 C-HEMBA1002177//TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).//6E-13//190aa//36%//P43694
 C-HEMBA1002191
 C-HEMBA1002199
 C-HEMBA1002212//TYROSINE-PROTEIN KINASE 2 (EC 2.7.1.112) (FRAGMENT).//3E-17//267aa//29%//P18161
 C-HEMBA1002237
 C-HEMBA1002265
 C-HEMBA1002267//Sus scrofa decorin mRNA, complete cds.//1.1E-46//302bp//90%//AF125537
 C-HEMBA1002349
 C-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//1847bp//99%//AF092563
 C-HEMBA1002419//TRICHOHYALIN.//1.9E-09//299aa//24%//P22793
 C-HEMBA1002430
 C-HEMBA1002439
 C-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.//4.2E-24//109aa//55%//Q00994
 C-HEMBA1002460
 C-HEMBA1002462
 C-HEMBA1002469//DXS8237E PROTEIN (FRAGMENT).//3.5E-50//199aa//61%//P98175

【0944】

【表641】

C-HEMBA1002475//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN). //1.1E-12//285aa//31%/P17437
 C-HEMBA1002477
 C-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1. //6.8E-53//257aa//36%/P48732
 C-HEMBA1002515
 C-HEMBA1002542
 C-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, complete cds. //6.8E-305//951bp//99%/AF075587
 C-HEMBA1002583
 C-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cds. //1.4E-253//1149bp//99%/AB011169
 C-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete cds. //0//1539bp//99%/AB018351
 C-HEMBA1002688
 C-HEMBA1002696
 C-HEMBA1002750
 C-HEMBA1002768//Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4). //1E-80//882bp//61%/AJ000414
 C-HEMBA1002770//Homo sapiens mRNA for KIAA0829 protein, partial cds. //0//1532bp//99%/AB020636
 C-HEMBA1002777
 C-HEMBA1002794
 C-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, complete cds. //8.2E-314//1437bp//99%/AF071185
 C-HEMBA1002818//Homo sapiens mRNA for fibulin-4. //2E-304//1383bp//99%/AJ132819
 C-HEMBA1002850
 C-HEMBA1002863
 C-HEMBA1002876//HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME 11. //1.5E-44//188aa//52%/Q09297
 C-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cds. //0//1483bp//100%/AB011148
 C-HEMBA1002937
 C-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKYRIN). //2E-34//300aa//34%/P16157
 C-HEMBA1002951//Homo sapiens mRNA for KIAA0903 protein, partial cds. //0//1752bp//99%/AB020710
 C-HEMBA1002954
 C-HEMBA1002971
 C-HEMBA1002973//CAMP-DEPENDENT 3', 5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1.4.17) (DPDE4). //1.2E-27//63aa//100%/P14646
 C-HEMBA1002997//CENTROMERIC PROTEIN E (CENP-E PROTEIN). //3.8E-25//534aa//24%/Q02224
 C-HEMBA1003033
 C-HEMBA1003035
 C-HEMBA1003041
 C-HEMBA1003046//MITOCHONDRIAL PROCESSING PROTEASE BETA SUBUNIT PRECURSOR (EC 3.4.24.64) (BETA-MPP) (P-52). //2.5E-263//489aa//99%/J075439
 C-HEMBA1003067
 C-HEMBA1003096
 C-HEMBA1003117
 C-HEMBA1003129
 C-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.13) (ATP-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPHOSPHORYLASE). //8.5E-51//221aa//33%/P41940
 C-HEMBA1003148//Homo sapiens mRNA full length insert cDNA clone EU ROIMAGE 381801. //0//1583bp//99%/AL079278
 C-HEMBA1003175
 C-HEMBA1003179//PROBABLE tRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLATE)-METHYLTRANSFERASE (EC 2.1.1.61). //5.9E-74//134aa//53%/P44551
 C-HEMBA1003199
 C-HEMBA1003222
 C-HEMBA1003235//TROPOMYOSIN. //0.000023//109aa//33%/Q02088
 C-HEMBA1003250//PROTEIN KINASE APK1A (EC 2.7.1.-). //7.2E-41//245aa//42%/Q06548
 C-HEMBA1003257
 C-HEMBA1003281//POLIOVIRUS RECEPTOR PRECURSOR. //6E-11//239aa//32%/P32506
 C-HEMBA1003286//Homo sapiens mRNA for beta-1,4-galactosyltransferase IV, complete cds. //5.4E-229//1043bp//99%/AB024436
 C-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete cds. //0//791bp//99%/AB011109
 C-HEMBA1003322
 C-HEMBA1003327
 C-HEMBA1003369//CENTROMERIC PROTEIN E (CENP-E PROTEIN). //0.0000002//248aa//23%/Q02224
 C-HEMBA1003370
 C-HEMBA1003380
 C-HEMBA1003395
 C-HEMBA1003402
 C-HEMBA1003408//Homo sapiens mRNA for KIAA0905 protein, complete cds. //0//1732bp//98%/AB020712
 C-HEMBA1003417//Homo sapiens mRNA: cDNA DKFZp586C021 (from clone D KFZp586C021). //1.6E-312//1414bp//99%/AL050287
 C-HEMBA1003418//TRICHOHYALIN. //8.7E-19//281aa//31%/P37709
 C-HEMBA1003433//Homo sapiens gene for NBS1, complete cds. //0//511bp//94%/AB013139
 C-HEMBA1003447
 C-HEMBA1003461
 C-HEMBA1003463
 C-HEMBA1003528
 C-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (ISLET-2). //8.8E-189//360aa//96%/P50480
 C-HEMBA1003555//NUCLEOTIDE-BINDING PROTEIN (NBP). //2.1E-68//251aa//52%/P53384
 C-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-2 SUBUNIT (G GAMMA-1). //1.2E-31//71aa//100%/P16874
 C-HEMBA1003568//52 KD RO PROTEIN (SJOGEREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)). //7.9E-49//279aa//32%/P19474
 C-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1. //6.9E-206//445aa//74%/Q13330
 C-HEMBA1003581//TALIN. //4.4E-45//52aa//98%/P26039
 C-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28RNP). //4.4E-10//118aa//35%/P19682
 C-HEMBA1003615
 C-HEMBA1003617//Homo sapiens HRHFB2157 mRNA, partial cds. //8.2E-178//501bp//97%/AB015344
 C-HEMBA1003621
 C-HEMBA1003662//TBX2 PROTEIN (T-BOX PROTEIN 2). //1.2E-75//151aa//99%/Q13207
 C-HEMBA1003690//HISTONE DEACETYLASE HDAC1. //2.1E-59//249aa//47%/P53973
 C-HEMBA1003711
 C-HEMBA1003807
 C-HEMBA1003864
 C-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 5B) (FRAGMENT). //3.8E-16//89aa//46%/P16372
 C-HEMBA1003959
 C-HEMBA1003989
 C-HEMBA1004074
 C-HEMBA1004097//Mus musculus putative transcription factor mRNA, complete cds. //8.5E-221//1188bp//78%/AF091234
 C-HEMBA1004146
 C-HEMBA1004199//Homo sapiens mRNA for KIAA0928 protein, partial cds. //0//1893bp//98%/AB023145
 C-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds. //0//1892bp//99%/U50748
 C-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, complete cds. //5.7E-217//1217bp//88%/AF095927
 C-HEMBA1004246
 C-HEMBA1004276//Homo sapiens AP-4 adaptor complex beta4 subunit mRNA, complete cds. //4.8E-257//738bp//99%/AF092094
 C-HEMBA1004289
 C-HEMBA1004509//Homo sapiens CGI-21 protein mRNA, complete cds. //0//1512bp//96%/AF132955
 C-HEMBA1004534//Homo sapiens gamma-filamin (ABPL) mRNA, complete cds. //1.2E-316//1445bp//99%/AF089841
 C-HEMBA1004596
 C-HEMBA1004693
 C-HEMBA1004736
 C-HEMBA1004753
 C-HEMBA1004756//Human transporter protein (g17) mRNA, complete cds. //9.1E-34//515bp//66%/U49082
 C-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, complete cds. //2.6E-246//1249bp//94%/L39060
 C-HEMBA1004763
 C-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG. //5.4E-111//314aa//58%/P08547
 C-HEMBA1004771
 C-HEMBA1004776
 C-HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT). //3.8E-69//198aa//66%/P50851
 C-HEMBA1004806
 C-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68). //8.2E-154//317aa//94%/Q00004
 C-HEMBA1004850
 C-HEMBA1004863//Homo sapiens mRNA: cDNA DKFZp586M2022 (from clone DKFZp586M2022). //0//1443bp//100%/AL080114

【0945】

【表642】

C-HEMBA1004923
 C-HEMBA1004929
 C-HEMBA1004930//265 PROTEASOME SUBUNIT 55B (K1AA0072) (HAI357).//3.3E-27//65aa//100%/Q16401
 C-HEMBA1004933
 C-HEMBA1004954
 C-HEMBA1004972//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//0.00000096//286aa//23%/P12036
 C-HEMBA1005475
 C-HEMBA1005581//Homo sapiens SLIT2 (SLIL2) mRNA, complete cds.//0//1721bp//100%/AF133270
 C-HEMBA1006248//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//8.6E-23//151aa//37%/P16372
 C-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1 a (PACS-1) mRNA, complete cds.//3.7E-22//1189bp//88%/AF076183
 C-HEMBA1006344//RADIXIN.//1.5E-31//333aa//28%/P26043
 C-HEMBA1006377
 C-HEMBA1006467
 C-HEMBA1006474//40 KD PROTEIN.//1.4E-39//292aa//34%/Q01552
 C-HEMBA1006530
 C-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NON ERYTHROID) (FRAGMENT).//0.00000043//111aa//40%/Q01485
 C-HEMBA1006795
 C-HEMBA1006877//OXYSTEROL-BINDING PROTEIN.//2E-59//378aa//39%/P16258
 C-HEMBA1006936
 C-HEMBA1007018//Homo sapiens dynein light chain-A mRNA, complete cds.//1.5E-26//1215bp//99%/AF078849
 C-HEMBA1007342
 C-HEMBA1008008
 C-HEMBA1008018
 C-HEMBA1008024
 C-HEMBA1008025
 C-HEMBA1008036
 C-HEMBA1008037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//2.8E-18//1582bp//80%/AF084928
 C-HEMBA1008083//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//1.9E-22//426aa//25%/P11799
 C-HEMBA1008103
 C-HEMBA1008119//Homo sapiens ASMTL gene.//0//1891bp//99%/Y15521
 C-HEMBA1008136
 C-HEMBA1008215
 C-HEMBA1008226//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE EEDB.5.//2.7E-12//112aa//47%/Q09530
 C-HEMBA1008244
 C-HEMBA1008265//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN ZC302.2 IN CHROMOSOME V.//6.1E-09//242aa//26%/Q23256
 C-HEMBA1008338
 C-HEMBA1008339
 C-HEMBA1008391
 C-HEMBA1008438
 C-HEMBA1008449
 C-HEMBA1008589
 C-HEMBA1008591
 C-HEMBA1008623
 C-HEMBA1008630
 C-HEMBA1008631//LONGEVITY-ASSURANCE PROTEIN 1 (LONGEVITY ASSURANCE FACTOR 1).//4.1E-19//232aa//28%/P78970
 C-HEMBA1008632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//2.2E-28//273aa//31%/P27671
 C-HEMBA1008671
 C-HEMBA1008673
 C-HEMBA1008705
 C-HEMBA1008706
 C-HEMBA1008725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//6.2E-13//692bp//93%/U53475
 C-HEMBA1008763//Homo sapiens CGI-89 protein mRNA, complete cds.//0//1676bp//96%/AF151847
 C-HEMBA1008781//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds.//1.2E-12//613bp//97%/AF111105
 C-HEMBA1008789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION.//5.1E-54//232aa//43%/P39956
 C-HEMBA1008807
 C-HEMBA1008810
 C-HEMBA1008848
 C-HEMBA1008852
 C-HEMBA1008870
 C-HEMBA1008887
 C-HEMBA1008908
 C-HEMBA1008927//Homo sapiens calsenilin mRNA, complete cds.//1.1E-70//595bp//76%/AF120102
 C-HEMBA1008947//Homo sapiens clone HAW100 putative ribonuclease III mRNA, complete cds.//0//2292bp//99%/AF116910
 C-HEMBA1008973//Mus musculus schlafen3 (Sln3) mRNA, complete cds.//3.4E-12//580bp//67%/AF099974
 C-HEMBA1008975
 C-HEMBA1008985//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//8.6E-18//178aa//30%/P28575
 C-HEMBA1008991
 C-HEMBA1009101//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.4E-73//230aa//45%/P51523
 C-HEMBA1009104
 C-HEMBA1009104
 C-HEMBA1009106//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120).//2.9E-19//264aa//34%/P46087
 C-HEMBA1009108//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds.//3.6E-52//331bp//80%/AF010144
 C-HEMBA1009108//Homo sapiens liprin-beta2 mRNA, partial cds.//2.4E-307//1447bp//97%/AF034803
 C-HEMBA10091096
 C-HEMBA10091105
 C-HEMBA1009117
 C-HEMBA1009116
 C-HEMBA1009137//Homo sapiens mRNA for putative phospholipase, complete cds.//0//3069bp//99%/AB019435
 C-HEMBA1009151//Rattus norvegicus golgi stacking protein homolog G RASP55 mRNA, complete cds.//4.2E-210//1835bp//76%/AF110267
 C-HEMBA1009153
 C-HEMBA1009169
 C-HEMBA1009175//ANKYRIN.//6.9E-11//169aa//31%/Q02357
 C-HEMBA1009182
 C-HEMBA1009199
 C-HEMBA1009210//Homo sapiens mRNA for KIAA0970 protein, complete cds.//0//1816bp//99%/AB023187
 C-HEMBA1009242//Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds.//1.8E-284//713bp//100%/AF089897
 C-HEMBA1009288//Homo sapiens CGI-32 protein mRNA, complete cds.//1.8E-274//642bp//99%/AF132966
 C-HEMBA1009289
 C-HEMBA1009294//GTP-BINDING PROTEIN TC10.//1.2E-79//196aa//80%/P17081
 C-HEMBA1009314//Mus musculus Dlf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//1.3E-129//724bp//86%/U92703
 C-HEMBA1009331
 C-HEMBA1009339//DXS8237E PROTEIN (FRAGMENT).//0.0000046//124aa//37%/P98175
 C-HEMBA1009345//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.1E-58//292bp//99%/AF097441
 C-HEMBA1009369
 C-HEMBA1009384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1586bp//99%/AF100757
 C-HEMBA1009387
 C-MAMMA1002317
 C-MAMMA1002319
 C-MAMMA1002385//RIBONUCLEOPROTEIN RB97D.//0.00000015//206aa//29%/Q02926
 C-NT2RM1000080//LINC-1 PROTEIN.//5.9E-25//211aa//31%/Q21190
 C-NT2RM1000242
 C-NT2RM1000257//MAGO NASHI PROTEIN.//7.9E-69//143aa//91%/P49028
 C-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V-ATPASE 28 KD ACCESSORY PROTEIN).//1.5E-106//118aa//97%/P39942
 C-NT2RM1000669
 C-NT2RM1000781
 C-NT2RM1000867//Homo sapiens HSPC033 mRNA, complete cds.//6.3E-172//798bp//99%/AF092138
 C-NT2RM1001008
 C-NT2RM1001044//Homo sapiens HSPC031 mRNA, complete cds.//0.00000002//980bp//95%/AF085360
 C-NT2RM1001074
 C-NT2RM1001115//ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14).//0.0000056//239aa//27%/P39942
 C-NT2RM2000006//Human DNA sequence from clone 796F18 on chromosome 1p36.11-36.33 Contains a pseudogene similar to NM52. ESTs and GSSs, complete sequence.//0//1740bp//99%/AL031291
 C-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE

【0946】

【表643】

(EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2). //2.2E-144//362aa//71%//P25167	7E-53//266aa//43%//P41877
C-NT2RM2000030//DYNEIN INTERMEDIATE CHAIN, CYTOSOLIC (DH IC) (CYTOPLASMIC DYNEIN INTERMEDIATE CHAIN). //0.00000043//136aa//31%//P54703	C-NT2RM2000795
C-NT2RM2000032	C-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-CO P). //9.5E-279//545aa//98%//P23514
C-NT2RM2000042	C-NT2RM2000837
C-NT2RM2000092//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8). //1.3E-36//160aa//40%//P50102	C-NT2RM2000951//Homo sapiens XYLB mRNA for xylulokinase, complete cds. //1.7E-200//927bp//99%//AB015046
C-NT2RM2000093	C-NT2RM2000952
C-NT2RM2000101	C-NT2RM2000984
C-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds. //0//1574bp//99%//AF067223	C-NT2RM2001004
C-NT2RM2000192	C-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1). //8.2E-154//285aa//99%//Q60809
C-NT2RM2000239	C-NT2RM2001065
C-NT2RM2000250//Homo sapiens mRNA: cDNA DKFZp564L232 (from clone D KFP564L232). //4.2E-314//1416bp//100%//AL080069	C-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOM E III. //2.4E-15//266aa//26%//P46577
C-NT2RM2000259	C-NT2RM2001131
C-NT2RM2000260//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN). //3.6E-19//181aa//34%//P14918	C-NT2RM2001141
C-NT2RM2000287	C-NT2RM2001152
C-NT2RM2000322//Homo sapiens mRNA for KIAA0859 protein, complete cds. //3.4E-294//863bp//99%//AB020666	C-NT2RM2001177//Homo sapiens mRNA: cDNA DKFZp586G1822 (from clone DKFZp586G1822). //2.1E-293//1335bp//99%//AL080109
C-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds. //0//1637bp//99%//AB011132	C-NT2RM2001194
C-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN. //1.8E-14//245aa//29%//P11274	C-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT). //1.3E-20//267aa//35%//P05143
C-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK 7 mRNA, partial cds. //0//1506bp//99%//U48251	C-NT2RM2001201//EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5). //0.0000015//95aa//35%//P48724
C-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLEOTIDE//1.7E-68//419aa//36%//P50849	C-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10). //3.6E-10//177aa//32%//P97924
C-NT2RM2000374	C-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMIDHYDROLASE). //1.3E-180//328aa//99%//P13264
C-NT2RM2000395	C-NT2RM2001243
C-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LAT E ENDOCYTIC INTERMEDIATE COMPONENT). //1.6E-54//344aa//33%//P32802	C-NT2RM2001247
C-NT2RM2000407	C-NT2RM2001256//PROTEIN TSG24 (MEIOTIC CHECK-POINT REGULATOR). //1.6E-166//312aa//98%//P53995
C-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73. //1E-222//237aa//89%//Q0469	C-NT2RM2001291
C-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION. //0.000001//157aa//28%//P36113	C-NT2RM2001306//Homo sapiens mRNA: cDNA DKFZp564I052 (from clone D KFP564I052). //0//1694bp//99%//AL080063
C-NT2RM2000469//NITROGEN PERMEASE REACTIVATOR PROTEIN (EC 2.7.1.-). //0.0000089//377aa//24%//P22211	C-NT2RM2001312
C-NT2RM2000490//SYNAPTOTAGMIN (P65). //1.8E-13//166aa//34%//P41823	C-NT2RM2001319
C-NT2RM2000502	C-NT2RM2001324//ZYXIN. //6.8E-55//200aa//41%//Q04584
C-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds. //0//1673bp//99%//AF061243	C-NT2RM2001345//VEGETATILE INCOMPATIBILITY PROTEIN MET-E-1. //0.0000029//334aa//22%//Q00808
C-NT2RM2000522//SKIN SECRETORY PROTEIN IP2 PRECURSOR (APEG PROTEIN). //1.3E-12//282aa//32%//P17437	C-NT2RM2001370
C-NT2RM2000540	C-NT2RM2001393
C-NT2RM2000567	C-NT2RM2001420
C-NT2RM2000569	C-NT2RM2001424//Homo sapiens mRNA: cDNA DKFZp586D0920 (from clone DKFZp586D0920). //0//1621bp//100%//AL050146
C-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCIN E-TRNA LIGASE) (ILERS). //1.7E-187//741aa//46%//P73505	C-NT2RM2001499//LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2). //7.4E-121//437aa//57%//P52569
C-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds. //0//3001bp//99%//D86987	C-NT2RM2001504
C-NT2RM2000588//HISTONE DEACETYLASE HDAC1. //2.8E-60//384aa//40%//P53973	C-NT2RM2001524
C-NT2RM2000594//Homo sapiens DNA cytosine-5 methyltransferase 3 beta 3 (DNMT3B) mRNA, complete cds. //0//2712bp//99%//AF156487	C-NT2RM2001544
C-NT2RM2000599//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds. //4.9E-70//838bp//69%//AF179221	C-NT2RM2001547//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1). //6.9E-27//90aa//42%//P38660
C-NT2RM2000624//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75). //4.4E-32//319aa//35%//Q08170	C-NT2RM2001575//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)). //4.3E-61//312aa//44%//P19474
C-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds. //0//3791bp//99%//AB018272	C-NT2RM2001582
C-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds. //0//2530bp//99%//AB014558	C-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds. //0//1000bp//100%//AB014610
C-NT2RM2000639	C-NT2RM2001896//CELL DIVISION PROTEIN FTSJ. //5.1E-26//204aa//34%//P28592
C-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds. //0//1543bp//99%//AB014576	C-NT2RM2001903//Homo sapiens mRNA for KIAA0462 protein, partial cds. //0//2390bp//99%//AB007931
C-NT2RM2000669	C-NT2RM2001930
C-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2). //3.7E-142//285aa//90%//P32391	C-NT2RM2001935
C-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1). //3.8E-23//184aa//36%//Q15404	C-NT2RM2001936//32.3 KD PROTEIN IN CWPI-MBRI INTERGENIC REGION. //2.7E-27//216aa//34%//P28320
C-NT2RM2000718//Homo sapiens HRHF82436 mRNA, partial cds. //4.4E-231//1065bp//99%//AB015342	C-NT2RM2001950//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION. //0.0000001//212aa//23%//P38250
C-NT2RM2000740//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L. //5.	C-NT2RM2001982
	C-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77). //1.9E-39//253aa//35%//P37838
	C-NT2RM2001997//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PD1) (EC 5.3.4.1). //1.3E-10//232aa//28%//Q12730
	C-NT2RM2001998//HYPOTHETICAL 85.7 KD PROTEIN IN C13G6.03 IN CHROMOSOM E I. //3.1E-12//206aa//30%//Q09782
	C-NT2RM2002004//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTOANTIGEN HOMOLOG). //0.00000029//83aa//44%//P40796
	C-NT2RM2002014//HYPOTHETICAL 81.4 KD PROTEIN IN GREB-FE0A INTERGENIC REGION. //1.1E-89//425aa//41%//P46837
	C-NT2RM2002030//Homo sapiens mRNA for Glutamine:fructose-6-phospha

【0947】

【表644】

te amidotransferase, complete cds.//0//1959bp//99%/AB016789	C-NT2RP1000191
C-NT2RM2002049	C-NT2RP1000202//ANKYRIN.//1E-25//302aa//34%/Q02357
C-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.//0.0000099//338aa//24%/Q07878	C-NT2RP1000243
C-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//5E-62//104aa//57%/Q61990	C-NT2RP1000259
C-NT2RM2002091	C-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//5.8E-114//616bp//93%/AF067730
C-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//0//1807bp//99%/AJ010840	C-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.3E-275//1249bp//99%/AF053551
C-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//0//1868bp//99%/AF030435	C-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//8.7E-47//155aa//58%/P32447
C-NT2RM2002128//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//4.9E-13//487aa//26%/P49695	C-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.7E-15//162aa//30%/P25343
C-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.//8E-31//105aa//47%/P47805	C-NT2RP1000357
C-NT2RM2002178//Homo sapiens mRNA: cDNA DKFZp434E0335 (from clone DKFZp434E0335).//0//1683bp//99%/AL117402	C-NT2RP1000376//Homo sapiens mRNA: cDNA DKFZp434A102 (from clone D KFZp434A102).//0//2265bp//95%/AL080187
C-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//7.1E-155//381aa//72%/P25167	C-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds.//0//1056bp//99%/AB011159
C-NT2RM4000061	C-NT2RP1000416
C-NT2RM4000104//ZINC FINGER PROTEIN 135.//1.5E-81//251aa//53%/P52742	C-NT2RP1000439//Xenopus laevis chromosome condensation protein XCA P-G mRNA, complete cds.//1.8E-94//1019bp//63%/AF111423
C-NT2RM4000139//R.norvegicus trg mRNA.//2.3E-114//1161bp//72%/X68101	C-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN).//2.4E-10//227aa//25%/Q08257
C-NT2RM4000169//INTRACELLULAR PROTEIN TRANSPORT PROTEIN US01.//4.8E-13//686aa//23%/P25386	C-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME III.//2.6E-94//254aa//47%/P34580
C-NT2RM4000191//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.//9.2E-75//439aa//41%/P16381	C-NT2RP1000478//TUBULIN BETA-5 CHAIN (CLASS-V).//4.5E-240//445aa//97%/P09653
C-NT2RM4000197	C-NT2RP1000481
C-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//0//1926bp//100%/AB018255	C-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds.//0//2728bp//99%/D87686
C-NT2RM4000229//Gallus gallus actin filament-associated protein (AFAP-110) mRNA, complete cds.//1.1E-27//633bp//64%/L20303	C-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.1E-27//193aa//35%/P49020
C-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//2.2E-276//1124bp//97%/M99438	C-NT2RP1000574//HOMEBOX PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//3.5E-75//151aa//94%/P97367
C-NT2RM4000344//Homo sapiens mRNA for ATP-dependent metalloprotease YME1L.//0//2030bp//99%/AJ132637	C-NT2RP1000581
C-NT2RM4000349//Homo sapiens HSPC028 mRNA, complete cds.//0//1827bp//99%/AF083246	C-NT2RP1000630//NECDIN.//2.4E-44//227aa//41%/P25233
C-NT2RM4000354//LETHAL(2) DENTICLELESS PROTEIN (DTL83 PROTEIN).//1.5E-21//208aa//35%/Q24371	C-NT2RP1000688
C-NT2RM4000386//Mus musculus mRNA for Ten-m3, complete cds.//0//2156bp//86%/AB025412	C-NT2RP1000695
C-NT2RM4000395	C-NT2RP1000733//Human mRNA for GSPT1-TK protein, complete cds.//0//2057bp//99%/E14379
C-NT2RM4000421//Homo sapiens mRNA for nuclear transport receptor.//0//1730bp//99%/AJ133769	C-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds.//0//2186bp//99%/AF101434
C-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME 1.//8E-20//393aa//24%/Q10297	C-NT2RP1000782//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%/Q35566
C-NT2RM4000471//Homo sapiens cysteine desulfurase (nifs) mRNA, complete cds.//0//2092bp//99%/AF097025	C-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//8.2E-83//334aa//50%/Q07960
C-NT2RM4000485//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE 18-6: PEPTIDE P-H].//4.8E-11//242aa//31%/P04280	C-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1494bp//99%/AF067223
C-NT2RM4000496//SAPI PROTEIN.//8.3E-53//434aa//29%/P39955	C-NT2RP1000846
C-NT2RM4000511	C-NT2RP1000851
C-NT2RM4000515//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H) (FRAGMENT).//1.1E-11//394aa//24%/P16884	C-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%/Q35566
C-NT2RM4000520	C-NT2RP1000915//AUTOANTIGEN NGP-1.//1.7E-19//343aa//25%/Q13823
C-NT2RM4000585	C-NT2RP1000947//Human E2 ubiquitin conjugating enzyme Ubch5B (UBCH5B) mRNA, complete cds.//4.6E-105//504bp//99%/U39317
C-NT2RM4000595//Homo sapiens leucine-rich repeats containing F-box protein FBL3 mRNA, complete cds.//1.1E-285//1293bp//99%/AF186273	C-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//1.4E-23//370aa//28%/Q04652
C-NT2RP1000018//Homo sapiens mRNA for KIAA0587 protein, partial cds.//0//1940bp//95%/AB014587	C-NT2RP1000958//AUTOANTIGEN NGP-1.//1.4E-19//343aa//25%/Q13823
C-NT2RP1000035//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%/AB020657	C-NT2RP1000959//Human acidic ribosomal phosphoprotein P0 mRNA, complete cds.//2.5E-236//966bp//99%/M17885
C-NT2RP1000040	C-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//8.9E-299//554aa//99%/P19338
C-NT2RP1000063	C-NT2RP1000980
C-NT2RP1000086//H. sapiens mRNA for zinc finger protein, Hsa12.//0//1162bp//99%/X98834	C-NT2RP1000988
C-NT2RP1000101	C-NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (T H1) mRNA, complete cds.//2.2E-78//1529bp//61%/L01790
C-NT2RP1000111//COP1 REGULATORY PROTEIN.//4E-116//296aa//51%/P93471	C-NT2RP1001014
C-NT2RP1000112	C-NT2RP1001395
C-NT2RP1000124	C-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//8.9E-141//396aa//67%/P91917
C-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//4.5E-50//181aa//60%/P51859	C-NT2RP1001424
C-NT2RP1000163//Homo sapiens mRNA for KIAA0948 protein, complete cds.//0//1889bp//98%/AB023165	C-NT2RP1001449
C-NT2RP1000170	C-NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative).//1.2E-137//629bp//100%/AJ005257
	C-NT2RP1001466
	C-NT2RP1001475
	C-NT2RP1001482

【0948】

【表645】

C-NT2RP1001494//MALE STERILITY PROTEIN 2.//7.2E-40//261aa//27%/Q08891	mRNA, complete cds.//0//1757bp//99%/AF102265
C-NT2RP1001543//MYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IP S).//1.6E-166//506aa//60%/P42803	C-NT2RP2000438
C-NT2RP1001548//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.6E-30//232aa//30%/Q35566	C-NT2RP2000448//KESI PROTEIN.//8.7E-54//392aa//38%/P35844
C-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA).//5.8E-121//271aa//89%/P47758	C-NT2RP2000503
C-NT2RP1001616	C-NT2RP2000510
C-NT2RP1001665//CALMODULIN.//0.0000051//83aa//30%/P02594	C-NT2RP2000516
C-NT2RP2000006//DNAJ PROTEIN (40 KD HEAT SHOCK CHAPERONE PROTEIN) (HSP40).//9.8E-17//79aa//55%/Q34136	C-NT2RP2000603
C-NT2RP2000007	C-NT2RP2000617
C-NT2RP2000008//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.4E-177//726aa//47%/P51523	C-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cds.//0//2482bp//99%/AB014514
C-NT2RP2000032//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//1.8E-22//184aa//34%/Q01730	C-NT2RP2000656
C-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) (mRNA, complete cds.//0//1390bp//98%/AF061749	C-NT2RP2000658
C-NT2RP2000054	C-NT2RP2000668//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.3E-27//349aa//32%/Q01577
C-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP- EPSILON).//9.4E-16//45aa//100%/P49446	C-NT2RP2000704
C-NT2RP2000067	C-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE).//2.7E-100//488aa//44%/Q32038
C-NT2RP2000070//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT P ROTEIN).//3.4E-51//383aa//32%/P33450	C-NT2RP2000764//NIFS PROTEIN.//6.6E-36//252aa//42%/P12623
C-NT2RP2000079	C-NT2RP2000809//Homo sapiens mRNA for KIAA0873 protein, partial cds.//0//3347bp//99%/AB020680
C-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cds.//0//2286bp//100%/AB018338	C-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//0.00000056//179aa//29%/Q99104
C-NT2RP2000091	C-NT2RP2000814//GELATION FACTOR (ACTIN BINDING PROTEIN 120) (ABP-1 20).//0.0000011//96aa//29%/P13466
C-NT2RP2000097	C-NT2RP2000816//MAGNESIUM-CHELATASE 30 KD SUBUNIT.//0.00000079//172aa//28%/P26174
C-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//0//2244bp//99%/AB018356	C-NT2RP2000819
C-NT2RP2000120	C-NT2RP2000841
C-NT2RP2000126//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SMF2L.//2.5E-117//541aa//42%/P41877	C-NT2RP2000845
C-NT2RP2000133//Homo sapiens mRNA for KIAA0989 protein, partial cds.//0//2286bp//99%/AB023206	C-NT2RP2000863
C-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN).//4.4E-226//423aa//99%/P35585	C-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2.//0//694aa//99%/Q05041
C-NT2RP2000153//GAR2 PROTEIN.//9.8E-23//311aa//28%/P41891	C-NT2RP2000892
C-NT2RP2000157//ML02 PROTEIN.//2.6E-11//62aa//40%/Q09329	C-NT2RP2000931//MATRIN 3.//2.4E-289//467aa//95%/P43244
C-NT2RP2000161//Homo sapiens mRNA for KIAA1008 protein, complete cds.//3.4E-315//1430bp//99%/AB023225	C-NT2RP2000932//Homo sapiens mRNA: cDNA DKFZp5640043 (from clone D KFZp5640043).//0//2487bp//99%/AL050390
C-NT2RP2000173	C-NT2RP2000938
C-NT2RP2000175	C-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete cds.//0//3458bp//99%/AB018298
C-NT2RP2000195	C-NT2RP2000965//Homo sapiens mRNA for fls353, complete cds.//0//1989bp//96%/AB024704
C-NT2RP2000205	C-NT2RP2000985
C-NT2RP2000208//Homo sapiens mRNA for KIAA0892 protein, partial cds.//0//2898bp//99%/AB020699	C-NT2RP2001036
C-NT2RP2000224//INSULIN RECEPTOR SUBSTRATE-1 (IRS-1).//0.000043//103aa//28%/P35568	C-NT2RP2001044
C-NT2RP2000232	C-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcript KIAA0488.//0//2749bp//99%/AB007957
C-NT2RP2000233	C-NT2RP2001065
C-NT2RP2000239	C-NT2RP2001070//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PNP/PNP OXIDASE).//5.8E-46//222aa//45%/Q20939
C-NT2RP2000248//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P 110 SUBUNIT).//3.4E-21//210aa//33%/P56558	C-NT2RP2001081//SYNAPTOTAGMIN IV.//4.2E-118//430aa//54%/P50232
C-NT2RP2000270	C-NT2RP2001094
C-NT2RP2000274	C-NT2RP2001119
C-NT2RP2000283	C-NT2RP2001127//Homo sapiens mRNA for PLU-1 protein.//0//2514bp//99%/AJ132440
C-NT2RP2000288//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMO SOME 1.//1.6E-27//576aa//25%/Q10297	C-NT2RP2001218
C-NT2RP2000297//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.3E-186//256aa//60%/Q99676	C-NT2RP2001245//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEAVY CHAIN) (NMHC).//2.2E-10//366aa//28%/P14105
C-NT2RP2000298	C-NT2RP2001381
C-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PRODH) mRNA, complete cds.//4.3E-279//1193bp//99%/U82381	C-NT2RP2001397//Homo sapiens mRNA: cDNA DKFZp434B174 (from clone D KFZp434B174).//0//1495bp//100%/AL080146
C-NT2RP2000328	C-NT2RP2001427
C-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//226aa//92%/P08760	C-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cds.//0//1748bp//99%/AB018340
C-NT2RP2000346//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN MYD116.//6.3E-115//674aa//46%/P17564	C-NT2RP2001675
C-NT2RP2000369	C-NT2RP2001721
C-NT2RP2000412	C-NT2RP2001907
C-NT2RP2000414//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F).//4.3E-228//415aa//100%/P52597	C-NT2RP2001969
C-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase	C-NT2RP2001976//Mus musculus calmodulin-binding protein SHA1 (Sha1) mRNA, complete cds.//4.7E-177//1538bp//74%/AF062378
	C-NT2RP2002046
	C-NT2RP2002154
	C-NT2RP2002208
	C-NT2RP2002270//AF-9 PROTEIN.//0.0000012//74aa//36%/P42568
	C-NT2RP2002312//Homo sapiens mRNA for CDS2 protein.//0//2333bp//99%/Y16521
	C-NT2RP2002325//Homo sapiens mRNA for Pexllp, complete cds.//8.4E-254//1158bp//99%/AB015594
	C-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced variant mRNA, complete cds.//4.3E-240//1105bp//99%/AF038958
	C-NT2RP2002426

【0949】

【表646】

C-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, complete cds.//0//2180bp//99%/AB005289	C-NT2RP2004802
C-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN BD416.5 IN CHROMOSOME X.//6.2E-19//288aa//26%/Q11073	C-NT2RP2004841
C-NT2RP2002595//PROBABLE CALCIUM-BINDING PROTEIN ALC-2 (PMP41) (ALG-257).//7.5E-35//181aa//42%/P12815	C-NT2RP2004936
C-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.-).//1.7E-51//326aa//38%/P55345	C-NT2RP2004959//P54 PROTEIN PRECURSOR.//0.00000095//297aa//20%/P13692
C-NT2RP2002621	C-NT2RP2004999
C-NT2RP2002672	C-NT2RP2005000
C-NT2RP2002701//HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME 11.//1.9E-14//210aa//30%/D14345	C-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//0//1694bp//99%/AB014515
C-NT2RP2002769	C-NT2RP2005012//Homo sapiens mRNA for SEC63 protein.//0//1693bp//99%/AJ011779
C-NT2RP2002862//60S ACIDIC RIBOSOMAL PROTEIN P0 (LIGHT-INDUCED 34 KD PROTEIN).//8.8E-10//203aa//27%/P29764	C-NT2RP2005037//ANTI-SILENCING PROTEIN 1.//3.3E-47//155aa//59%/P32447
C-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA. complete cds.//1.9E-136//623bp//100%/AF038392	C-NT2RP2005126//H. sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//0//2388bp//98%/X98743
C-NT2RP2002954	C-NT2RP2005140
C-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//4.6E-80//147aa//100%/P51669	C-NT2RP2005147
C-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//0.00000001//98aa//36%/P10129	C-NT2RP2005159
C-NT2RP2002985//Homo sapiens mRNA for Kelch motif containing protein, complete cds.//0//2209bp//99%/AB026190	C-NT2RP2005239//Homo sapiens cysteine desulfurase (nifs) mRNA, complete cds.//0//2087bp//99%/AF097025
C-NT2RP2003108	C-NT2RP2005270
C-NT2RP2003117	C-NT2RP2005276//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2122bp//99%/D89053
C-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//2.3E-82//642bp//68%/AF079765	C-NT2RP2005293
C-NT2RP2003125//RING CANAL PROTEIN (KELCH PROTEIN).//2.4E-38//539aa//25%/Q04652	C-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1515bp//99%/AB014576
C-NT2RP2003177	C-NT2RP2005358//Homo sapiens methyl-CoG binding domain-containing protein MBD3 (MBD3) mRNA, complete cds.//0//2199bp//99%/AF072247
C-NT2RP2003194	C-NT2RP2005393//AUTOANTIGEN NGP-1.//7.2E-39//224aa//35%/Q13823
C-NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.//0//1580bp//99%/AF151811	C-NT2RP2005436//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.2E-13//185aa//38%/Q08170
C-NT2RP2003295//Homo sapiens RNP mRNA for RPB5 mediating protein, complete cds.//0//1526bp//99%/AB006572	C-NT2RP2005441
C-NT2RP2003329//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.//3.6E-14//332aa//32%/P26337	C-NT2RP2005453
C-NT2RP2003367	C-NT2RP2005464
C-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//5E-131//269aa//91%/P38378	C-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2.//3E-44//252aa//41%/P38127
C-NT2RP2003446	C-NT2RP2005472
C-NT2RP2003533	C-NT2RP2005495
C-NT2RP2003543//HYPOTHETICAL tRNA/tRNA METHYLTRANSFERASE SLR1673 (EC 2.1.1.-).//1.7E-17//148aa//34%/P74261	C-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55).//5.2E-81//166aa//88%/P36876
C-NT2RP2003596	C-NT2RP2005509//Homo sapiens CGI-45 protein mRNA, complete cds.//0//1825bp//99%/AF151803
C-NT2RP2003629	C-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//3994bp//99%/AF092563
C-NT2RP2003687	C-NT2RP2005525//Mus musculus kanadaplin mRNA, complete cds.//2.4E-304//1687bp//85%/AF035526
C-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//5.4E-29//85aa//72%/Q05481	C-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//0//2856bp//99%/AB007963
C-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//1.7E-75//147aa//93%/P51669	C-NT2RP2005549//PUTATIVE LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXAL LYASE).//2E-20//181aa//36%/Q39366
C-NT2RP2003793	C-NT2RP2005555
C-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//1.5E-23//200aa//30%/Q09175	C-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds.//1E-46//576bp//70%/AF062529
C-NT2RP2003986	C-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//8.9E-313//1455bp//98%/AF062085
C-NT2RP2004042	C-NT2RP2005622
C-NT2RP2004316//Homo sapiens chromosome 1 clone J549L20, WORKING DRAFT SEQUENCE, in unordered pieces.//8.2E-202//926bp//100%/AL096820	C-NT2RP2005635//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).//1E-11//128aa//36%/P47623
C-NT2RP2004389//PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR.//9.3E-15//126aa//39%/P38120	C-NT2RP2005637
C-NT2RP2004392//tRNA PROTEIN.//1.4E-11//143aa//27%/P36044	C-NT2RP2005640
C-NT2RP2004463	C-NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).//1.2E-13//74aa//45%/P56101
C-NT2RP2004602	C-NT2RP2005669//Homo sapiens mRNA for DEDD protein.//3.9E-209//957bp//99%/AJ010973
C-NT2RP2004614//Homo sapiens mRNA for KIAA0922 protein, partial cds.//0//2040bp//99%/AB023139	C-NT2RP2005675//Homo sapiens growth suppressor related (DCC-1R) mRNA, complete cds.//4.4E-200//908bp//99%/AF089814
C-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//8.5E-233//1061bp//99%/AJ006291	C-NT2RP2005683
C-NT2RP2004689//HYPOTHETICAL 192.5 KD PROTEIN C6G9.10C IN CHROMOSOME 1.//5.6E-64//616aa//33%/Q92355	C-NT2RP2005690
C-NT2RP2004791//PUTATIVE LEUCYL-tRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.4) (LEUCINE--tRNA LIGASE) (LEURS).//9.5E-73//153aa//59%/Q10490	C-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//0//1684bp//99%/AB018342
C-NT2RP2004799//PROBABLE SUCCINYL-CoA LIGASE (GDP-FORMING), BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUCCINYL-CoA SYNTHETASE, BETA CHAIN) (SCS-BETA).//3.7E-135//414aa//62%/P53588	C-NT2RP2005723//HNRNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (DOP1 PROTEIN).//0.000000003//169aa//28%/P38074
	C-NT2RP2005748
	C-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//0//1968bp//99%/AF068868
	C-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA.

【0950】

【表647】

complete cds.//0//1966bp//99%/AF082516
 C-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A (EIF-4A).//1.7E-61//374aa//38%/P47943
 C-NT2RP2005767//G. gallus PB1 gene.//5E-163//1158bp//81%/X90849
 C-NT2RP2005773//Homo sapiens pyrroline 5-carboxylate reductase iso form (P5CR2) mRNA, complete cds.//2.7E-180//656bp//99%/AF151351
 C-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN-BINDING PROTEIN) (SABP).//2.1E-213//249aa//85%/Q02038
 C-NT2RP2005781
 C-NT2RP2005804
 C-NT2RP2005835//SHP1 PROTEIN.//1.8E-28//208aa//32%/P34223
 C-NT2RP2005853
 C-NT2RP2005868
 C-NT2RP2005886
 C-NT2RP2005890
 C-NT2RP2005901//Homo sapiens mRNA for KIAA0971 protein, complete cds.//0//1977bp//99%/AB023188
 C-NT2RP2005933//NUCLEOPORIN NUP57 (NUCLEAR PORE PROTEIN NUP57).//5E-11//155aa//34%/P48837
 C-NT2RP2006038
 C-NT2RP2006043//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.5E-13//185aa//38%/Q08170
 C-NT2RP2006052
 C-NT2RP2006069
 C-NT2RP2006071
 C-NT2RP2006100//Homo sapiens mRNA: cDNA DKFp5648102 (from clone D KFP5648102).//0//1759bp//99%/AL049970
 C-NT2RP2006106
 C-NT2RP2006141
 C-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds.//3.3E-189//899bp//97%/AB014554
 C-NT2RP2006196
 C-NT2RP2006200
 C-NT2RP2006219//H. sapiens mRNA for DGC6 protein.//1.1E-214//1026bp//97%/X96484
 C-NT2RP2006237
 C-NT2RP2006238
 C-NT2RP2006275//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//2E-59//388aa//32%/P46821
 C-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.8E-274//1236bp//99%/AF035262
 C-NT2RP2006333
 C-NT2RP2006365
 C-NT2RP2006393
 C-NT2RP2006436//ANTERIOR-RESTRICTED HOMEOBOX PROTEIN (RATHKE POUCH HOMEO BOX).//0.0000034//50aa//50%/Q61658
 C-NT2RP2006456
 C-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//0//2181bp//99%/AJ006266
 C-NT2RP2006467
 C-NT2RP2006472
 C-NT2RP2006565//Sus scrofa mRNA for SCAMP1 protein.//0//1276bp//84%/Y15710
 C-NT2RP2006571//CYTOCHROME P450 2C1 (EC 1.14.14.1) (CYP11C1) (P450-NMB) (OLFACTIVE).//4.2E-134//486aa//50%/P24461
 C-NT2RP2006573//2'-3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC 3.1.4.37) (CNP).//0.000055//169aa//25%/P09543
 C-NT2RP3000031//Homo sapiens mRNA for KIAA0901 protein, complete cds.//0//2547bp//99%/AB020708
 C-NT2RP3000072
 C-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//0//1404bp//97%/AB011164
 C-NT2RP3000220
 C-NT2RP3000251
 C-NT2RP3000252//Homo sapiens GTP-binding protein MGB mRNA, complete cds.//0//2388bp//99%/AF120334
 C-NT2RP3000312
 C-NT2RP3000320//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Spl.//0//1544bp//100%/AJ242978
 C-NT2RP3000333
 C-NT2RP3000348
 C-NT2RP3000350//PROBABLE GTP-BINDING PROTEIN HP0303.//0.00000028//185aa//31%/Q25074
 C-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//226aa//92%/P08750
 C-NT2RP3000361//Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1/Zer1 and Prp6.//0//2072bp//98%/AB019219
 C-NT2RP3000366//RAS-RELATED PROTEIN RAB-18.//2.1E-107//206aa//99%/P35293
 C-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DE AH BOX PROTEIN 13).//1.7E-139//679aa//41%/Q43143
 C-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//0//2364bp//99%/AF071185
 C-NT2RP3000484
 C-NT2RP3000527//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//4.8E-28//536aa//27%/P28160
 C-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//1.9E-12//192aa//30%/P15151
 C-NT2RP3000596//TRICHOHYALIN.//2.5E-17//304aa//28%/Q07283
 C-NT2RP3000599
 C-NT2RP3000632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3E-140//499aa//46%/P51523
 C-NT2RP3000644
 C-NT2RP3000661
 C-NT2RP3000665
 C-NT2RP3000690
 C-NT2RP3000759//ADP-RIBOSYLATION FACTOR.//7E-28//176aa//34%/Q94650
 C-NT2RP3000825//NEUROGENIC LOCUS NOTCH 3 PROTEIN.//2.5E-36//417aa//31%/Q61982
 C-NT2RP3000836
 C-NT2RP3000841
 C-NT2RP3000850
 C-NT2RP3000852
 C-NT2RP3000859
 C-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//6.9E-69//1611bp//61%/U53445
 C-NT2RP3000869
 C-NT2RP3000901
 C-NT2RP3000917//Homo sapiens Dnal-like protein mRNA, complete cds.//0//3199bp//99%/AF064257
 C-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//2.7E-185//585bp//88%/AF015264
 C-NT2RP3000980
 C-NT2RP3000994//MATERNAL EFFECT PROTEIN STAUFEN.//0.0000006//78aa//48%/P25159
 C-NT2RP3001004
 C-NT2RP3001081
 C-NT2RP3001084
 C-NT2RP3001096//Rattus norvegicus leprecan (leprel) mRNA, complete cds.//1.7E-94//787bp//66%/AF087433
 C-NT2RP3001107//PEREGRIN (BR140 PROTEIN).//3E-44//260aa//40%/P55201
 C-NT2RP3001109
 C-NT2RP3001116
 C-NT2RP3001119
 C-NT2RP3001133
 C-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//0//2802bp//99%/AB018305
 C-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//0//2732bp//99%/AJ006266
 C-NT2RP3001176//HYPOTHETICAL 65.3 KD PROTEIN IN MADI-SCY1 INTERGENIC REGION.//1.7E-10//196aa//27%/P53154
 C-NT2RP3001214
 C-NT2RP3001216//CYCLICIN I (MULTIPLE-BAND POLYPEPTIDE I) (FRAGMENT).//0.000023//137aa//33%/P35663
 C-NT2RP3001221//GAMMA-BUTYROBETAININE, 2-OXOGLUTARATE DIOXYGENASE (EC 1.14.11.1) (GAMMA-BUTYROBETAININE HYDROXYLASE).//1.9E-31//353aa//30%/P80193
 C-NT2RP3001236
 C-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP1.2) (MAP1(X)) [CONTAINS: LIGHT CHAIN LC1].//1.2E-166//395aa//51%/P14873
 C-NT2RP3001260//Homo sapiens mRNA for KIAA0911 protein, complete cds.//0//2497bp//99%/AB020718
 C-NT2RP3001307
 C-NT2RP3001325
 C-NT2RP3001384//Homo sapiens NAKAP95 mRNA for neighbor of A-kinase anchoring protein 95, complete cds.//0//1213bp//99%/AB025905
 C-NT2RP3001392
 C-NT2RP3001396
 C-NT2RP3001398//TRANSCRIPTIONAL REPRESSOR CTCF.//1.3E-61//374aa//36%/P49711
 C-NT2RP3001407//SCY1 PROTEIN.//0.0000033//143aa//25%/P53009
 C-NT2RP3001420

【0951】

【表648】

C-NT2RP3001426//DNAJ PROTEIN (FRAGMENT).//1E-16//77aa//46%/033529	C-NT2RP4000312//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE).//1.5E-26//237aa//28%/Q01631
C-NT2RP3001427//WERNER SYNDROME HELICASE HOMOLOG.//2.7E-10//159aa//33%/009053	C-NT2RP4000323//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KERATIN).//0.0000003//101aa//32%/P26372
C-NT2RP3001457	C-NT2RP4000355
C-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A.//9.1E-13//87aa//43%/P11632	C-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds.//0//4074bp//99%/AB018281
C-NT2RP3001495//Human oxidoreductase (HHCMA56) mRNA, complete cds.//0//1475bp//99%/U13395	C-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds.//0//4782bp//99%/AF044195
C-NT2RP3001497//Homo sapiens multiple membrane spanning receptor T RCB (TRCB) mRNA, complete cds.//0//2295bp//99%/AF064801	C-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1).//2.6E-77//262aa//54%/075570
C-NT2RP3001529//SPODB-ASSOCIATED GTP-BINDING PROTEIN.//1E-61//345aa//42%/P20964	C-NT2RP4000376//Homo sapiens mRNA for phospholipase A2 activating protein.//0//2412bp//99%/AJ238243
C-NT2RP3001621	C-NT2RP4000381
C-NT2RP3001629	C-NT2RP4000398//ZINC FINGER PROTEIN 140.//2.9E-110//435aa//50%/P52738
C-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210.//6.8E-18//91aa//38%/Q92609	C-NT2RP4000415
C-NT2RP3001646//WD-40 REPEAT PROTEIN MS12.//8.8E-09//132aa//31%/Q22468	C-NT2RP4000417//MANNOsyl-OLIGOSACCHARIDE ALPHA-1,2-MANNOsIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOsIDASE) (FRAGMENT).//2.6E-51//438aa//33%/P45701
C-NT2RP3001676	C-NT2RP4000448//Homo sapiens mRNA: cDNA DKFZp566C0746 (from clone DKFZp566C0746).//0//3991bp//99%/AL050078
C-NT2RP3001679	C-NT2RP4000449
C-NT2RP3001799//MYOSIN HEAVY CHAIN, STRIATED MUSCLE.//1.6E-11//348aa//27%/P24733	C-NT2RP4000455//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO.//0.000003//175aa//27%/P09309
C-NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN).//7.4E-18//249aa//30%/Q04652	C-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15) (DEUBIQUITINATING ENZYME 15).//2.5E-37//291aa//38%/P50101
C-NT2RP3001896	C-NT2RP4000480
C-NT2RP3001915	C-NT2RP4000481//ATP-DEPENDENT RNA HELICASE DOB1 (RNA TRANSPORT REGULATOR NTR4).//1.9E-67//721aa//29%/Q09475
C-NT2RP3001929	C-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1).//8.8E-50//214aa//50%/P40484
C-NT2RP3003193//ZINC FINGER PROTEIN 135.//7.3E-98//269aa//62%/P52742	C-NT2RP4000500
C-NT2RP3004466	C-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1.//1.5E-106//495aa//45%/P45818
C-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35.//3.3E-113//466aa//42%/P34110	C-NT2RP4000524
C-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds.//0//1520bp//99%/AB014532	C-NT2RP4000541
C-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds.//0//974bp//95%/AB011126	C-NT2RP4000556//SUR4 PROTEIN (SRE1 PROTEIN).//7.4E-14//233aa//31%/P40319
C-NT2RP3004569//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NON ERYTHROID).//0.00000038//150aa//28%/Q01484	C-NT2RP4000560
C-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF15) mRNA, complete cds.//0//1770bp//99%/AF026445	C-NT2RP4000588
C-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds.//0//1639bp//99%/AB007946	C-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//2.9E-188//863bp//99%/AF067730
C-NT2RP3004594//Homo sapiens mRNA for AMD-1 protein.//0//1807bp//99%/AJ006266	C-NT2RP4000638
C-NT2RP3004617//ZINC-BINDING PROTEIN A33.//7.2E-75//464aa//35%/Q02084	C-NT2RP4000648//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPO.//0.0000037//175aa//27%/P09309
C-NT2RP3004618//Homo sapiens putative RNA-binding protein Q99 mRNA A, complete cds.//0//3972bp//98%/AF093097	C-NT2RP4000657//SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN SPS E.//1.1E-32//350aa//30%/P39625
C-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN).//1.7E-72//254aa//45%/P54352	C-NT2RP4000704
C-NT2RP3004688//CHLORINE CHANNEL PROTEIN P64.//2.6E-98//239aa//64%/P35526	C-NT2RP4000713//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//1.1E-13//295aa//27%/Q11073
C-NT2RP4000051//SYNAPTONEMAL COMPLEX PROTEIN SC65.//4.9E-51//335aa//37%/Q64375	C-NT2RP4000724//RETROVIRUS-RELATED ENV POLYPROTEIN.//3.2E-191//199aa//78%/P10267
C-NT2RP4000078//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//3013bp//99%/AB020657	C-NT2RP4000728//Homo sapiens mRNA for KIAA0931 protein, partial cds.//0//3392bp//95%/AB023148
C-NT2RP4000109//Homo sapiens mRNA for MECF5, partial cds.//0//2161bp//99%/AB011538	C-NT2RP4000737
C-NT2RP4000111//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//728aa//99%/Q10568	C-NT2RP4000739//Homo sapiens mRNA for KIAA1012 protein, complete cds.//0//3574bp//99%/AB023229
C-NT2RP4000129	C-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION.//0.00000032//67aa//31%/P53915
C-NT2RP4000147//Drosophila melanogaster putative ARF1 GTPase activating protein (ARF1-GAP) mRNA, complete cds.//3.8E-28//528bp//67%/AF011427	C-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds.//0//1927bp//99%/AB007939
C-NT2RP4000150	C-NT2RP4000833
C-NT2RP4000151	C-NT2RP4000837//Homo sapiens mRNA for zinc finger protein SALL1.//4.3E-94//810bp//65%/Y18265
C-NT2RP4000159	C-NT2RP4000839//VEGETATILE INCOMPATIBILITY PROTEIN MET-E-1.//8.5E-21//271aa//28%/Q00808
C-NT2RP4000185	C-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//5.7E-82//324aa//48%/Q09175
C-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds.//0//4149bp//99%/AB014600	C-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT).//4.1E-85//174aa//55%/P16415
C-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA).//5.9E-15//104aa//40%/P15287	C-NT2RP4000878//MYELOID UPREGULATED PROTEIN.//6.2E-91//173aa//87%/Q35682
C-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP).//0//1932bp//99%/AJ006470	C-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN).//9.6E-96//513aa//42%/P22314
C-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1).//2.7E-84//208aa//76%/Q03173	C-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 KD PROTEIN).//2.6E-26//227aa//36%/Q06828
C-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9).//5.5E-29//153aa//43%/Q23968	
C-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G.09C IN CHROMOSOME 1.//3.5E-297//1024aa//55%/P87115	

【0952】

【表649】

C-NT2RP4000927//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1).//1.5E-76//346aa//43%/Q61068	C-NT2RP4001373
C-NT2RP4000928//Homo sapiens mRNA for CDS2 protein.//0.72487bp//99%/Y16521	C-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2.7.1.112) (TYROSINE- PROTEIN KINASE 1).//9.2E-17//146aa//35%/P18160
C-NT2RP4000929//PUTATIVE ATP-DEPENDENT RNA HELICASE MJ1505.//0.0000014//185aa//25%/Q58900	C-NT2RP4001379//HYPOTHETICAL 49.1 KD PROTEIN C11D3.06 IN CHROMOSOM E 1.//2E-53//436aa//30%/Q10085
C-NT2RP4000955	C-NT2RP4001407//Homo sapiens mRNA for KIAA0923 protein, complete c ds.//0.72716bp//99%/AB023140
C-NT2RP4000973//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//1.4E-26//90aa//42%/P38660	C-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT).//7.7E-19//422aa//82%/Q14141
C-NT2RP4000975	C-NT2RP4001433//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.2E-138//419aa//54%/Q99676
C-NT2RP4000979	C-NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.//2.7E-66//738bp//71%/AF129131
C-NT2RP4000984	C-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSOR (EC 1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE).//0.7962aa//78%/Q02218
C-NT2RP4000989//UNC-47 PROTEIN.//0.000082//173aa//25%/P34579	C-NT2RP4001498//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//1E-27//374aa//29%/P39010
C-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0.7838aa//87%/P70700	C-NT2RP4001502
C-NT2RP4001004//VACUOLAR PROTEIN 8.//3.7E-16//401aa//26%/P39968	C-NT2RP4001507
C-NT2RP4001006	C-NT2RP4001524
C-NT2RP4001010//Homo sapiens mRNA for KIAA0964 protein, complete c ds.//0.72482bp//99%/AB023181	C-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INT ERGENIC REGION.//5.7E-54//242aa//38%/P25656
C-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUCINE--TRNA LIGASE).//1.5E-92//443aa//44%/Q09996	C-NT2RP4001551//Homo sapiens chromatin-specific transcription elon gation factor FACT 140 kDa subunit mRNA, complete cds.//0.73202bp//99%/AF152961
C-NT2RP4001057	C-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).//4.7E-09//216aa//24%/P96902
C-NT2RP4001064//SYNAPTONEMAL COMPLEX PROTEIN SC65.//6.7E-51//335aa//37%/Q64375	C-NT2RP4001567//ARMADILLO SEGMENT POLARITY PROTEIN.//0.0000054//213aa//26%/Q02453
C-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-ATPASE).//1.3E-123//563aa//46%/P13586	C-NT2RP4001568//ZINC FINGER PROTEIN GCS1.//1.8E-10//109aa//36%/P35197
C-NT2RP4001080//Homo sapiens mRNA for Rod1, complete cds.//0.71439bp//99%/AB023967	C-NT2RP4001571
C-NT2RP4001086	C-NT2RP4001574//Homo sapiens coat protein gamma-cop mRNA, complete cds.//0.73046bp//99%/AF100756
C-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADEMOSINE DEAMINASE) (RNA EDITING ENZYME 1).//2.6E-17//21aa//36%/P51400	C-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein.//0.71087bp//87%/AJ223830
C-NT2RP4001100	C-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCIN E--TRNA LIGASE) (ILERS).//1.7E-141//373aa//47%/P73505
C-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1.9E-115//224aa//100%/P38378	C-NT2RP4001610//Homo sapiens mRNA for KIAA0869 protein, partial c ds.//0.71897bp//99%/AB020676
C-NT2RP4001122//TIPO PROTEIN.//1.4E-65//253aa//41%/O15736	C-NT2RP4001614
C-NT2RP4001126//TRICHOHYALIN.//2.9E-18//380aa//26%/Q07283	C-NT2RP4001634
C-NT2RP4001138	C-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/MMS19.//5.1E-46//234aa//32%/P40469
C-NT2RP4001143//SUCCINYL-DIAMINOPIMELATE DESUCCINYLASE (EC 3.5.1.18) (SDAP).//0.0000021//93aa//33%/P44514	C-NT2RP4001644//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).//6.4E-19//111aa//45%/P25323
C-NT2RP4001146//SCF1 PROTEIN.//1.3E-104//236aa//52%/P33750	C-NT2RP4001677
C-NT2RP4001149	C-NT2RP4001679
C-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (N R-CAM) (BRAYO).//3.4E-29//385aa//29%/P35331	C-NT2RP4001696//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR. 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//4E-10//243aa//25%/Q10568
C-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PR ECURSOR (CTPT).//4.7E-29//227aa//35%/P52178	C-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.//3E-10//128aa//32%/Q10282
C-NT2RP4001206//Drosophila melanogaster strawberry notch (sno) mRNA A, complete cds.//4.4E-104//1460bp//65%/U95760	C-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECU RSOR (EC 2.4.1.-) (DUGT).//6.4E-170//1168aa//33%/Q09332
C-NT2RP4001207	C-NT2RP4001739
C-NT2RP4001210	C-NT2RP4001753//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3.9E-236//665aa//58%/P51523
C-NT2RP4001219//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.2E-27//90aa//42%/P38660	C-NT2RP4001760//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTO R (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN).//4.1E-16//263aa//27%/P98174
C-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).//1.8E-103//508aa//43%/Q04652	C-NT2RP4001790//Homo sapiens mRNA for KIAA1015 protein, complete c ds.//0.73144bp//99%/AB023232
C-NT2RP4001235	C-NT2RP4001803
C-NT2RP4001256	C-NT2RP4001822//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//241aa//30%/Q35566
C-NT2RP4001260//Homo sapiens mRNA for KIAA0875 protein, partial cd s.//0.72876bp//99%/AB020682	C-NT2RP4001823//MICROFIL-BRIL-ASSOCIATED GLYCOPROTEIN 4.//1.1E-19//77aa//54%/P55083
C-NT2RP4001274//Human transporter protein (gl7) mRNA, complete cd s.//4.4E-58//1196bp//61%/U49082	C-NT2RP4001828
C-NT2RP4001276//TRICHOHYALIN.//7.9E-09//126aa//32%/Q07283	C-NT2RP4001838//Homo sapiens CoREST protein (COREST) mRNA, complet e cds.//6.3E-99//555bp//73%/AF155595
C-NT2RP4001313//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MOM38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT).//5.9E-17//296aa//29%/P24391	C-NT2RP4001861//TRICHOHYALIN.//1E-35//307aa//34%/P37709
C-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5.//8.5E-213//1129bp//92%/AJ001119	C-NT2RP4001893//Homo sapiens mRNA: cDNA DKFZp5640043 (from clone D KFZp5640043).//0.71306bp//98%/AL050390
C-NT2RP4001339//Human ovarian cancer downregulated myosin heavy ch ain homolog (Doc1) mRNA, complete cds.//1.4E-58//2425bp//59%/U53445	C-NT2RP4001896//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//0.00000014//345aa//25%/Q00808
C-NT2RP4001353	C-NT2RP4001901
C-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRR EC PROTEIN).//1.6E-19//222aa//30%/Q08180	C-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.3E-38//258

【0953】

【表650】

aa//32%/Q12024	C-OVARC1000443//Homo sapiens mRNA: cDNA DKFZp434A073 (from clone D
C-NT2RP4001938//TRANSCRIPTIONAL REPRESSOR CTCF.//9.8E-60//303aa//3	KFZp434A073).//0//1216bp//99%/AL080126
8%/P49711	C-OVARC1000461
C-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.	C-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//1.2E-25//227aa//2
1.1.77) (PROTEIN- BETA-ASPARTATE METHYLTRANSFERASE) (PINT) (PROTEI	5%/P11075
N L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL	C-OVARC1000466
METHYLTRANSFERASE).//1.5E-13//211aa//28%/Q43209	C-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.4
C-NT2RP4001950//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//1.2E-13//35	8) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE VHR).//3.1
6aa//27%/P13816	E-10//125aa//35%/P51452
C-NT2RP4001953	C-OVARC1000479//Homo sapiens mRNA for KIAA0829 protein, partial cd
C-NT2RP4001966	s.//0//1919bp//99%/AB020636
C-NT2RP4001975	C-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.2
C-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN).//6.9E-24//370a	E-157//892bp//91%/AF051850
a//27%/Q04652	C-OVARC1000564
C-NT2RP4002052	C-OVARC1000576
C-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DE	C-OVARC1000588
AH BOX PROTEIN 13).//1E-137//679aa//40%/Q43143	C-OVARC1000605
C-NT2RP4002071	C-OVARC1000640
C-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10)	C-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA fo
(HPF7).//3E-150//722aa//39%/Q05481	r GRB-7 SH2 domain protein, complete cds.//0//1812bp//98%/D43772
C-NT2RP4002081//TRANSCRIPTION INITIATION FACTOR IIA ALPHA AND BETA	C-OVARC1000661
CHAINS (TFIIA P35 AND P19 SUBUNITS) (TFIIA-42) (TFIIA).//0.00000	C-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.1E-46//121aa//79%/P
67//250aa//31%/P52655	08886
C-NT2RP4002298	C-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//1.2E-17//127aa//33%/
C-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-).//1.5E-63//159aa//	Q58343
53%/P38938	C-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//1.5E-178//11
C-NT2RP4002791	13bp//86%/AF001533
C-NT2RP4002888//Homo sapiens mRNA: cDNA DKFZp434F172 (from clone D	C-OVARC1001038//Homo sapiens mRNA for Ariadne-2 protein.//0//1172b
KFZp434F172).//0//2557bp//99%/AL080202	p//97%/AJ130978
C-NT2RP4002905	C-OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds.//1
C-NT2RP5003461//RLR1 PROTEIN.//9.7E-22//177aa//27%/P53552	E-215//1027bp//98%/AF132946
C-NT2RP5003477//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1.//5.5	C-OVARC1001162
E-15//280aa//27%/Q00808	C-OVARC1001243
C-NT2RP5003492	C-OVARC1001296
C-NT2RP5003500	C-OVARC1001360
C-NT2RP5003506	C-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor i
C-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR	nvolved in B-CLL.//6E-148//683bp//99%/AJ224819
).//3.3E-23//219aa//40%/P37116	C-OVARC1001425
C-NT2RP5003524	C-PLACE1000005
C-NT2RP5003534	C-PLACE1000066//SSU72 PROTEIN.//1.1E-39//206aa//43%/P53538
C-OVARC1000006//HISTONE H2A.1.//1.1E-55//117aa//99%/P02262	C-PLACE1000142//3-HYDROXYBUTYRYL-COA DEHYDRATASE (EC 4.2.1.55) (CR
C-OVARC1000013//APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1).//	OTONASE).//2.8E-29//134aa//43%/P52046
0.000042//102aa//32%/Q14727	C-PLACE1000184//Homo sapiens mRNA for KIAA0832 protein, complete c
C-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//2.6	ds.//5.5E-312//141bp//99%/AB020639
E-295//1393bp//97%/AF058922	C-PLACE1000185
C-OVARC1000035	C-PLACE1000213//Homo sapiens mRNA for KIAA0977 protein, complete c
C-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.2	ds.//0//1904bp//99%/AB023194
7.1) (RNASE LE).//0.0000032//60aa//45%/P80022	C-PLACE1000347
C-OVARC1000087//HISTONE MACRO-H2A.1.//1.6E-12//174aa//26%/Q02874	C-PLACE1000374
C-OVARC1000091//HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN)	C-PLACE1000380//Homo sapiens mRNA for KIAA0853 protein, partial cd
(HFC1) (VCAF) (CFF).//8.4E-14//259aa//30%/P51610	s.//0//2208bp//99%/AB020660
C-OVARC1000113	C-PLACE1000383//Homo sapiens mRNA for MTMR1 protein.//0//753bp//99
C-OVARC1000139//Homo sapiens CGI-21 protein mRNA, complete cds.//0	%/AJ224979
//1562bp//99%/AF132955	C-PLACE1000401//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//2.
C-OVARC1000148	7E-30//352aa//31%/P15151
C-OVARC1000151//Homo sapiens partial mRNA for putative protein p38	C-PLACE1000406//PTB-ASSOCIATED SPLICING FACTOR (PSF).//1.2E-132//3
interacting with transcription factor Spl.//2.5E-95//461bp//98%/	34aa//72%/P23246
AJ242975	C-PLACE1000420//7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3. .6.
C-OVARC1000168	-) (8-OXO-DGTPASE).//0.0000028//134aa//29%/P53368
C-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA,	C-PLACE1000435
complete cds.//1.8E-32//511bp//65%/AF068332	C-PLACE1000444
C-OVARC1000212	C-PLACE1000562
C-OVARC1000241//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (AR	C-PLACE1000564
NT INTERACTING PROTEIN) (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALP	C-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GU
HA).//8.2E-120//351aa//54%/Q16665	ANINE NUCLEOTIDE- BINDING PROTEIN 1).//1.6E-270//437aa//86%/P3245
C-OVARC1000288//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22)	5
(POLYPEPTIDASE) (LEUCINE AMINOPEPTIDASE IV) (LAPIV) (AMINOPEPTIDAS	C-PLACE1000596//Homo sapiens mRNA for KIAA0850 protein, complete c
E 111) (AMINOPEPTIDASE YSC1).//5.4E-53//384aa//30%/P14904	ds.//0//2393bp//99%/AB020657
C-OVARC1000304//PROTEIN MOV-10.//1.1E-249//519aa//87%/P23249	C-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA,
C-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2).//2.7E-40//154aa//	complete cds.//2E-55//779bp//67%/AF044201
38%/P29363	C-PLACE1000636//MALE STERILITY PROTEIN 2.//1.2E-39//261aa//27%/Q0
C-OVARC1000321	8891
C-OVARC1000326	C-PLACE1000716
C-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGEN	C-PLACE1000748
IC REGION.//5.9E-14//200aa//27%/P40004	C-PLACE1000755//Homo sapiens mRNA for Helicase-MOI, complete cds./
C-OVARC1000347	4.6E-250//1189bp//97%/AB028449
C-OVARC1000384	C-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cd
C-OVARC1000411	s.//0//2002bp//99%/AB014548
C-OVARC1000420	C-PLACE1000798
C-OVARC1000437//TENSIN.//7.9E-181//340aa//84%/Q04205	C-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN YHR14

【0954】

【表651】

8W.//2.5E-49//181aa//54%/P32899
 C-PLACE1000909//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//2.6E-19//404aa//26%/P39010
 C-PLACE1000948
 C-PLACE1000972
 C-PLACE1000977//BETA-CHIMAERIN (BETA-CHIMERIN).//4.4E-22//129aa//35%/Q03070
 C-PLACE1001000
 C-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//Q//1500bp//99%/AF065485
 C-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN).//4.3E-54//257aa//46%/Q04652
 C-PLACE1001383//ZINC-FINGER PROTEIN UBI-04 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQUIEM).//3E-33//138aa//42%/Q61103
 C-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//2.3E-61//132aa//46%/Q12929
 C-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22_N_12, complete sequence.//0//2118bp//99%/AC005412
 C-PLACE1001412
 C-PLACE1001484//Homo sapiens chromosome 20 clone 387E22. WORKING DRAFT SEQUENCE, in unordered pieces.//0//1440bp//99%/AL031660
 C-PLACE1001503
 C-PLACE1001570
 C-PLACE1001610
 C-PLACE1001692//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//4E-81//263aa//56%/P08635
 C-PLACE1001729
 C-PLACE1001739//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.//3.5E-75//439aa//41%/P16381
 C-PLACE1001781//PROBABLE PHOSPHOMANNOMUTASE (EC 5.4.2.8) (PMM).//5.4E-63//427aa//35%/Q57290
 C-PLACE1001810
 C-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//0//1995bp//99%/AF058953
 C-PLACE1001869//L-RIBULOKINASE (EC 2.7.1.16).//2E-27//270aa//31%/P94524
 C-PLACE1001912//Homo sapiens clone 24963 mRNA sequence, complete cds.//0//1196bp//99%/AF131737
 C-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//1729bp//99%/AF099935
 C-PLACE1001928
 C-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//1.4E-78//496aa//37%/Q49091
 C-PLACE1002046//LIGATIN (FRAGMENT).//1.7E-240//560aa//80%/Q61211
 C-PLACE1002072
 C-PLACE1002073//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLATE CYCLASE).//0.0000053//188aa//29%/P49606
 C-PLACE1002140
 C-PLACE1002163
 C-PLACE1002170
 C-PLACE1002433
 C-PLACE1002438//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//0.0000042//133aa//29%/Q13105
 C-PLACE1002465
 C-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//6.7E-214//956bp//94%/AB018256
 C-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//0//1750bp//99%/AF068180
 C-PLACE1002722//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//9E-45//305aa//33%/Q15391
 C-PLACE1002794
 C-PLACE1002815
 C-PLACE1002839
 C-PLACE1002851
 C-PLACE1002941
 C-PLACE1002996
 C-PLACE1003045
 C-PLACE1003092
 C-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//2.6E-79//253aa//60%/Q13268
 C-PLACE1003108
 C-PLACE1003145
 C-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PUB2).//3.8E-37//143aa//51%/P42743
 C-PLACE1003190//SOF1 PROTEIN.//1.9E-110//325aa//48%/P33750
 C-PLACE1003200
 C-PLACE1003296//Homo sapiens mRNA: cDNA DKFp434G173 (from clone D KF2p434G173).//0//1706bp//99%/AL080133
 C-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//6.9E-206//396aa//86%/P51522
 C-PLACE1003334
 C-PLACE1003342
 C-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//0//2435bp//99%/U92715
 C-PLACE1003369
 C-PLACE1003602//Homo sapiens mRNA expressed in placenta.//5.9E-278//1275bp//99%/D83200
 C-PLACE1003611
 C-PLACE1003625//ARMADILLO SEGMENT POLARITY PROTEIN.//3.2E-10//380aa//25%/P18824
 C-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//8E-19//209aa//34%/Q08170
 C-PLACE1003711
 C-PLACE1003723
 C-PLACE1003762
 C-PLACE1003771
 C-PLACE1003784
 C-PLACE1003923
 C-PLACE1003936
 C-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN).//2.4E-124//326aa//73%/P80385
 C-PLACE1004104
 C-PLACE1004114
 C-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA CHAIN 4).//6.1E-181//340aa//96%/P29387
 C-PLACE1004149
 C-PLACE1004156
 C-PLACE1004161
 C-PLACE1004183//Homo sapiens for TOM1-like protein.//0//1279bp//97%/AJ010071
 C-PLACE1004197//BUTYROPHEIN PRECURSOR (BT).//4.5E-10//208aa//27%/Q62556
 C-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds.//0//1882bp//99%/AF069493
 C-PLACE1004258
 C-PLACE1004270//TRANSMEMBRANE PROTEASE, SERINE 2 (EC 3.4.21.-).//9.7E-36//389aa//31%/O15393
 C-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, complete cds.//0//1498bp//99%/AF084830
 C-PLACE1004289
 C-PLACE1004302//SOF1 PROTEIN.//1.9E-110//325aa//48%/P33750
 C-PLACE1004316//H. sapiens mRNA for apoptosis specific protein.//0//1767bp//99%/Y11588
 C-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//0//2512bp//99%/AF100153
 C-PLACE1004376
 C-PLACE1004388
 C-PLACE1004405
 C-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-).//1.2E-39//385aa//33%/Q63448
 C-PLACE1004437//Human NAD+-specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds.//0//985bp//99%/U49283
 C-PLACE1004451
 C-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0000002//218aa//23%/P25823
 C-PLACE1004473
 C-PLACE1004510//Homo sapiens cofactor of initiator function (CIF15 D) mRNA, complete//1.3E-209//954bp//99%/AF026445
 C-PLACE1004516
 C-PLACE1004548
 C-PLACE1004564//CLEFTAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//525aa//99%/Q10568
 C-PLACE1004629//PROTEIN OS-9 PRECURSOR.//7.7E-18//264aa//32%/Q13438
 C-PLACE1004645
 C-PLACE1004646//B. taurus mRNA for retinal pigment epithelial membrane receptor p63.//4.4E-42//985bp//59%/X66277
 C-PLACE1004664
 C-PLACE1004672
 C-PLACE1004674//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//1.6E-95//191aa//96%/P12815
 C-PLACE1004691
 C-PLACE1004722
 C-PLACE1004736
 C-PLACE1004740
 C-PLACE1004743//PROBABLE N-END-RECOGNIZING PROTEIN (UBIQUITIN-PROTEIN LIGASE E3 COMPONENT) (N-RECOGNIN).//4.4E-35//578aa//27%/O60152

【0955】

【表652】

C-PLACE1004751//Homo sapiens mRNA for alpha2,3-sialyltransferase 5 T3Gai VI, complete cds.//7.1E-224//790bp//98%//AB022918	C-PLACE1005936
C-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-CHIMAERIN).//1.9E-32//259aa//32%//P30337	C-PLACE1005951
C-PLACE1004804//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE).//4.7E-65//695aa//29%//Q01631	C-PLACE1005953//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//6.7E-30//98aa//37%//P43636
C-PLACE1004814//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//5.9E-19//196aa//36%//Q08170	C-PLACE1005955//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE).//5.4E-54//455aa//32%//P14904
C-PLACE1004824	C-PLACE1005966//TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TAFII-90).//0.00000014//254aa//25%//P38129
C-PLACE1004868//MALE STERILITY PROTEIN 2.//3.9E-39//261aa//27%//Q08891	C-PLACE1005990
C-PLACE1004885	C-PLACE1006011//Homo sapiens mRNA for poly(ADP-ribose) polymerase-2.//0//1564bp//99%//AJ236876
C-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//9.3E-11//94aa//47%//Q42643	C-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.7E-161//744bp//99%//X99906
C-PLACE1004918//L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDH-A).//4.9E-48//198aa//44%//P06151	C-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.5E-148//681bp//99%//AF039023
C-PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//1853bp//98%//AF099936	C-PLACE1006139
C-PLACE1004934	C-PLACE1006159
C-PLACE1004937//SEL-10 PROTEIN.//6.3E-125//357aa//58%//Q93794	C-PLACE1006167
C-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//2E-14//205aa//26%//Q11073	C-PLACE1006170//Homo sapiens mRNA for KIAA0899 protein, partial cds.//4.5E-293//953bp//99%//AB020706
C-PLACE1004982	C-PLACE1006195
C-PLACE1005026	C-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//2.7E-116//496aa//48%//Q09747
C-PLACE1005027	C-PLACE1006225
C-PLACE1005046	C-PLACE1006236
C-PLACE1005077	C-PLACE1006239//BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN).//2E-16//244aa//31%//P28675
C-PLACE1005101//Homo sapiens (clone zap128) mRNA, 3' end of cds.//1E-209//1031bp//96%//L40401	C-PLACE1006246
C-PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN).//2.6E-56//565aa//30%//Q04652	C-PLACE1006325//Homo sapiens mRNA: cDNA DKFpZp564J142 (from clone D KFp564J142).//3.8E-278//1271bp//99%//AL080066
C-PLACE1005111	C-PLACE1006335
C-PLACE1005181	C-PLACE1006357
C-PLACE1005187//APAG PROTEIN.//3.8E-13//122aa//36%//P05636	C-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.//0//1168bp//99%//AF062085
C-PLACE1005206	C-PLACE1006412
C-PLACE1005232	C-PLACE1006414
C-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.3E-27//349aa//32%//Q01577	C-PLACE1006438//ZINC FINGER PROTEIN 165.//2.5E-45//122aa//43%//P49910
C-PLACE1005261	C-PLACE1006445
C-PLACE1005266	C-PLACE1006470
C-PLACE1005277//Homo sapiens mRNA for KIAA0610 protein, partial cds.//3.2E-297//1341bp//100%//AB011182	C-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//7.7E-55//142aa//85%//Q90595
C-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.3E-13//269aa//28%//P53352	C-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.1E-229//367aa//96%//Q00004
C-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//226aa//92%//P08760	C-PLACE1006492
C-PLACE1005308	C-PLACE1006531
C-PLACE1005313	C-PLACE1006552
C-PLACE1005327	C-PLACE1006598//Homo sapiens clone NH0310K15, WORKING DRAFT SEQUENCE. 4 unordered pieces.//0//2182bp//99%//AC007383
C-PLACE1005335	C-PLACE1006615
C-PLACE1005373//TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//8.6E-09//194aa//27%//Q33335	C-PLACE1006626//Homo sapiens mRNA for KIAA0928 protein, partial cds.//0//1760bp//99%//AB023145
C-PLACE1005374	C-PLACE1006673
C-PLACE1005480	C-PLACE1006678//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.8E-24//734bp//62%//AB015630
C-PLACE1005481	C-PLACE1006704
C-PLACE1005494//Homo sapiens mRNA for transient receptor potential protein TRP6.//0//1649bp//99%//AJ006276	C-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//6.9E-13//177aa//33%//Q59263
C-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME III.//5.6E-52//173aa//57%//Q09251	C-PLACE1006782
C-PLACE1005550	C-PLACE1006819//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.8E-213//732aa//80%//P08547
C-PLACE1005554	C-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN).//2E-15//188aa//29%//P35123
C-PLACE1005623	C-PLACE1006883
C-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//0//2130bp//99%//AF083255	C-PLACE1006901
C-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE).//2.1E-148//321aa//83%//P31350	C-PLACE1006917//HSH49 PROTEIN.//5.5E-12//97aa//35%//Q99181
C-PLACE1005730	C-PLACE1006932
C-PLACE1005755	C-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME III.//6.7E-48//278aa//41%//Q10000
C-PLACE1005763//S-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//2.5E-79//209aa//53%//P08635	C-PLACE1006956//ATP-DEPENDENT PERMEASE MDL1.//1.3E-86//522aa//36%//P97998
C-PLACE1005803	C-PLACE1006958//Homo sapiens mRNA for heat shock protein apg-1, complete cds.//0//1770bp//99%//AB023421
C-PLACE1005804//Homo sapiens alpha 1,2-mannosidase IB mRNA, complete cds.//1.1E-217//994bp//99%//AF027156	C-PLACE1006961
C-PLACE1005851	C-PLACE1006962
C-PLACE1005921//AIGI PROTEIN.//3E-31//284aa//31%//P54120	C-PLACE1006966
C-PLACE1005923	C-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE)
C-PLACE1005925	
C-PLACE1005934	

【0956】

【表653】

NSE PROTEIN 12) (DER12). //3.2E-35//180aa//33%/Q14542	YOSIN 11). //2.6E-14//370aa//25%/Q99323
C-PLACE1007021	C-PLACE1007954
C-PLACE1007105	C-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRn
C-PLACE1007178	A. complete cds. //0//2252bp//99%/AF084530
C-PLACE1007226//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III	C-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 8B (P
OXIDASE (EC 1.-.-.-) (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE). //	DE8B) mRNA, partial cds. //0//2300bp//99%/AF079529
/1E-42//370aa//31%/P54304	C-PLACE1007969//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP
C-PLACE1007238	M). //1.1E-36//202aa//48%/P52272
C-PLACE1007239//Homo sapiens mRNA for transcription elongation fac	C-PLACE1007990
tor S-II, hS-II-T1, complete cds. //6.5E-216//1068bp//96%/D50495	C-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSY
C-PLACE1007242	N-110) (SYNAPTIC DENSITY PROTEIN PSD-93). //6.1E-14//128aa//39%/Q6
C-PLACE1007243//UNC-47 PROTEIN. //0.00000017//211aa//27%/P34579	3622
C-PLACE1007257//Homo sapiens mRNA for dia-12c protein. //0//2052bp//	C-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUE
99%/Y15908	CE, 4 unordered pieces. //0//1833bp//99%/AC005628
C-PLACE1007274	C-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN N
C-PLACE1007282	UPI07) (107 KD NUCLEOPORIN) (P105). //4.6E-318//613aa//94%/P52590
C-PLACE1007301	C-PLACE1008095
C-PLACE1007317//Drosophila melanogaster Adrift (adrift) mRNA, comp	C-PLACE1008122
lete cds. //4.1E-17//1037bp//56%/AF117649	C-PLACE1008129
C-PLACE1007342	C-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOM
C-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EB	E 111). //1.3E-24//395aa//31%/Q09531
BP) mRNA, complete cds. //0//2366bp//99%/AF096870	C-PLACE1008177//TRICHOHYALIN. //2.3E-29//487aa//26%/P37709
C-PLACE1007367	C-PLACE1008209
C-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-1	C-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMM
3. //0.0000044//127aa//30%/P27715	A-COP). //1.3E-283//671aa//77%/P53620
C-PLACE1007386	C-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-). //2.3E-18//16
C-PLACE1007402	Zaa//37%/P12689
C-PLACE1007409//WHITE PROTEIN. //1.1E-64//428aa//32%/Q17320	C-PLACE1008280
C-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-	C-PLACE1008309
CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEX	C-PLACE1008329
ING PROTEIN-2) (ADABP). //8.8E-25//140aa//35%/P27487	C-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial c
C-PLACE1007450	s. //0//1853bp//100%/AB014579
C-PLACE1007452	C-PLACE1008398//GENE 33 POLYPEPTIDE. //7.3E-114//243aa//87%/P05432
C-PLACE1007460	C-PLACE1008401
C-PLACE1007484	C-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTO
C-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTO	SIS ASSOCIATED PROTEIN) (TAP). //0//698aa//95%/P41541
R (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG). //5.4E-53	C-PLACE1008429//ANKYRIN HOMOLOG PRECURSOR. //3.1E-11//189aa//32%/Q
//426aa//33%/P52734	06527
C-PLACE1007507	C-PLACE1008457
C-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19)	C-PLACE1008465
(K19) (CK 19). //1.4E-85//385aa//45%/P08728	C-PLACE1008488
C-PLACE1007524	C-PLACE1008524//Human DNA sequence from clone 34821 on chromosome
C-PLACE1007537//Homo sapiens ankyrin repeat-containing protein AS	5p12.1-21.1. Contains part of a gene for a novel protein with ZUS
B-2 mRNA, complete cds. //8.9E-316//1485bp//98%/AF159164	domain similar to part of Tight Junction Protein 201 (TJPI) and UM
C-PLACE1007544	C5 Homologs. the gene for a novel BZRP (peripheral benzodiazepine
C-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R05D3.4 IN CHROMOSOME	recepto//0//1980bp//99%/AL031778
111. //1E-49//361aa//36%/P34537	C-PLACE1008531
C-PLACE1007583	C-PLACE1008532
C-PLACE1007598//ZINC FINGER PROTEIN 184 (FRAGMENT). //1.6E-143//666	C-PLACE1008533//101 KD MALARIA ANTIGEN (P101) (ACIDIC BASIC REPEAT
aa//44%/Q99676	ANTIGEN). //1.1E-09//62aa//48%/P22620
C-PLACE1007618//Homo sapiens mRNA for KIAA0977 protein, complete c	C-PLACE1008568
ds. //0//713bp//99%/AB023194	C-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN N
C-PLACE1007621	UPI55) (155 KD NUCLEOPORIN) (P140). //7.8E-236//453aa//96%/P37199
C-PLACE1007632//POLIOVIRUS RECEPTOR PRECURSOR. //0.000001//228aa//	C-PLACE1008621
31%/P32506	C-PLACE1008626
C-PLACE1007645	C-PLACE1008627//Homo sapiens mRNA for cysteine-rich protein. //0//1
C-PLACE1007649//Homo sapiens mRNA for KIAA0977 protein, complete c	850bp//99%/AJ006591
ds. //0//1952bp//99%/AB023194	C-PLACE1008629
C-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTO	C-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA,
ANTIGEN HOMOLOG). //8.7E-09//279aa//28%/Q26457	complete cds. //0//1548bp//100%/AF044333
C-PLACE1007690	C-PLACE1008693
C-PLACE1007697//GCN20 PROTEIN. //7.6E-119//717aa//38%/P43535	C-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S pr
C-PLACE1007706//Homo sapiens metalloprotease 1 (MPI) mRNA, complet	otein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitoch
e cds. //0//3431bp//99%/AF061243	ondrial protein, complete cds. //0//3002bp//99%/AF038406
C-PLACE1007725	C-PLACE1008790//IMPORTIN ALPHA-6 SUBUNIT (KARYOPHERIN ALPHA-6 SUBU
C-PLACE1007729//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-). //1.5E-4	NIT) (IMPORTIN ALPHA S2). //3.1E-280//533aa//98%/D35345
4//231aa//42%/P10265	C-PLACE1008808//Homo sapiens mRNA for cell cycle checkpoint protei
C-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete c	n rad1A. //2.3E-269//1225bp//99%/AJ004974
ds. //9.2E-294//1504bp//94%/AB014585	C-PLACE1008813
C-PLACE1007746	C-PLACE1008854
C-PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds. //0//1836bp	C-PLACE1008867
//99%/AB019602	C-PLACE1008887
C-PLACE1007810	C-PLACE1008902
C-PLACE1007843	C-PLACE1008925
C-PLACE1007846//Homo sapiens genomic DNA of 21q22.2 Down Syndrome	C-PLACE1009020//NIFS PROTEIN. //3.9E-55//279aa//41%/P12623
region, segment 3/13. //0//1751bp//99%/AP000010	C-PLACE1009027//Homo sapiens mRNA for doublecortin. //0//1919bp//99
C-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete c	%//AJ003112
ds. //0//3112bp//99%/AB018309	C-PLACE1009045
C-PLACE1007897	C-PLACE1009060//BRO1 PROTEIN. //6.7E-19//567aa//24%/P48582
C-PLACE1007946//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (M	C-PLACE1009090

【0957】

【表654】

C-PLACE1009091	//Q62671
C-PLACE1009094//FURIN-LIKE PROTEASE 2 PRECURSOR (EC 3.4.21.75) (FU RIN 2).//1.9E-44//480aa//30%/P30432	C-PLACE1010102
C-PLACE1009099//ZINC FINGER PROTEIN 41 (FRAGMENT).//1.1E-179//452a a//67%/P51814	C-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).//7.3E-114//537 aa//44%/Q04652
C-PLACE1009110	C-PLACE1010106//Homo sapiens mRNA: cDNA DKFZp586M1418 (from clone DKFZp586M1418).//0//1974bp//99%/AL049385
C-PLACE1009111	C-PLACE1010134//TRANSCRIPTION REGULATORY PROTEIN SNF2 (SWI/SNF COM PLEX COMPONENT SNF2) (REGULATORY PROTEIN SWI2) (REGULATORY PROTEIN GAM1) (TRANSCRIPTION FACTOR TYE3).//1.7E-20//156aa//42%/P22082
C-PLACE1009130//UBIQUITIN-PROTEIN LIGASE E3A (EC 6.3.2.-) (ONCOGEN IC PROTEIN-ASSOCIATED PROTEIN E6-AP).//2E-68//181aa//43%/Q05086	C-PLACE1010148//CYCLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//0.00000 46//431aa//23%/P35662
C-PLACE1009158	C-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN)./ /9.8E-11//95aa//49%/Q01130
C-PLACE1009166	C-PLACE1010202
C-PLACE1009174	C-PLACE1010261//SEGREGATION DISTORTER PROTEIN.//1.6E-77//214aa//62 %/P25722
C-PLACE1009186	C-PLACE1010274//Homo sapiens mRNA: cDNA DKFZp5640123 (from clone D KFZp5640123).//0//1964bp//99%/AL080122
C-PLACE1009190	C-PLACE1010293
C-PLACE1009230	C-PLACE1010321//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PR ECURSOR (CTPT).//1.1E-09//350aa//22%/P52178
C-PLACE1009319//Rattus norvegicus outer membrane protein (OMP25) m RNA, complete cds: nuclear gene for mitochondrial product.//2.1E-1 32//1229bp//75%/AF107295	C-PLACE1010324
C-PLACE1009328	C-PLACE1010329
C-PLACE1009335	C-PLACE1010362//1-PHOSPHATIDYLINOSITOL PHOSPHODIESTERASE PRECURSOR (EC 3.1.4.10) (PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (P I-PLC).//0.00000002//126aa//29%/P34024
C-PLACE1009338	C-PLACE1010364
C-PLACE1009368//METAL HOMEOSTASIS FACTOR ATX2.//2.5E-10//151aa//29 %/Q12067	C-PLACE1010383
C-PLACE1009375	C-PLACE1010481//Homo sapiens mRNA for KIAA0836 protein, partial cd s.//0//2121bp//99%/AB020643
C-PLACE1009388	C-PLACE1010491
C-PLACE1009404//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOS OME 1.//0.00000047//165aa//33%/Q09820	C-PLACE1010492
C-PLACE1009434	C-PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induc ed by progesterone), complete cds.//0//1981bp//99%/AB022718
C-PLACE1009443	C-PLACE1010529
C-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//7.8E-71//82aa//89%/ P42356	C-PLACE1010547//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.0 000012//616aa//24%/P25386
C-PLACE1009459	C-PLACE1010599//Homo sapiens Pex14 mRNA for peroxisomal membrane a nchor protein, complete cds.//0//1904bp//99%/AB017546
C-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//3.1 E-289//550aa//93%/P54319	C-PLACE1010616
C-PLACE1009476//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CH ROMOSOME III.//3.9E-40//179aa//37%/P34580	C-PLACE1010622//TROPONIN T, CARDIAC MUSCLE ISOFORMS (TNYC).//0.000 00016//120aa//28%/P02642
C-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FACTOR).//8.1E-99//228aa//75%/Q09418	C-PLACE1010629
C-PLACE1009542	C-PLACE1010630
C-PLACE1009571	C-PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS13.//5.7E-75//423aa//39 %/Q01755
C-PLACE1009581	C-PLACE1010714
C-PLACE1009596//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1.//5.1 E-54//291aa//40%/Q00808	C-PLACE1010720//Homo sapiens mRNA for chromosome-associated polype ptide-C, complete cds.//4E-299//1091bp//99%/AB019987
C-PLACE1009607	C-PLACE1010743//Homo sapiens myosin-IXb splice variant (Myo9b) mRN A, partial cds.//8.9E-91//668bp//82%/AF020267
C-PLACE1009621	C-PLACE1010771//M. musculus HCMGP mRNA.//7.4E-168//966bp//89%/X680 61
C-PLACE1009622//MATERNAL EFFECT PROTEIN STAUFEN.//1.3E-60//209aa// 41%/P25159	C-PLACE1010786
C-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN)./ /1.5E-285//538aa//99%/P55161	C-PLACE1010800
C-PLACE1009665	C-PLACE1010811
C-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//0// 1854bp//100%/AF062534	C-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.3E-143//407aa//58%/Q05481
C-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING P ROTEIN C12G12.13C IN CHROMOSOME 1.//7E-33//166aa//43%/Q09876	C-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cd s.//0//1885bp//99%/AB011182
C-PLACE1009721//MSF1 PROTEIN.//1.7E-22//176aa//33%/P35200	C-PLACE1010900
C-PLACE1009731//AIG1 PROTEIN.//1.6E-22//274aa//28%/P54120	C-PLACE2000050
C-PLACE1009763//Homo sapiens mRNA for Nedd8-activating enzyme hUba 3, complete cds.//4.3E-294//1329bp//100%/AB012190	C-PLACE4000522//NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (XOTCH PROTEIN).//2.4E-191//828aa//48%/P21783
C-PLACE1009794	C-PLACE4000590
C-PLACE1009845//Homo sapiens mRNA for KIAA0905 protein, complete c ds.//0//2685bp//99%/AB020712	C-PLACE4000638
C-PLACE1009886	C-PLACE4000650//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN).// 7.9E-17//201aa//34%/P49816
C-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN IN SEH1-PRP20 INT ERGENIC REGION.//1.9E-108//277aa//43%/P53145	C-Y79AA1001647
C-PLACE1009971	
C-PLACE1009992//LIMULUS CLOTTING FACTOR C PRECURSOR (EC 3.4.21.84)//4.6E-59//450aa//34%/P28175	
C-PLACE1009995//Homo sapiens mRNA: cDNA DKFZp5640123 (from clone D KFZp5640123).//0//1962bp//99%/AL080122	
C-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds.//5.2E-70//136bp//73%/U48288	
C-PLACE1010023	
C-PLACE1010031	
C-PLACE1010053//M. musculus Spnr mRNA for RNA binding protein.//6E- 279//1402bp//94%/X84692	
C-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2019bp//99%/AF065482	
C-PLACE1010076	
C-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-).//1.4E-268//506aa//98%	

【0229】

全長塩基配列及び推定アミノ酸配列に対する同源性検索結果データ

各データは、配列名、ヒットデータのDefinition、P値、比較配列の長
さ、同源性、ヒットデータのAccession No.の順に//で区切って記載した。C-HEMBA1000005//DNAJ PROTEIN HOMOLOG MTJ1.//1.9E-250//554aa//85%/
Q61712
C-HEMBA1000030

【0958】

【表655】

C-HEMBA1000046	C-HEMBA1001286//COMPLEMENT DECAY-ACCELERATING FACTOR PRECURSOR.//0.0000002//198aa//29%/Q60401
C-HEMBA1000050	C-HEMBA1001303
C-HEMBA1000076	C-HEMBA1001310
C-HEMBA1000156//NEUROFILAMENT TRIPLET M PROTEIN (160 KD NEUROFILAMENT PROTEIN) (NF-M).//1.9E-12//368aa//24%/P08553	C-HEMBA1001326
C-HEMBA1000158//HEPATOCTE NUCLEAR FACTOR 3-GAMMA (HNF-3G).//5E-16//166aa//36%/P35584	C-HEMBA1001351//Homo sapiens VAMP-associated protein of 33 kDa (VA P-33) mRNA, complete cds.//1.4E-133//614bp//99%/AF057358
C-HEMBA1000168//CYCLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//2.9E-14//303aa//25%/P35662	C-HEMBA1001387//GTP-BINDING PROTEIN TC10.//2.9E-64//104aa//82%/P17081
C-HEMBA1000185//RAS-RELATED PROTEIN RAL-A.//3.4E-12//125aa//31%/P48555	C-HEMBA1001388
C-HEMBA1000193	C-HEMBA1001398
C-HEMBA1000227	C-HEMBA1001405
C-HEMBA1000288	C-HEMBA1001407
C-HEMBA1000302	C-HEMBA1001413
C-HEMBA1000304	C-HEMBA1001415
C-HEMBA1000307//CARNITINE DEFICIENCY-ASSOCIATED PROTEIN EXPRESSED IN VENTRICLE 1//5.2E-49//107aa//91%/O35594	C-HEMBA1001446
C-HEMBA1000369//Novel human mRNA similar to mouse gene PICK1 (TR:Q62083).//0//1950bp//98%/AL049654	C-HEMBA1001450
C-HEMBA1000387	C-HEMBA1001455
C-HEMBA1000392	C-HEMBA1001510//CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-6 (FRAGMENT).//1.7E-16//63aa//61%/P18850
C-HEMBA1000460	C-HEMBA1001526//PERIPLASMIC [FE] HYDROGENASE 1 (EC 1.18.99.1).//4.9E-31//399aa//29%/P29166
C-HEMBA1000488//RING CANAL PROTEIN (KELCH PROTEIN).//3.3E-45//481aa//29%/Q04652	C-HEMBA1001533
C-HEMBA1000491//RAS-LIKE PROTEIN 2.//2E-22//188aa//31%/P22279	C-HEMBA1001579//Homo sapiens mRNA for KIA0850 protein, complete cds.//0//1662bp//99%/AB020657
C-HEMBA1000501	C-HEMBA1001581
C-HEMBA1000508	C-HEMBA1001595//SEPTIN 2 HOMOLOG (FRAGMENT).//4.9E-156//348aa//83%/Q14141
C-HEMBA1000520	C-HEMBA1001635//TESTIS SPECIFIC PROTEIN A (ZINC FINGER PROTEIN TSG A).//1.6E-10//155aa//28%/Q63679
C-HEMBA1000531//HEAT SHOCK 70 KD PROTEIN COGNATE 1 (HEAT SHOCK 70 KD PROTEIN 70C) (FRAGMENTS).//2.6E-12//73aa//41%/P02826	C-HEMBA1001661//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT P ROTEIN).//4.6E-36//365aa//33%/P33450
C-HEMBA1000534	C-HEMBA1001702
C-HEMBA1000555	C-HEMBA1001714//Homo sapiens mRNA: cDNA DKFZp564G0422 (from clone DKFZp564G0422).//0//1845bp//99%/AL050386
C-HEMBA1000568	C-HEMBA1001731
C-HEMBA1000588	C-HEMBA1001744//SCY1 PROTEIN.//9.9E-32//481aa//25%/P53009
C-HEMBA1000608//HYPOTHETICAL PROTEIN KIA0411 (FRAGMENT).//1.8E-55//179aa//61%/O43295	C-HEMBA1001809//IMMEDIATE-EARLY PROTEIN IE180.//3.8E-11//206aa//36%/P11675
C-HEMBA1000636	C-HEMBA1001815
C-HEMBA1000682	C-HEMBA1001819//ZINC FINGER PROTEIN 184 (FRAGMENT).//2.9E-135//459aa//52%/Q99676
C-HEMBA1000686	C-HEMBA1001847//ZINC FINGER PROTEIN 29 (ZFP-29).//7.6E-64//221aa//55%/Q07230
C-HEMBA1000719	C-HEMBA1001864
C-HEMBA1000727	C-HEMBA1001869//TRITHORAX PROTEIN.//0.000096//166aa//27%/P20659
C-HEMBA1000752	C-HEMBA1001896//DIMETHYLGLYCINE DEHYDROGENASE PRECURSOR (EC 1.5.9.2) (ME2GLYDH).//9.3E-36//395aa//26%/Q63342
C-HEMBA1000817	C-HEMBA1001987
C-HEMBA1000851	C-HEMBA1002018
C-HEMBA1000867	C-HEMBA1002049
C-HEMBA1000869	C-HEMBA1002084
C-HEMBA1000872	C-HEMBA1002125
C-HEMBA1000910//MELANOMA-ASSOCIATED ANTIGEN B1 (MAGE-B1 ANTIGEN) (MAGE-XP ANTIGEN).//1.6E-30//127aa//40%/P43366	C-HEMBA1002161//MYOSIN HEAVY CHAIN, CARDIAC MUSCLE BETA ISOFORM.//1.4E-51//180aa//56%/P79293
C-HEMBA1000918	C-HEMBA1002177//TRANSCRIPTION FACTOR GATA-4 (GATA BINDING FACTOR-4).//6E-13//190aa//36%/P43594
C-HEMBA1000919//HYPOTHETICAL 65.5 KD TRP-ASP REPEATS CONTAINING PROTEIN F02E8.5 IN CHROMOSOME X.//1E-10//288aa//23%/Q19124	C-HEMBA1002191
C-HEMBA1000946	C-HEMBA1002199
C-HEMBA1000968	C-HEMBA1002212//TYROSINE-PROTEIN KINASE 2 (EC 2.7.1.112) (FRAGMENT).//3E-17//267aa//29%/P18161
C-HEMBA1000971	C-HEMBA1002237
C-HEMBA1000975	C-HEMBA1002265
C-HEMBA1001009	C-HEMBA1002267//Sus scrofa decorin mRNA, complete cds.//1.1E-46//302bp//90%/AF125537
C-HEMBA1001022	C-HEMBA1002349
C-HEMBA1001043//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NON ERYTHROID) (FRAGMENT).//1.4E-12//131aa//38%/Q01485	C-HEMBA1002363//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//1847bp//99%/AF092563
C-HEMBA1001052	C-HEMBA1002419//TRICHOHYALIN.//1.9E-09//299aa//24%/P22793
C-HEMBA1001080	C-HEMBA1002430
C-HEMBA1001085	C-HEMBA1002439
C-HEMBA1001088//PINCH PROTEIN (PARTICULARLY INTERESTING NEW CYS-HIS PROTEIN).//3.5E-50//176aa//57%/P48059	C-HEMBA1002458//OVARIAN GRANULOSA CELL 13.0 KD PROTEIN HGR74.//4.2E-24//109aa//55%/Q00994
C-HEMBA1001109	C-HEMBA1002460
C-HEMBA1001122	C-HEMBA1002462
C-HEMBA1001133	C-HEMBA1002469//DXS8237E PROTEIN (FRAGMENT).//3.5E-50//199aa//61%/P98175
C-HEMBA1001137//ZINC FINGER PROTEIN 33A (ZINC FINGER PROTEIN K0X31) (KIA0065) (HAD946) (FRAGMENT).//1.5E-116//197aa//58%/Q06730	C-HEMBA1002475//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN).//1.1E-12//285aa//31%/P17437
C-HEMBA1001140	C-HEMBA1002477
C-HEMBA1001174//ADP-RIBOSYLATION FACTOR-LIKE PROTEIN S.//6.8E-79//178aa//80%/P51646	
C-HEMBA1001197//Homo sapiens mRNA for KIA0871 protein, complete cds.//9.5E-257//1307bp//94%/AB020678	
C-HEMBA1001235	
C-HEMBA1001257//Homo sapiens mRNA 2-methylacyl-CoA racemase.//0//1672bp//99%/AJ130733	
C-HEMBA1001281	

【0959】

【表656】

C-HEMBA1002495//LIGHT-MEDIATED DEVELOPMENT PROTEIN DET1.//6.8E-53/ /257aa//36%/P48732	ds.//0//1732bp//98%/AB020712
C-HEMBA1002515	C-HEMBA1003417//Homo sapiens mRNA: cDNA DKFp586C021 (from clone O KF2p586C021).//1.6E-312//1414bp//99%/AL050287
C-HEMBA1002542	C-HEMBA1003418//TRICHOHYALIN.//8.7E-19//281aa//31%/P37709
C-HEMBA1002569//Homo sapiens protein associated with Myc mRNA, com plete cds.//6.8E-305//951bp//99%/AF075587	C-HEMBA1003433//Homo sapiens gene for NBS1, complete cds.//0//511b p//94%/AB013139
C-HEMBA1002583	C-HEMBA1003447
C-HEMBA1002609//Homo sapiens mRNA for KIAA0597 protein, partial cd s.//1.4E-253//1149bp//99%/AB011169	C-HEMBA1003461
C-HEMBA1002624//Homo sapiens mRNA for KIAA0808 protein, complete c ds.//0//1539bp//99%/AB018351	C-HEMBA1003463
C-HEMBA1002688	C-HEMBA1003528
C-HEMBA1002696	C-HEMBA1003545//INSULIN GENE ENHANCER PROTEIN ISL-2 (ISLET-2).//8. 8E-189//360aa//96%/P50480
C-HEMBA1002750	C-HEMBA1003555//NUCLEOTIDE-BINDING PROTEIN (NBP).//2.1E-68//251aa/ /52%/P53384
C-HEMBA1002768//Homo sapiens mRNA for Cdc42-interacting protein 4 (CIP4).//1E-80//882bp//61%/AJ000414	C-HEMBA1003560//GUANINE NUCLEOTIDE-BINDING PROTEIN G(I)/G(S)/G(O) GAMMA-2 SUBUNIT (G GAMMA-1).//1.2E-31//71aa//100%/P16874
C-HEMBA1002770//Homo sapiens mRNA for KIAA0829 protein, partial cd s.//0//1532bp//99%/AB020636	C-HEMBA1003568//52 KD RO PROTEIN (SJOGREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)).//7.9E-49//279aa//32%/P19474
C-HEMBA1002777	C-HEMBA1003569//METASTASIS-ASSOCIATED PROTEIN MTA1.//6.9E-206//445 aa//74%/Q13330
C-HEMBA1002794	C-HEMBA1003581//TALIN.//4.4E-45//52aa//98%/P26039
C-HEMBA1002810//Homo sapiens formin binding protein 21 mRNA, compl ete cds.//8.2E-314//1437bp//99%/AF071185	C-HEMBA1003591//CHLOROPLAST 28 KD RIBONUCLEOPROTEIN PRECURSOR (28R NP).//4.4E-10//118aa//35%/P19682
C-HEMBA1002818//Homo sapiens mRNA for fibulin-4.//2E-304//1383bp// 99%/AJ132819	C-HEMBA1003615
C-HEMBA1002850	C-HEMBA1003617//Homo sapiens HRIHFB2157 mRNA, partial cds.//8.2E-1 78//501bp//97%/AB015344
C-HEMBA1002863	C-HEMBA1003621
C-HEMBA1002876//HYPOTHETICAL 26.4 KD PROTEIN EEED8.8 IN CHROMOSOME 11.//1.5E-44//188aa//52%/Q09297	C-HEMBA1003662//TBX2 PROTEIN (T-BOX PROTEIN 2).//1.2E-75//151aa//9 9%/Q13207
C-HEMBA1002935//Homo sapiens mRNA for KIAA0576 protein, partial cd s.//0//1483bp//100%/AB011148	C-HEMBA1003690//HISTONE DEACETYLASE HDAC1.//2.1E-59//249aa//47%/P5 3973
C-HEMBA1002937	C-HEMBA1003711
C-HEMBA1002939//ANKYRIN R (ANKYRINS 2.1 AND 2.2) (ERYTHROCYTE ANKY RIN).//2E-34//300aa//34%/P16157	C-HEMBA1003807
C-HEMBA1002951//Homo sapiens mRNA for KIAA0903 protein, partial cd s.//0//1752bp//99%/AB020710	C-HEMBA1003864
C-HEMBA1002954	C-HEMBA1003953//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//3.8E-16//89aa//46%/P16372
C-HEMBA1002971	C-HEMBA1003959
C-HEMBA1002973//CAMP-DEPENDENT 3',5'-CYCLIC PHOSPHODIESTERASE 4B (EC 3.1.4.17) (DPOE4).//1.2E-27//63aa//100%/P14646	C-HEMBA1003989
C-HEMBA1002997//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//3.8E-25// 534aa//24%/Q02224	C-HEMBA1004074
C-HEMBA1003033	C-HEMBA1004097//Mus musculus putative transcription factor mRNA, c omplete cds.//8.5E-22//1188bp//78%/AF091234
C-HEMBA1003035	C-HEMBA1004146
C-HEMBA1003041	C-HEMBA1004199//Homo sapiens mRNA for KIAA0928 protein, partial cd s.//0//1893bp//98%/AB023145
C-HEMBA1003046//MITOCHONDRIAL PROCESSING PROTEASE BETA SUBUNIT PRE CURSOR (EC 3.4.24.64) (BETA-MPP) (P-52).//2.5E-263//489aa//99%/O7 5439	C-HEMBA1004207//Homo sapiens leptin receptor short form (db) mRNA, complete cds.//0//1892bp//99%/U50748
C-HEMBA1003067	C-HEMBA1004227//Rattus norvegicus protein phosphatase 2C mRNA, com plete cds.//5.7E-217//1217bp//88%/AF095927
C-HEMBA1003096	C-HEMBA1004246
C-HEMBA1003117	C-HEMBA1004276//Homo sapiens AP-4 adaptor complex beta4 subunit mR NA, complete cds.//4.8E-257//738bp//99%/AF092094
C-HEMBA1003129	C-HEMBA1004289
C-HEMBA1003136//MANNOSE-1-PHOSPHATE GUANYLTRANSFERASE (EC 2.7.7.1 3) (ATP-MANNOSE-1-PHOSPHATE GUANYLYLTRANSFERASE) (NDP-HEXOSE PYROPH OSPHORYLASE).//8.5E-51//221aa//33%/P41940	C-HEMBA1004509//Homo sapiens CGI-21 protein mRNA, complete cds.//0 //1512bp//96%/AF132955
C-HEMBA1003148//Homo sapiens mRNA full length insert cDNA clone EU ROIMAGE 381801.//0//1583bp//99%/ALD79278	C-HEMBA1004534//Homo sapiens gamma-filamin (ABPL) mRNA, complete c ds.//1.2E-316//1445bp//99%/AF089841
C-HEMBA1003175	C-HEMBA1004596
C-HEMBA1003179//PROBABLE TRNA (5-METHYLAMINOMETHYL-2-THIOURIDYLAT E)-METHYLTRANSFERASE (EC 2.1.1.61).//5.9E-74//134aa//53%/P44551	C-HEMBA1004693
C-HEMBA1003199	C-HEMBA1004736
C-HEMBA1003222	C-HEMBA1004753
C-HEMBA1003235//TROPOMYOSIN.//0.000023//109aa//33%/Q02088	C-HEMBA1004756//Human transporter protein (glt) mRNA, complete cd s.//9.1E-34//515bp//66%/U49082
C-HEMBA1003250//PROTEIN KINASE APK1A (EC 2.7.1.-).//7.2E-41//245aa //42%/Q06548	C-HEMBA1004758//Homo sapiens transcription factor SL1 mRNA, comple te cds.//2.6E-246//1249bp//94%/L39060
C-HEMBA1003257	C-HEMBA1004763
C-HEMBA1003281//POLIOVIRUS RECEPTOR PRECURSOR.//6E-11//239aa//32%/ /P32506	C-HEMBA1004768//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//5.4E-111//3 14aa//58%/P08547
C-HEMBA1003286//Homo sapiens mRNA for beta-1,4-galactosyltransfera se IV, complete cds.//5.4E-229//1043bp//99%/AB024436	C-HEMBA1004771
C-HEMBA1003291//Homo sapiens mRNA for KIAA0537 protein, complete c ds.//0//791bp//99%/AB011109	C-HEMBA1004776
C-HEMBA1003322	C-HEMBA1004795//CDC4-LIKE PROTEIN (FRAGMENT).//3.8E-69//198aa//66% //P50851
C-HEMBA1003327	C-HEMBA1004806
C-HEMBA1003369//CENTROMERIC PROTEIN E (CENP-E PROTEIN).//0.000000 2//248aa//23%/Q02224	C-HEMBA1004847//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68). //8.2E-154//317aa//94%/Q00004
C-HEMBA1003370	C-HEMBA1004850
C-HEMBA1003380	C-HEMBA1004853//Homo sapiens mRNA: cDNA DKFp586M2022 (from clone DKFp586M2022).//0//1443bp//100%/AL080114
C-HEMBA1003395	C-HEMBA1004923
C-HEMBA1003402	C-HEMBA1004929
C-HEMBA1003408//Homo sapiens mRNA for KIAA0905 protein, complete c	C-HEMBA1004930//26S PROTEASOME SUBUNIT 55B (KIAA0072) (HA1357).//

【0960】

【表657】

3.3E-27//65aa//100%/Q16401
C-HEMBA1004933
C-HEMBA1004954
C-HEMBA1004972//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H).//0.00000096//286aa//23%/P12036
C-HEMBA1005475
C-HEMBA1005581//Homo sapiens SLIT2 (SLIL2) mRNA, complete cds.//0//1721bp//100%/AF133270
C-HEMBA1006248//ZINC FINGER PROTEIN MFG-1 (ZINC FINGER PROTEIN 58) (FRAGMENT).//8.6E-23//151aa//37%/P16372
C-HEMBA1006310//Rattus norvegicus cytosolic sorting protein PACS-1 a (PACS-1) mRNA, complete cds.//3.7E-225//1189bp//88%/AF076183
C-HEMBA1006344//RADIXIN.//1.5E-31//333aa//28%/P26043
C-HEMBA1006377
C-HEMBA1006467
C-HEMBA1006474//40 KD PROTEIN.//1.4E-39//292aa//34%/Q01552
C-HEMBA1006530
C-HEMBA1006737//ANKYRIN, BRAIN VARIANT 2 (ANKYRIN B) (ANKYRIN, NON ERYTHROID) (FRAGMENT).//0.000000043//111aa//40%/Q01485
C-HEMBA1006795
C-HEMBA1006877//OXYSTEROL-BINDING PROTEIN.//2E-59//378aa//39%/P16258
C-HEMBA1006936
C-HEMBA1007018//Homo sapiens dynein light chain-A mRNA, complete cds.//1.5E-267//1215bp//99%/AF078849
C-HEMBA1007342
C-HEMBA10000008
C-HEMBA10000018
C-HEMBA10000024
C-HEMBA10000025
C-HEMBA10000036
C-HEMBA10000037//Homo sapiens erythroblast macrophage protein EMP mRNA, complete cds.//2.8E-187//1582bp//80%/AF084928
C-HEMBA10000083//MYOSIN LIGHT CHAIN KINASE, SMOOTH MUSCLE AND NON-MUSCLE ISOZYMES (EC 2.7.1.117) (MLCK) [CONTAINS: TELOKIN].//1.9E-22//426aa//25%/P11799
C-HEMBA1000103
C-HEMBA1000119//Homo sapiens ASMTL gene.//0//1891bp//99%/Y15521
C-HEMBA1000136
C-HEMBA1000215
C-HEMBA1000226//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE EEDD8.5.//2.7E-12//112aa//47%/Q09530
C-HEMBA1000244
C-HEMBA1000266//HYPOTHETICAL 54.5 KD TRP-ASP REPEATS CONTAINING PROTEIN 2C302.2 IN CHROMOSOME V.//6.1E-09//242aa//26%/Q23256
C-HEMBA1000338
C-HEMBA1000339
C-HEMBA1000391
C-HEMBA1000438
C-HEMBA1000449
C-HEMBA1000589
C-HEMBA1000591
C-HEMBA1000623
C-HEMBA1000630
C-HEMBA1000631//LONGEVITY-ASSURANCE PROTEIN 1 (LONGEVITY ASSURANCE FACTOR 1).//4.1E-19//232aa//28%/P78970
C-HEMBA1000632//GUANINE NUCLEOTIDE RELEASING PROTEIN (GNRP).//2.2E-28//273aa//31%/P27671
C-HEMBA1000671
C-HEMBA1000673
C-HEMBA1000705
C-HEMBA1000706
C-HEMBA1000725//Rattus norvegicus GTPase Rab8b (Rab8b) mRNA, complete cds.//6.2E-130//692bp//93%/U53475
C-HEMBA1000763//Homo sapiens CGI-89 protein mRNA, complete cds.//0//1676bp//96%/AF151847
C-HEMBA1000781//Homo sapiens mitogen-activated protein kinase kinase kinase MEKK2 mRNA, complete cds.//1.2E-126//613bp//97%/AF111105
C-HEMBA1000789//PUTATIVE 90.2 KD ZINC FINGER PROTEIN IN CCA1-ADK2 INTERGENIC REGION.//5.1E-54//232aa//43%/P39956
C-HEMBA1000807
C-HEMBA1000810
C-HEMBA1000848
C-HEMBA1000852
C-HEMBA1000870
C-HEMBA1000887
C-HEMBA1000908
C-HEMBA1000927//Homo sapiens calseinin mRNA, complete cds.//1.1E-70//595bp//76%/AF120102
C-HEMBA1000947//Homo sapiens clone HAW100 putative ribonuclease II mRNA, complete cds.//0//2292bp//99%/AF116910
C-HEMBA1000973//Mus musculus schlafen3 (Sln3) mRNA, complete cds.//3.4E-120//580bp//67%/AF099974
C-HEMBA1000975
C-HEMBA1000985//MIPP PROTEIN (MURINE IAP-PROMOTED PLACENTA-EXPRESSED PROTEIN).//8.6E-18//178aa//30%/P28575
C-HEMBA1000991
C-HEMBA1001011//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//1.4E-73//230aa//45%/P51523
C-HEMBA1001014
C-HEMBA1001024
C-HEMBA1001056//PROLIFERATING-CELL NUCLEOLAR ANTIGEN P120 (PROLIFERATION-ASSOCIATED NUCLEOLAR PROTEIN P120).//2.9E-19//264aa//34%/P46087
C-HEMBA1001058//Homo sapiens neuronal thread protein AD7c-NTP mRNA, complete cds.//3.6E-52//331bp//80%/AF010144
C-HEMBA1001068//Homo sapiens liprin-beta2 mRNA, partial cds.//2.4E-307//1447bp//97%/AF034803
C-HEMBA1001096
C-HEMBA1001105
C-HEMBA1001117
C-HEMBA1001126
C-HEMBA1001137//Homo sapiens mRNA for putative phospholipase, complete cds.//0//3069bp//99%/AB019435
C-HEMBA1001151//Rattus norvegicus golgi stacking protein homolog GRASP55 mRNA, complete cds.//4.2E-210//1835bp//76%/AF110267
C-HEMBA1001153
C-HEMBA1001169
C-HEMBA1001175//ANKYRIN.//6.9E-11//169aa//31%/Q02357
C-HEMBA1001182
C-HEMBA1001199
C-HEMBA1001210//Homo sapiens mRNA for KIAA0970 protein, complete cds.//0//1816bp//99%/AB023187
C-HEMBA1001242//Homo sapiens topoisomerase-related function protein (TRF4-2) mRNA, partial cds.//1.8E-284//713bp//100%/AF089897
C-HEMBA1001288//Homo sapiens CGI-32 protein mRNA, complete cds.//1.8E-274//642bp//99%/AF132966
C-HEMBA1001289
C-HEMBA1001294//GTP-BINDING PROTEIN TC10.//1.2E-79//196aa//80%/P17081
C-HEMBA1001314//Mus musculus Olf-1/EBF-like-3 transcription factor (O/E-3) mRNA, complete cds.//1.3E-129//724bp//86%/U92703
C-HEMBA1001331
C-HEMBA1001339//DXS0237E PROTEIN (FRAGMENT).//0.0000046//124aa//37%/P98175
C-HEMBA1001346//Homo sapiens phenylalanine-tRNA synthetase (FARS1) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.1E-58//292bp//99%/AF097441
C-HEMBA1001369
C-HEMBA1001384//Homo sapiens COP9 complex subunit 4 mRNA, complete cds.//0//1586bp//99%/AF100757
C-HEMBA1001387
C-MAHMA1002317
C-MAHMA1002319
C-MAHMA1002385//RIBONUCLEOPROTEIN RB97D.//0.00000015//206aa//29%/Q02926
C-NT2RM1000080//UNC-1 PROTEIN.//5.9E-25//211aa//31%/Q21190
C-NT2RM1000242
C-NT2RM1000257//MAGO NASHI PROTEIN.//7.9E-69//143aa//91%/P49028
C-NT2RM1000280//VACUOLAR ATP SYNTHASE SUBUNIT D (EC 3.6.1.34) (V-ATPASE D SUBUNIT) (V-ATPASE 28 KD ACCESSORY PROTEIN).//1.5E-106//118aa//97%/P39942
C-NT2RM1000669
C-NT2RM1000781
C-NT2RM1000867//Homo sapiens HSPC033 mRNA, complete cds.//6.3E-172//798bp//99%/AF092138
C-NT2RM1001008
C-NT2RM1001044//Homo sapiens HSPC031 mRNA, complete cds.//0.00000002//980bp//95%/AF085360
C-NT2RM1001074
C-NT2RM1001115//ENDOCHITINASE 2 PRECURSOR (EC 3.2.1.14).//0.0000058//239aa//27%/P
C-NT2RM2000006//Human DNA sequence from clone 796F18 on chromosome 1p36.11-36.33 Contains a pseudogene similar to MMS2, ESTs and GSS s. complete sequence.//0//1740bp//99%/AL031291
C-NT2RM2000013//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//2.2E-144//362aa//71%/P25167
C-NT2RM2000030//DYNEIN INTERMEDIATE CHAIN, CYTOSOLIC (DM IC) (CYTO

【0961】

【表658】

PLASMIC DYNEIN INTERMEDIATE CHAIN) //0.0000043//136aa//31%/P54703	P) //9.5E-279//545aa//98%/P23514
C-NT2RM2000032	C-NT2RM2000837
C-NT2RM2000042	C-NT2RM2000951//Homo sapiens TYLB mRNA for tylosukinase, complete cds. //1.7E-200//927bp//99%/AB015046
C-NT2RM2000092//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 8 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 8) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 8) (DEUBIQUITINATING ENZYME 8) //1.3E-36//160aa//40%/P50102	C-NT2RM2000952
C-NT2RM2000093	C-NT2RM2000984
C-NT2RM2000101	C-NT2RM2001004
C-NT2RM2000191//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds. //0//1574bp//99%/AF067223	C-NT2RM2001035//CCR4-ASSOCIATED FACTOR 1 (CAF1) //8.2E-154//285aa//99%/Q60809
C-NT2RM2000192	C-NT2RM2001065
C-NT2RM2000239	C-NT2RM2001100//HYPOTHETICAL 39.7 KD PROTEIN C34E10.2 IN CHROMOSOM E 111. //2.4E-15//266aa//26%/P46577
C-NT2RM2000250//Homo sapiens mRNA: cDNA DKFZp564L232 (from clone D KFP564L232) //4.2E-314//1416bp//100%/AL080069	C-NT2RM2001131
C-NT2RM2000259	C-NT2RM2001141
C-NT2RM2000260//EXTENSIN PRECURSOR (PROLINE-RICH GLYCOPROTEIN) //3.6E-19//181aa//34%/P14918	C-NT2RM2001152
C-NT2RM2000287	C-NT2RM2001177//Homo sapiens mRNA: cDNA DKFZp586G1822 (from clone DKFZp586G1822) //2.1E-293//1335bp//99%/AL080109
C-NT2RM2000322//Homo sapiens mRNA for KIAA0859 protein, complete cds. //3.4E-294//863bp//99%/AB020666	C-NT2RM2001194
C-NT2RM2000359//Homo sapiens mRNA for KIAA0560 protein, complete cds. //0//1637bp//99%/AB011132	C-NT2RM2001196//PROLINE-RICH PROTEIN MP-3 (FRAGMENT) //1.3E-20//267aa//35%/P05143
C-NT2RM2000363//BREAKPOINT CLUSTER REGION PROTEIN //1.8E-14//245aa//29%/P11274	C-NT2RM2001201//EUKARYOTIC TRANSLATION INITIATION FACTOR 5 (EIF-5) //0.0000015//95aa//35%/P48724
C-NT2RM2000368//Homo sapiens protein kinase C-binding protein RACK 7 mRNA, partial cds. //0//1506bp//99%/U48251	C-NT2RM2001221//KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10) //3.6E-10//177aa//32%/P97924
C-NT2RM2000371//POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE (EC 2.7.7.8) (POLYNUCLEOTIDE) //1.7E-68//419aa//36%/P50849	C-NT2RM2001238//GLUTAMINASE, KIDNEY ISOFORM PRECURSOR (EC 3.5.1.2) (GLS) (L-GLUTAMINE AMIDOHYDROLASE) //1.3E-180//328aa//99%/P13264
C-NT2RM2000374	C-NT2RM2001243
C-NT2RM2000395	C-NT2RM2001247
C-NT2RM2000402//ENDOSOMAL P24A PROTEIN PRECURSOR (70 KD ENDOMEMBRANE PROTEIN) (PHEROMONE ALPHA-FACTOR TRANSPORTER) (ACIDIC 24 KD LAT E ENDOCYTIC INTERMEDIATE COMPONENT) //1.6E-54//344aa//33%/P32802	C-NT2RM2001256//PROTEIN TSC24 (MEIOTIC CHECK POINT REGULATOR) //1.6E-166//312aa//98%/P53995
C-NT2RM2000407	C-NT2RM2001291
C-NT2RM2000422//SODIUM- AND CHLORIDE-DEPENDENT TRANSPORTER NTT73. //1E-222//237aa//89%/Q08469	C-NT2RM2001306//Homo sapiens mRNA: cDNA DKFZp564I052 (from clone: D KFP564I052) //0//1694bp//99%/AL080063
C-NT2RM2000452//HYPOTHETICAL 63.6 KD PROTEIN IN YPT52-GCN3 INTERGENIC REGION //0.000001//157aa//28%/P36113	C-NT2RM2001312
C-NT2RM2000469//NITROGEN PERMEASE REACTIVATOR PROTEIN (EC 2.7.1.-) //0.0000089//377aa//24%/P22211	C-NT2RM2001319
C-NT2RM2000490//SYNAPTOTAGMIN (P65) //1.8E-13//166aa//34%/P41823	C-NT2RM2001324//ZYXIN //6.8E-55//200aa//41%/Q04584
C-NT2RM2000502	C-NT2RM2001345//VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1 //0.0000029//334aa//22%/Q00808
C-NT2RM2000504//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds. //0//1673bp//99%/AF061243	C-NT2RM2001370
C-NT2RM2000522//SKIN SECRETORY PROTEIN XP2 PRECURSOR (APEG PROTEIN) //1.3E-12//282aa//32%/P17437	C-NT2RM2001393
C-NT2RM2000540	C-NT2RM2001420
C-NT2RM2000567	C-NT2RM2001424//Homo sapiens mRNA: cDNA DKFZp586D0920 (from clone DKFZp586D0920) //0//1621bp//100%/AL050146
C-NT2RM2000569	C-NT2RM2001499//LOW-AFFINITY CATIONIC AMINO ACID TRANSPORTER-2 (CAT-2) (CAT2) //7.4E-121//437aa//57%/P52569
C-NT2RM2000577//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCINE--TRNA LIGASE) (ILERS) //1.7E-187//741aa//46%/P73505	C-NT2RM2001504
C-NT2RM2000581//Homo sapiens mRNA for KIAA0214 protein, complete cds. //0//3001bp//99%/D86987	C-NT2RM2001524
C-NT2RM2000588//HISTONE DEACETYLASE HDAC1 //2.8E-60//384aa//40%/P53973	C-NT2RM2001544
C-NT2RM2000594//Homo sapiens DNA cytosine-5 methyltransferase 3 beta 3 (DNMT3B) mRNA, complete cds. //0//2712bp//99%/AF156487	C-NT2RM2001547//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1) //6.9E-27//90aa//42%/P38660
C-NT2RM2000599//Homo sapiens F-box protein Lilina (LILINA) mRNA, complete cds. //4.9E-70//838bp//69%/AF179221	C-NT2RM2001575//52 KD RO PROTEIN (SJOJREN SYNDROME TYPE A ANTIGEN (SS-A)) (RO(SS-A)) //4.3E-61//312aa//44%/P19474
C-NT2RM2000624//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75) //4.4E-32//319aa//35%/Q08170	C-NT2RM2001582
C-NT2RM2000635//Homo sapiens mRNA for KIAA0729 protein, partial cds. //0//3791bp//99%/AB018272	C-NT2RM2001886//Homo sapiens mRNA for KIAA0710 protein, complete cds. //0//1000bp//100%/AB014610
C-NT2RM2000636//Homo sapiens mRNA for KIAA0658 protein, partial cds. //0//2530bp//99%/AB014558	C-NT2RM2001896//CELL DIVISION PROTEIN FTSJ //5.1E-26//204aa//34%/P28692
C-NT2RM2000639	C-NT2RM2001903//Homo sapiens mRNA for KIAA0452 protein, partial cds. //0//2390bp//99%/AB007931
C-NT2RM2000649//Homo sapiens mRNA for KIAA0676 protein, partial cds. //0//1543bp//99%/AB014576	C-NT2RM2001930
C-NT2RM2000669	C-NT2RM2001935
C-NT2RM2000691//ACTIN-LIKE PROTEIN 3 (ACTIN-2) //3.7E-142//285aa//90%/P32391	C-NT2RM2001936//32.3 KD PROTEIN IN CWPI-MBR1 INTERGENIC REGION. //2.7E-21//216aa//34%/P28320
C-NT2RM2000714//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1) //3.8E-23//184aa//36%/Q15404	C-NT2RM2001950//HYPOTHETICAL 105.9 KD PROTEIN IN AAC3-RFC5 INTERGENIC REGION //0.000001//212aa//23%/P38250
C-NT2RM2000718//Homo sapiens HRIHF82436 mRNA, partial cds. //4.4E-23//1065bp//99%/AB015342	C-NT2RM2001982
C-NT2RM2000740//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SNF2L //5.7E-53//266aa//43%/P41877	C-NT2RM2001989//NUCLEOLAR PROTEIN NOP4 (NUCLEOLAR PROTEIN NOP77) //1.9E-39//253aa//35%/P37838
C-NT2RM2000795	C-NT2RM2001997//PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (EC 5.3.4.1) //1.3E-10//232aa//28%/Q12730
C-NT2RM2000821//COATOMER BETA SUBUNIT (BETA-COAT PROTEIN) (BETA-CO	C-NT2RM2001998//HYPOTHETICAL 85.7 KD PROTEIN C13G6.03 IN CHROMOSOM E 1 //3.1E-12//206aa//30%/Q09782
	C-NT2RM2002004//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTO ANTIGEN HOMOLOG) //0.00000029//83aa//44%/P40796
	C-NT2RM2002014//HYPOTHETICAL 81.4 KD PROTEIN IN GREB-FEOA INTERGENIC REGION //1.1E-89//425aa//41%/P46837
	C-NT2RM2002030//Homo sapiens mRNA for Glutamine:fructose-6-phosphate amidotransferase, complete cds. //0//1959bp//99%/AB016789
	C-NT2RM2002049
	C-NT2RM2002055//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS13.

【0962】

【表659】

//0.0000099//338aa//24%/Q07878	C-NT2RP1000259
C-NT2RM2002088//PUTATIVE HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN X (HNRNP X) (CBP).//5E-62//104aa//57%/Q61990	C-NT2RP1000272//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds.//5.8E-114//616bp//93%/AF067730
C-NT2RM2002091	C-NT2RP1000326//Homo sapiens metaxin 2 (MTX2) mRNA, nuclear gene encoding mitochondrial protein, complete cds.//1.3E-275//1249bp//99%/AF053551
C-NT2RM2002100//Homo sapiens mRNA for ATP-dependent RNA helicase, partial.//0//1807bp//99%/AJ010840	C-NT2RP1000333//ANTI-SILENCING PROTEIN 1.//8.7E-47//155aa//58%/P32447
C-NT2RM2002109//Homo sapiens glioma amplified on chromosome 1 protein (GAC1) mRNA, complete cds.//0//1868bp//99%/AF030435	C-NT2RP1000348//REDUCED VIABILITY UPON STARVATION PROTEIN 161.//1.7E-15//162aa//30%/P25343
C-NT2RM2002128//PUTATIVE SERINE/THREONINE-PROTEIN KINASE PKWA (EC 2.7.1.-).//4.9E-13//487aa//26%/P49695	C-NT2RP1000357
C-NT2RM2002142//GASTRULATION SPECIFIC PROTEIN G12.//8E-31//105aa//47%/P47805	C-NT2RP1000376//Homo sapiens mRNA: cDNA DKFZp434A102 (from clone DKFZp434A102).//0//2265bp//95%/AL080187
C-NT2RM2002178//Homo sapiens mRNA: cDNA DKFZp434E0335 (from clone DKFZp434E0335).//0//1683bp//99%/AL117402	C-NT2RP1000413//Homo sapiens mRNA for KIAA0587 protein, complete cds.//0//1056bp//99%/AB011159
C-NT2RM4000024//DNA-DIRECTED RNA POLYMERASE III 128 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE III SUBUNIT 2).//7.1E-155//381aa//72%/P25167	C-NT2RP1000416
C-NT2RM40000061	C-NT2RP1000439//Xenopus laevis chromosome condensation protein XCA P-G mRNA, complete cds.//1.8E-94//1019bp//63%/AF111423
C-NT2RM4000104//ZINC FINGER PROTEIN 135.//1.5E-81//251aa//53%/P52742	C-NT2RP1000443//QUINONE OXIDOREDUCTASE (EC 1.6.5.5) (NADPH:QUINONE REDUCTASE) (ZETA-CRYSTALLIN).//2.4E-10//227aa//25%/Q08257
C-NT2RM4000139//R.norvegicus trg mRNA.//2.3E-114//1161bp//72%/X58101	C-NT2RP1000470//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME 111.//2.6E-94//254aa//47%/P34580
C-NT2RM4000169//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//4.8E-13//686aa//23%/P25386	C-NT2RP1000478//TUBULIN BETA-5 CHAIN (CLASS-V).//4.5E-240//445aa//97%/P09653
C-NT2RM4000191//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.//9.2E-75//439aa//41%/P16381	C-NT2RP1000481
C-NT2RM4000197	C-NT2RP1000493//Homo sapiens mRNA for KIAA0017 protein, complete cds.//0//2728bp//99%/D87686
C-NT2RM4000210//Homo sapiens mRNA for KIAA0712 protein, complete cds.//0//1926bp//100%/AB018255	C-NT2RP1000547//COP-COATED VESICLE MEMBRANE PROTEIN P24 PRECURSOR (FRAGMENT).//1.1E-27//193aa//35%/P49020
C-NT2RM4000229//Callus gallus actin filament-associated protein (A-FAP-110) mRNA, complete cds.//1.1E-27//633bp//64%/L20303	C-NT2RP1000574//HOMEOBOX PROTEIN MEIS2 (MEIS1-RELATED PROTEIN 1).//3.5E-75//151aa//94%/P97367
C-NT2RM4000290//Human transducin-like enhancer protein (TLE3) mRNA, complete cds.//2.2E-276//1124bp//97%/M99438	C-NT2RP1000581
C-NT2RM4000344//Homo sapiens mRNA for ATP-dependent metalloproteinase YME1L.//0//2030bp//99%/AJ132637	C-NT2RP1000630//NECDIN.//2.4E-44//227aa//41%/P25233
C-NT2RM4000349//Homo sapiens HSPC028 mRNA, complete cds.//0//1827bp//99%/AF083246	C-NT2RP1000688
C-NT2RM4000354//LETHAL(2) DENTICLELESS PROTEIN (DTL83 PROTEIN).//1.5E-21//208aa//35%/Q24371	C-NT2RP1000695
C-NT2RM4000386//Mus musculus mRNA for Ten-m3, complete cds.//0//2156bp//86%/AB025412	C-NT2RP1000733//Human mRNA for GSPT1-TK protein, complete cds.//0//2057bp//99%/E14379
C-NT2RM4000395	C-NT2RP1000738//Homo sapiens Wolf-Hirschhorn syndrome candidate 2 protein (WHSC2) mRNA, complete cds.//0//2186bp//99%/AF101434
C-NT2RM4000421//Homo sapiens mRNA for nuclear transport receptor.//0//1730bp//99%/AJ133769	C-NT2RP1000782//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%/Q35566
C-NT2RM4000457//HYPOTHETICAL 111.9 KD PROTEIN C22H10.03C IN CHROMOSOME 1.//8E-20//393aa//24%/Q10297	C-NT2RP1000825//GTPASE-ACTIVATING PROTEIN RHOGAP (RHO-RELATED SMALL GTPASE PROTEIN ACTIVATOR) (CDC42 GTPASE-ACTIVATING PROTEIN) (P50-RHOGAP).//8.2E-83//334aa//50%/Q07960
C-NT2RM4000471//Homo sapiens cysteine desulfurase (nifs) mRNA, complete cds.//0//2092bp//99%/AF097025	C-NT2RP1000833//Homo sapiens cGMP phosphodiesterase A1 (PDE9A) mRNA, complete cds.//0//1494bp//99%/AF067223
C-NT2RM4000486//SALIVARY PROLINE-RICH PROTEIN PRECURSOR (CLONES CP3, CP4 AND CP5) [CONTAINS: BASIC PEPTIDE 18-6; PEPTIDE P-H].//4.8E-11//242aa//31%/P04280	C-NT2RP1000846
C-NT2RM4000496//SAP1 PROTEIN.//8.3E-53//434aa//29%/P39955	C-NT2RP1000851
C-NT2RM4000511	C-NT2RP1000856//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//232aa//30%/Q35566
C-NT2RM4000515//NEUROFILAMENT TRIPLET H PROTEIN (200 KD NEUROFILAMENT PROTEIN) (NF-H) (FRAGMENT).//1.1E-11//394aa//24%/P16884	C-NT2RP1000915//AUTOANTIGEN NGP-1.//1.7E-19//343aa//25%/Q13823
C-NT2RM4000520	C-NT2RP1000947//Human E2 ubiquitin conjugating enzyme UbcH5B (UBCH5B) mRNA, complete cds.//4.6E-105//504bp//99%/U39317
C-NT2RM4000585	C-NT2RP1000954//RING CANAL PROTEIN (KELCH PROTEIN).//1.4E-23//370aa//28%/Q04652
C-NT2RM4000595//Homo sapiens leucine-rich repeats containing F-box protein FBL3 mRNA, complete cds.//1.1E-285//1293bp//99%/AF186273	C-NT2RP1000958//AUTOANTIGEN NGP-1.//1.4E-19//343aa//25%/Q13823
C-NT2RP1000018//Homo sapiens mRNA for KIAA0687 protein, partial cds.//0//1940bp//95%/AB014587	C-NT2RP1000959//Human acidic ribosomal phosphoprotein P0 mRNA, complete cds.//2.5E-236//966bp//99%/M17885
C-NT2RP1000035//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//1652bp//99%/AB020657	C-NT2RP1000966//NUCLEOLIN (PROTEIN C23).//8.9E-299//554aa//99%/P19338
C-NT2RP1000040	C-NT2RP1000980
C-NT2RP1000063	C-NT2RP1000988
C-NT2RP1000086//H.sapiens mRNA for zinc finger protein, Hsa12.//0//1162bp//99%/P98834	C-NT2RP1001011//Drosophila melanogaster putative 43 kDa protein (TH1) mRNA, complete cds.//2.2E-78//1529bp//61%/L01790
C-NT2RP1000101	C-NT2RP1001014
C-NT2RP1000111//COPI REGULATORY PROTEIN.//4E-116//296aa//51%/P93471	C-NT2RP1001395
C-NT2RP1000112	C-NT2RP1001410//PUTATIVE GTP-BINDING PROTEIN W08E3.3.//8.9E-141//396aa//67%/P91917
C-NT2RP1000124	C-NT2RP1001424
C-NT2RP1000130//HEPATOMA-DERIVED GROWTH FACTOR (HDGF).//4.5E-50//181aa//60%/P51859	C-NT2RP1001449
C-NT2RP1000163//Homo sapiens mRNA for KIAA0948 protein, complete cds.//0//1889bp//98%/AB023165	C-NT2RP1001457//Homo sapiens partial mRNA for beta-transducin family protein (putative).//1.2E-137//629bp//100%/AJ005257
C-NT2RP1000170	C-NT2RP1001466
C-NT2RP1000191	C-NT2RP1001475
C-NT2RP1000202//ANKYRIN.//1E-25//302aa//34%/Q02357	C-NT2RP1001482
C-NT2RP1000243	C-NT2RP1001494//MALE STERILITY PROTEIN 2.//7.2E-40//261aa//27%/Q08891
	C-NT2RP1001543//WYO-INOSITOL-1-PHOSPHATE SYNTHASE (EC 5.5.1.4) (IP

【0963】

【表660】

S).//1.6E-166//506aa//60%/P42803	C-NT2RP2000503
C-NT2RP1001546//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.6E-30//232aa//30%/O35566	C-NT2RP2000510
C-NT2RP1001569//SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA).//5.8E-121//271aa//89%/P47758	C-NT2RP2000516
C-NT2RP1001616	C-NT2RP2000603
C-NT2RP1001665//CALMODULIN.//0.0000051//83aa//30%/P02594	C-NT2RP2000617
C-NT2RP2000006//DNAJ PROTEIN (40 KD HEAT SHOCK CHAPERONE PROTEIN) (HSP40).//9.8E-17//79aa//55%/O34136	C-NT2RP2000634//Homo sapiens mRNA for KIAA0614 protein, partial cd s.//0//2482bp//99%/AB014514
C-NT2RP2000007	C-NT2RP2000656
C-NT2RP2000008//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//2.4E-177//726aa//47%/P51523	C-NT2RP2000658
C-NT2RP2000032//RAS SUPPRESSOR PROTEIN 1 (RSU-1) (RSP-1 PROTEIN) (RSP-1).//1.8E-22//184aa//34%/Q01730	C-NT2RP2000668//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.3E-27//349aa//32%/Q01577
C-NT2RP2000045//Homo sapiens tumorous imaginal discs protein Tid56 homolog (TID1) mRNA, complete cds.//0//1390bp//98%/AF061749	C-NT2RP2000704
C-NT2RP2000054	C-NT2RP2000710//ASPARTYL-TRNA SYNTHETASE (EC 6.1.1.12) (ASPARTATE--TRNA LIGASE).//2.7E-100//488aa//44%/O32038
C-NT2RP2000056//PROTEIN-TYROSINE PHOSPHATASE EPSILON PRECURSOR (EC 3.1.3.48) (R-PTP- EPSILON).//9.4E-16//45aa//100%/P49446	C-NT2RP2000764//WIFS PROTEIN.//6.6E-36//252aa//42%/P12623
C-NT2RP2000067	C-NT2RP2000809//Homo sapiens mRNA for KIAA0873 protein, partial cd s.//0//3347bp//99%/AB020680
C-NT2RP2000070//CADHERIN-RELATED TUMOR SUPPRESSOR PRECURSOR (FAT P ROEIN).//3.4E-51//383aa//32%/P33450	C-NT2RP2000812//DILUTE MYOSIN HEAVY CHAIN, NON-MUSCLE (MYOSIN 5A).//0.00000056//179aa//29%/Q99104
C-NT2RP2000079	C-NT2RP2000814//GELATIN FACTOR (ACTIN BINDING PROTEIN 120) (ABP-1 20).//0.0000011//96aa//29%/P13466
C-NT2RP2000088//Homo sapiens mRNA for KIAA0795 protein, partial cd s.//0//2286bp//100%/AB018338	C-NT2RP2000816//MAGNESIUM-CHELATASE 30 KD SUBUNIT.//0.00000079//172aa//28%/P26174
C-NT2RP2000091	C-NT2RP2000819
C-NT2RP2000097	C-NT2RP2000841
C-NT2RP2000114//Homo sapiens mRNA for GM3 synthase, complete cds.//0//2244bp//99%/AB018356	C-NT2RP2000845
C-NT2RP2000120	C-NT2RP2000863
C-NT2RP2000126//POSSIBLE GLOBAL TRANSCRIPTION ACTIVATOR SMF2L.//2.5E-117//541aa//42%/P41877	C-NT2RP2000880//PROBABLE TRANSLATION INITIATION FACTOR IF-2.//0//694aa//99%/O60841
C-NT2RP2000133//Homo sapiens mRNA for KIAA0989 protein, partial cd s.//0//2286bp//99%/AB023206	C-NT2RP2000892
C-NT2RP2000147//CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIAN CHAIN).//4.4E-226//423aa//99%/P35585	C-NT2RP2000931//MATRIN 3.//2.4E-289//467aa//95%/P43244
C-NT2RP2000153//GAR2 PROTEIN.//9.8E-23//311aa//28%/P41891	C-NT2RP2000932//Homo sapiens mRNA: cDNA DKFZp5640043 (from clone D KFZp5640043).//0//2487bp//99%/AL050390
C-NT2RP2000157//ML02 PROTEIN.//2.6E-11//62aa//40%/Q09329	C-NT2RP2000938
C-NT2RP2000161//Homo sapiens mRNA for KIAA1008 protein, complete c ds.//3.4E-315//1430bp//99%/AB023225	C-NT2RP2000943//Homo sapiens mRNA for KIAA0755 protein, complete c ds.//0//3458bp//99%/AB018298
C-NT2RP2000173	C-NT2RP2000965//Homo sapiens mRNA for fls353, complete cds.//0//1989bp//96%/AB024704
C-NT2RP2000195	C-NT2RP2000985
C-NT2RP2000205	C-NT2RP2001036
C-NT2RP2000208//Homo sapiens mRNA for KIAA0892 protein, partial cd s.//0//2898bp//99%/AB020699	C-NT2RP2001044
C-NT2RP2000224//INSULIN RECEPTOR SUBSTRATE-1 (IRS-1).//0.000043//103aa//28%/P35568	C-NT2RP2001056//Homo sapiens mRNA, chromosome 1 specific transcrip t KIAA0488.//0//2749bp//99%/AB007957
C-NT2RP2000232	C-NT2RP2001065
C-NT2RP2000233	C-NT2RP2001070//PUTATIVE PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (EC 1.4.3.5) (PMP/PMP OXIDASE).//5.8E-46//222aa//45%/Q20939
C-NT2RP2000239	C-NT2RP2001081//SYNAPTOTACMIN IV.//4.2E-118//430aa//54%/P50232
C-NT2RP2000248//UDP-N-ACETYLGLUCOSAMINE--PEPTIDE N-ACETYLGLUCOSAM I NYLTRANSFERASE 110 KD SUBUNIT (EC 2.4.1.-) (O-GLCNAC TRANSFERASE P 110 SUBUNIT).//3.4E-21//210aa//33%/P56558	C-NT2RP2001094
C-NT2RP2000270	C-NT2RP2001119
C-NT2RP2000274	C-NT2RP2001127//Homo sapiens mRNA for PLU-1 protein.//0//2514bp//99%/AJ132440
C-NT2RP2000283	C-NT2RP2001218
C-NT2RP2000288//HYPOTHETICAL I11.9 KD PROTEIN C22H10.03C IN CHROMO SOME 1.//1.6E-27//576aa//25%/Q10297	C-NT2RP2001245//MYOSIN HEAVY CHAIN, NONMUSCLE (CELLULAR MYOSIN HEA VY CHAIN) (NMHC).//2.2E-10//366aa//28%/P14105
C-NT2RP2000297//ZINC FINGER PROTEIN 184 (FRAGMENT).//3.3E-186//256aa//60%/Q99676	C-NT2RP2001381
C-NT2RP2000298	C-NT2RP2001397//Homo sapiens mRNA: cDNA DKFZp434B174 (from clone D KFZp434B174).//0//1495bp//100%/AL080146
C-NT2RP2000310//Human proline dehydrogenase/proline oxidase (PROD H) mRNA, complete cds.//4.3E-279//1193bp//99%/U82381	C-NT2RP2001427
C-NT2RP2000328	C-NT2RP2001601//Homo sapiens mRNA for KIAA0797 protein, partial cd s.//0//1748bp//99%/AB018340
C-NT2RP2000329//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//226aa//92%/P08760	C-NT2RP2001675
C-NT2RP2000346//MYELOID DIFFERENTIATION PRIMARY RESPONSE PROTEIN M YD116.//6.3E-115//674aa//46%/P17564	C-NT2RP2001721
C-NT2RP2000369	C-NT2RP2001907
C-NT2RP2000412	C-NT2RP2001969
C-NT2RP2000414//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN F (HNRNP F).//4.3E-228//415aa//100%/P52597	C-NT2RP2001976//Mus musculus calmodulin-binding protein SHAL (Sha l) mRNA, complete cds.//4.7E-177//1538bp//74%/AF062378
C-NT2RP2000422//Homo sapiens N-acetylglucosamine-phosphate mutase mRNA, complete cds.//0//1757bp//99%/AF102265	C-NT2RP2002046
C-NT2RP2000438	C-NT2RP2002154
C-NT2RP2000448//XES1 PROTEIN.//8.7E-54//392aa//38%/P35844	C-NT2RP2002208
	C-NT2RP2002270//AF-9 PROTEIN.//0.0000012//74aa//36%/P42568
	C-NT2RP2002312//Homo sapiens mRNA for CDS2 protein.//0//2333bp//99%/Y16521
	C-NT2RP2002325//Homo sapiens mRNA for Pex1lp, complete cds.//8.4E-254//1158bp//99%/AB015594
	C-NT2RP2002385//Homo sapiens synaptic glycoprotein SC2 spliced var iant mRNA, complete cds.//4.3E-240//1105bp//99%/AF038958
	C-NT2RP2002426
	C-NT2RP2002479//Homo sapiens mRNA for ABC transporter 7 protein, c omplete cds.//0//2180bp//99%/AB005289
	C-NT2RP2002537//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME

【0964】

【表661】

X.//6.2E-19//288aa//26%/Q11073	C-NT2RP2004959//P54 PROTEIN PRECURSOR.//0.00000095//297aa//20%/P13692
C-NT2RP2002595//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//7.5E-35//181aa//42%/P12815	C-NT2RP2004999
C-NT2RP2002618//PROTEIN ARGININE N-METHYLTRANSFERASE 2 (EC 2.1.1.-).//1.7E-51//326aa//38%/P55345	C-NT2RP2005000
C-NT2RP2002621	C-NT2RP2005001//Homo sapiens mRNA for KIAA0615 protein, complete cds.//0//1694bp//99%/AB014515
C-NT2RP2002672	C-NT2RP2005012//Homo sapiens mRNA for SEC63 protein.//0//1693bp//99%/AJ011779
C-NT2RP2002701//HYPOTHETICAL 38.1 KD PROTEIN C2F12.15C IN CHROMOSOME 11.//1.9E-14//210aa//30%/O14345	C-NT2RP2005037//ANTI-SILENCING PROTEIN 1.//3.3E-47//155aa//59%/P32447
C-NT2RP2002769	C-NT2RP2005126//H. sapiens mRNA for RNA helicase (Myc-regulated dead box protein).//0//2388bp//98%/X98743
C-NT2RP2002862//60S ACIDIC RIBOSOMAL PROTEIN P0 (LIGHT-INDUCED 34 KD PROTEIN).//8.8E-10//203aa//27%/P29764	C-NT2RP2005140
C-NT2RP2002928//Homo sapiens pre-mRNA splicing factor (PRP17) mRNA, complete cds.//1.9E-136//623bp//100%/AF038392	C-NT2RP2005147
C-NT2RP2002954	C-NT2RP2005159
C-NT2RP2002959//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//4.6E-80//147aa//100%/P51669	C-NT2RP2005239//Homo sapiens cysteine desulfurase (nifs) mRNA, complete cds.//0//2087bp//99%/AF097025
C-NT2RP2002980//30S RIBOSOMAL PROTEIN S10.//0.00000001//98aa//36%/P10129	C-NT2RP2005270
C-NT2RP2002986//Homo sapiens mRNA for Kelch motif containing protein, complete cds.//0//2209bp//99%/AB026190	C-NT2RP2005276//Homo sapiens mRNA for Acyl-CoA synthetase 3, complete cds.//0//2122bp//99%/D89053
C-NT2RP2003108	C-NT2RP2005293
C-NT2RP2003117	C-NT2RP2005315//Homo sapiens mRNA for KIAA0676 protein, partial cds.//0//1515bp//99%/AB014576
C-NT2RP2003121//Mus musculus enhancer of polycomb (Epc1) mRNA, complete cds.//2.3E-82//642bp//68%/AF079765	C-NT2RP2005358//Homo sapiens methyl-CpG binding domain-containing protein MB03 (MB03) mRNA, complete cds.//0//2199bp//99%/AF072247
C-NT2RP2003125//RING CANAL PROTEIN (KELCH PROTEIN).//2.4E-38//539aa//25%/Q04652	C-NT2RP2005393//AUTOANTIGEN NGP-1.//7.2E-39//224aa//35%/Q13823
C-NT2RP2003177	C-NT2RP2005436//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.2E-13//185aa//38%/Q08170
C-NT2RP2003194	C-NT2RP2005441
C-NT2RP2003265//Homo sapiens CGI-53 protein mRNA, complete cds.//0//1580bp//99%/AF151811	C-NT2RP2005453
C-NT2RP2003295//Homo sapiens RMP mRNA for RPB5 mediating protein, complete cds.//0//1526bp//99%/AB006572	C-NT2RP2005464
C-NT2RP2003329//PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.//3.6E-14//332aa//32%/P26337	C-NT2RP2005465//MITOCHONDRIAL CARRIER PROTEIN RIM2.//3E-44//252aa//41%/P38127
C-NT2RP2003367	C-NT2RP2005472
C-NT2RP2003433//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//5E-131//269aa//91%/P38378	C-NT2RP2005495
C-NT2RP2003446	C-NT2RP2005498//PROTEIN PHOSPHATASE PP2A, 55 KD REGULATORY SUBUNIT, ALPHA ISOFORM (PROTEIN PHOSPHATASE PP2A B SUBUNIT ALPHA ISOFORM) (ALPHA-PR55).//5.2E-81//166aa//88%/P36876
C-NT2RP2003533	C-NT2RP2005509//Homo sapiens CGI-45 protein mRNA, complete cds.//0//1825bp//99%/AF151803
C-NT2RP2003543//HYPOTHETICAL TRNA/RRNA METHYLTRANSFERASE SLR1673 (EC 2.1.1.-).//1.7E-17//148aa//34%/P74261	C-NT2RP2005520//Homo sapiens chromosome-associated protein-E (hCAP-E) mRNA, complete cds.//0//3994bp//99%/AF092563
C-NT2RP2003596	C-NT2RP2005525//Mus musculus kanadaplin mRNA, complete cds.//2.4E-304//1687bp//85%/AF035526
C-NT2RP2003629	C-NT2RP2005540//Homo sapiens mRNA for KIAA0494 protein, complete cds.//0//2856bp//99%/AB007963
C-NT2RP2003687	C-NT2RP2005549//PUTATIVE LACTOYLGLUTATHIONE LYASE (EC 4.4.1.5) (METHYLGLYOXALASE) (ALDOKETOMUTASE) (GLYOXALASE I) (GLX I) (KETONE-ALDEHYDE MUTASE) (S-D-LACTOYLGLUTATHIONE METHYLGLYOXALASE).//2E-0//181aa//36%/Q39366
C-NT2RP2003714//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//5.4E-29//85aa//72%/Q05481	C-NT2RP2005555
C-NT2RP2003737//UBIQUITIN-CONJUGATING ENZYME E2-17 KD 2 (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (E2(17)KB 2).//1.7E-75//147aa//93%/P51669	C-NT2RP2005557//Homo sapiens clone 486790 diphosphoinositol polyphosphate phosphohydrolase mRNA, complete cds.//1E-46//576bp//70%/AF062529
C-NT2RP2003793	C-NT2RP2005620//Homo sapiens epsin 2a mRNA, complete cds.//8.9E-313//1455bp//98%/AF062085
C-NT2RP2003952//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B).//1.5E-23//200aa//30%/Q09175	C-NT2RP2005622
C-NT2RP2003986	C-NT2RP2005635//PROBABLE NH(3)-DEPENDENT NAD(+) SYNTHETASE (EC 6.3.5.1).//1E-11//128aa//36%/P47623
C-NT2RP2004042	C-NT2RP2005637
C-NT2RP2004316//Homo sapiens chromosome 1 clone J549L20, WORKING DRAFT SEQUENCE, in unordered pieces.//8.2E-202//926bp//100%/AL096820	C-NT2RP2005640
C-NT2RP2004389//PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S9 PRECURSOR.//9.3E-15//126aa//39%/P38120	C-NT2RP2005654//CYSTEINE STRING PROTEIN (CCCS1).//1.2E-13//74aa//45%/P56101
C-NT2RP2004392//MNNA PROTEIN.//1.4E-11//143aa//27%/P36044	C-NT2RP2005669//Homo sapiens mRNA for DEDD protein.//3.9E-209//957bp//99%/AJ010973
C-NT2RP2004463	C-NT2RP2005675//Homo sapiens growth suppressor related (DOC-1R) mRNA, complete cds.//4.4E-200//908bp//99%/AF089814
C-NT2RP2004602	C-NT2RP2005683
C-NT2RP2004614//Homo sapiens mRNA for KIAA0922 protein, partial cds.//0//2040bp//99%/AB023139	C-NT2RP2005690
C-NT2RP2004655//Homo sapiens mRNA for leucine rich protein.//8.5E-233//1061bp//99%/AJ006291	C-NT2RP2005712//Homo sapiens mRNA for KIAA0799 protein, partial cds.//0//1684bp//99%/AB018342
C-NT2RP2004689//HYPOTHETICAL 192.5 KD PROTEIN C6G9.10C IN CHROMOSOME 1.//5.6E-64//616aa//33%/Q92355	C-NT2RP2005723//HMNP ARGININE N-METHYLTRANSFERASE (EC 2.1.1.-) (ODPI PROTEIN).//0.00000003//169aa//28%/P38074
C-NT2RP2004791//PUTATIVE LEUCYL-TRNA SYNTHETASE, CYTOPLASMIC (EC 6.1.1.4) (LEUCINE--TRNA LIGASE) (LEURS).//9.5E-73//153aa//59%/Q10490	C-NT2RP2005748
C-NT2RP2004799//PROBABLE SUCCINYL-COA LIGASE [GDP-FORMING], BETA-CHAIN PRECURSOR (EC 6.2.1.4) (SUCCINYL-COA SYNTHETASE, BETA CHAIN) (SCS-BETA).//3.7E-135//414aa//62%/P53588	C-NT2RP2005752//Homo sapiens TNFR-related death receptor-6 (DR6) mRNA, complete cds.//0//1968bp//99%/AF068868
C-NT2RP2004802	C-NT2RP2005753//Homo sapiens I-1 receptor candidate protein mRNA, complete cds.//0//1966bp//99%/AF082516
C-NT2RP2004841	C-NT2RP2005763//EUKARYOTIC INITIATION FACTOR 4A (EIF-4A).//1.7E-61//374aa//38%/P47943
C-NT2RP2004936	

【0965】

【表662】

C-NT2RP2005767//G. gallus PBI gene.//5E-163//1158bp//81%/X90849	C-NT2RP3000397//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DE AH BOX PROTEIN 13)//1.7E-139//679aa//41%/043143
C-NT2RP2005773//Homo sapiens pyrroline 5-carboxylate reductase iso form (P5CR2) mRNA, complete cds.//2.7E-180//656bp//99%/AF151351	C-NT2RP3000403//Homo sapiens formin binding protein 21 mRNA, complete cds.//0//2364bp//99%/AF071185
C-NT2RP2005775//NEUROLYSIN PRECURSOR (EC 3.4.24.16) (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) (MICROSOMAL ENDOPEPTIDASE) (MEP) (SOLUBLE ANGIOTENSIN-BINDING PROTEIN) (SABP).//2.1E-213//249aa//85%/Q02038	C-NT2RP3000484
C-NT2RP2005781	C-NT2RP3000527//ZINC FINGER PROTEIN 43 (ZINC PROTEIN HTF6).//4.8E-28//536aa//27%/P28160
C-NT2RP2005804	C-NT2RP3000531//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN).//1.9E-12//192aa//30%/P15151
C-NT2RP2005835//SHP1 PROTEIN.//1.8E-28//208aa//32%/P34223	C-NT2RP3000596//TRICHOHYALIN.//2.5E-17//304aa//28%/Q07283
C-NT2RP2005853	C-NT2RP3000599
C-NT2RP2005868	C-NT2RP3000632//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2).//3E-140//499aa//46%/P51523
C-NT2RP2005886	C-NT2RP3000644
C-NT2RP2005890	C-NT2RP3000661
C-NT2RP2005901//Homo sapiens mRNA for KIAA0971 protein, complete cds.//0//1977bp//99%/AB023188	C-NT2RP3000665
C-NT2RP2005933//NUCLEOPORIN NUP57 (NUCLEAR PORE PROTEIN NUP57).//5E-11//155aa//34%/P48837	C-NT2RP3000690
C-NT2RP2006038	C-NT2RP3000759//ADP-RIBOSYLATION FACTOR.//7E-28//176aa//34%/Q94650
C-NT2RP2006043//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//1.5E-13//185aa//38%/Q08170	C-NT2RP3000825//NEUROGENIC LOCUS NOTCH 3 PROTEIN.//2.5E-36//417aa//31%/Q61982
C-NT2RP2006052	C-NT2RP3000836
C-NT2RP2006069	C-NT2RP3000841
C-NT2RP2006071	C-NT2RP3000850
C-NT2RP2006100//Homo sapiens mRNA: cDNA DKFZp5648102 (from clone D KFZp5648102).//0//1759bp//99%/AL049970	C-NT2RP3000852
C-NT2RP2006106	C-NT2RP3000859
C-NT2RP2006141	C-NT2RP3000868//Human ovarian cancer downregulated myosin heavy chain homolog (Doc1) mRNA, complete cds.//6.9E-69//1611bp//61%/U53445
C-NT2RP2006186//Homo sapiens mRNA for KIAA0654 protein, partial cds.//3.3E-189//899bp//97%/AB014554	C-NT2RP3000869
C-NT2RP2006196	C-NT2RP3000901
C-NT2RP2006200	C-NT2RP3000917//Homo sapiens Dhml-like protein mRNA, complete cds.//0//3199bp//99%/AF064257
C-NT2RP2006219//H. sapiens mRNA for DGCR6 protein.//1.1E-214//1026bp//97%/X96484	C-NT2RP3000919//Rattus norvegicus golgi peripheral membrane protein p65 (GRASP65) mRNA, complete cds.//2.7E-185//585bp//88%/AF015264
C-NT2RP2006237	C-NT2RP3000980
C-NT2RP2006238	C-NT2RP3000994//MATERNAL EFFECT PROTEIN STAUFEN.//0.00000006//78aa//48%/P25159
C-NT2RP2006275//MICROTUBULE-ASSOCIATED PROTEIN 1B [CONTAINS: LIGHT CHAIN LC1].//2E-59//388aa//32%/P46821	C-NT2RP3001004
C-NT2RP2006312//Homo sapiens BAF57 (BAF57) gene, complete cds.//2.8E-274//1236bp//99%/AF035262	C-NT2RP3001081
C-NT2RP2006333	C-NT2RP3001084
C-NT2RP2006365	C-NT2RP3001096//Rattus norvegicus leprecan (leprel) mRNA, complete cds.//1.7E-94//787bp//66%/AF087433
C-NT2RP2006393	C-NT2RP3001107//PEREGRIN (BR140 PROTEIN).//3E-44//260aa//40%/P55201
C-NT2RP2006436//ANTERIOR-RESTRICTED HOMEOBOX PROTEIN (RATHKE POUCH HOMEO BOX).//0.00000034//50aa//50%/Q61658	C-NT2RP3001109
C-NT2RP2006456	C-NT2RP3001116
C-NT2RP2006464//Homo sapiens mRNA for AND-1 protein.//0//2181bp//99%/AJ006266	C-NT2RP3001119
C-NT2RP2006467	C-NT2RP3001133
C-NT2RP2006472	C-NT2RP3001140//Homo sapiens mRNA for KIAA0762 protein, partial cds.//0//2802bp//99%/AB018305
C-NT2RP2006565//Sus scrofa mRNA for SCAMP1 protein.//0//1276bp//84%/Y15710	C-NT2RP3001155//Homo sapiens mRNA for AND-1 protein.//0//2732bp//99%/AJ006266
C-NT2RP2006571//CYTOCHROME P450 2G1 (EC 1.14.14.1) (CYP11G1) (P450-NMB) (OLFACTIVE).//4.2E-134//486aa//50%/P24461	C-NT2RP3001176//HYPOTHETICAL 65.3 KD PROTEIN IN MAD1-SCY1 INTERGENIC REGION.//1.7E-10//196aa//27%/P53154
C-NT2RP2006573//2',3'-CYCLIC NUCLEOTIDE 3'-PHOSPHODIESTERASE (EC 3.1.4.37) (CNP).//0.0000055//169aa//25%/P09543	C-NT2RP3001214
C-NT2RP3000031//Homo sapiens mRNA for KIAA0901 protein, complete cds.//0//2547bp//99%/AB020708	C-NT2RP3001216//CYCLICIN 1 (MULTIPLE-BAND POLYPEPTIDE 1) (FRAGMENT).//0.0000023//137aa//33%/P35663
C-NT2RP3000072	C-NT2RP3001221//GAMMA-BUTYROBETAIN, 2-OXOGLUTARATE DIOXYGENASE (EC 1.14.11.1) (GAMMA-BUTYROBETAIN HYDROXYLASE).//1.9E-31//353aa//30%/P80193
C-NT2RP3000142//Homo sapiens mRNA for KIAA0592 protein, partial cds.//0//1404bp//97%/AB011164	C-NT2RP3001236
C-NT2RP3000220	C-NT2RP3001239//MICROTUBULE-ASSOCIATED PROTEIN 1B (MAP1.2) (MAP1(X)) [CONTAINS: LIGHT CHAIN LC1].//1.2E-166//395aa//51%/P14873
C-NT2RP3000251	C-NT2RP3001260//Homo sapiens mRNA for KIAA0911 protein, complete cds.//0//2497bp//99%/AB020718
C-NT2RP3000252//Homo sapiens GTP-binding protein NCB mRNA, complete cds.//0//2388bp//99%/AF120334	C-NT2RP3001307
C-NT2RP3000312	C-NT2RP3001325
C-NT2RP3000320//Homo sapiens partial mRNA for putative p621 protein which interacts with transcription factor Spl.//0//1544bp//100%/AJ242978	C-NT2RP3001384//Homo sapiens NAKAP95 mRNA for neighbor of A-kinase anchoring protein 95, complete cds.//0//1213bp//99%/AB025905
C-NT2RP3000333	C-NT2RP3001392
C-NT2RP3000348	C-NT2RP3001396
C-NT2RP3000350//PROBABLE GTP-BINDING PROTEIN HP0303.//0.000000028//185aa//31%/Q25074	C-NT2RP3001398//TRANSCRIPTIONAL REPRESSOR CTCF.//1.3E-61//374aa//36%/P49711
C-NT2RP3000359//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//226aa//92%/P08760	C-NT2RP3001407//SCY1 PROTEIN.//0.0000033//143aa//25%/P53009
C-NT2RP3000361//Homo sapiens mRNA, complete cds, similar to yeast pre-mRNA splicing factors, Prp1/Zer1 and Prp6.//0//2072bp//98%/AB019219	C-NT2RP3001420
C-NT2RP3000366//RAS-RELATED PROTEIN RAB-1B.//2.1E-107//206aa//99%/P35293	C-NT2RP3001426//DNAJ PROTEIN (FRAGMENT).//1E-16//177aa//46%/Q33529
	C-NT2RP3001427//WERNER SYNDROME HELICASE HOMOLOG.//2.7E-10//159aa//33%/Q09053

【0966】

【表663】

C-NT2RP3001457	ATIN)../0.000003//101aa//32%/P26372
C-NT2RP3001472//NONHISTONE CHROMOSOMAL PROTEIN 6A../9.1E-13//87aa//43%/P11632	C-NT2RP4000355
C-NT2RP3001495//Human oxidoreductase (HICMA56) mRNA, complete cds../0//1475bp//99%/U13395	C-NT2RP4000360//Homo sapiens mRNA for KIAA0738 protein, complete cds../0//4074bp//99%/AB018281
C-NT2RP3001497//Homo sapiens multiple membrane spanning receptor TRCB (TRCB) mRNA, complete cds../0//2295bp//99%/AF064801	C-NT2RP4000367//Homo sapiens IkappaB kinase complex associated protein (IKAP) mRNA, complete cds../0//4782bp//99%/AF044195
C-NT2RP3001529//SPOOB-ASSOCIATED GTP-BINDING PROTEIN../1E-61//345aa//42%/P20964	C-NT2RP4000370//MITOCHONDRIAL PEPTIDE CHAIN RELEASE FACTOR 1 PRECURSOR (MRF-1)../2.6E-77//262aa//54%/075570
C-NT2RP3001621	C-NT2RP4000376//Homo sapiens mRNA for phospholipase A2 activating protein../0//2412bp//99%/AJ238243
C-NT2RP3001629	C-NT2RP4000381
C-NT2RP3001642//HYPOTHETICAL PROTEIN KIAA0210../6.8E-18//91aa//38%/Q92609	C-NT2RP4000398//ZINC FINGER PROTEIN 140../2.9E-110//435aa//50%/P52738
C-NT2RP3001646//WD-40 REPEAT PROTEIN MS12../8.8E-09//132aa//31%/Q22468	C-NT2RP4000415
C-NT2RP3001676	C-NT2RP4000417//MANNOSE-OLIGOSACCHARIDE ALPHA-1,2-MANNOSIDASE (EC 3.2.1.113) (MAN(9)-ALPHA-MANNOSIDASE) (FRAGMENT)../2.6E-51//438aa//33%/P45701
C-NT2RP3001679	C-NT2RP4000448//Homo sapiens mRNA: cDNA DKFZp566G0746 (from clone DKFZp566G0746)../0//3991bp//99%/AL050078
C-NT2RP3001799//MYOSIN HEAVY CHAIN, STRIATED MUSCLE../1.6E-11//348aa//27%/P24733	C-NT2RP4000449
C-NT2RP3001819//RING CANAL PROTEIN (KELCH PROTEIN)../7.4E-18//249aa//30%/Q04652	C-NT2RP4000455//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPD../0.000003//175aa//27%/P09309
C-NT2RP3001896	C-NT2RP4000457//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 15 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 15) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 15) (DEUBIQUITINATING ENZYME 15)../2.5E-37//291aa//38%/P50101
C-NT2RP3001915	C-NT2RP4000480
C-NT2RP3001929	C-NT2RP4000481//ATP-DEPENDENT RNA HELICASE DOB1 (RNA TRANSPORT REGULATOR NTR4)../1.9E-67//721aa//29%/Q09475
C-NT2RP3003193//ZINC FINGER PROTEIN 135../7.3E-98//269aa//62%/P52742	C-NT2RP4000498//MOB1 PROTEIN (MPS1 BINDER 1)../8.8E-50//214aa//50%/P40484
C-NT2RP3004466	C-NT2RP4000500
C-NT2RP3004480//VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN VPS35../3.3E-113//466aa//42%/P34110	C-NT2RP4000518//ATP-DEPENDENT RNA HELICASE ROK1../1.5E-106//495aa//45%/P45818
C-NT2RP3004539//Homo sapiens mRNA for KIAA0632 protein, partial cds../0//1520bp//99%/AB014532	C-NT2RP4000524
C-NT2RP3004544//Homo sapiens mRNA for KIAA0554 protein, partial cds../0//974bp//95%/AB011126	C-NT2RP4000541
C-NT2RP3004569//ANKYRIN, BRAIN VARIANT 1 (ANKYRIN B) (ANKYRIN, NON ERYTHROID)../0.00000038//150aa//28%/Q01484	C-NT2RP4000556//SUR4 PROTEIN (SRE1 PROTEIN)../7.4E-14//233aa//31%/P40319
C-NT2RP3004572//Homo sapiens cofactor of initiator function (CIF15) mRNA, complete cds../0//1770bp//99%/AF026445	C-NT2RP4000560
C-NT2RP3004578//Homo sapiens mRNA for KIAA0477 protein, complete cds../0//1639bp//99%/AB007946	C-NT2RP4000588
C-NT2RP3004594//Homo sapiens mRNA for AMD-1 protein../0//1807bp//99%/AJ006266	C-NT2RP4000614//Homo sapiens TLS-associated protein TASR-2 mRNA, complete cds../2.9E-188//863bp//99%/AF067730
C-NT2RP3004617//ZINC-BINDING PROTEIN A33../7.2E-75//464aa//35%/Q02084	C-NT2RP4000638
C-NT2RP3004618//Homo sapiens putative RNA-binding protein Q99 mRNA A, complete cds../0//3972bp//98%/AF093097	C-NT2RP4000648//TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICPD../0.000003//175aa//27%/P09309
C-NT2RP3004669//ETHANOLAMINE KINASE (EC 2.7.1.82) (EASILY SHOCKED PROTEIN)../1.7E-72//254aa//45%/P54352	C-NT2RP4000657//SPORE COAT POLYSACCHARIDE BIOSYNTHESIS PROTEIN SPS E../1.1E-32//350aa//30%/P39625
C-NT2RP4000008//CHLORINE CHANNEL PROTEIN P64../2.6E-98//239aa//64%/P35526	C-NT2RP4000704
C-NT2RP4000051//SYNAPTONEMAL COMPLEX PROTEIN SC55../4.9E-51//335aa//37%/Q64375	C-NT2RP4000713//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X../1.1E-13//295aa//27%/Q11073
C-NT2RP4000078//Homo sapiens mRNA for KIAA0850 protein, complete cds../0//3013bp//99%/AB020657	C-NT2RP4000724//RETROVIRUS-RELATED ENV POLYPROTEIN../3.2E-191//199aa//78%/P10267
C-NT2RP4000109//Homo sapiens mRNA for MECF5, partial cds../0//2161bp//99%/AB011538	C-NT2RP4000728//Homo sapiens mRNA for KIAA0931 protein, partial cds../0//3392bp//95%/AB023148
C-NT2RP4000111//CLEFTAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT)../0//728aa//99%/Q10568	C-NT2RP4000737
C-NT2RP4000129	C-NT2RP4000739//Homo sapiens mRNA for KIAA1012 protein, complete cds../0//3574bp//99%/AB023229
C-NT2RP4000147//Drosophila melanogaster putative ARF1 GTPase activating protein (ARF1-GAP) mRNA, complete cds../3.8E-28//528bp//67%/AF011427	C-NT2RP4000781//HYPOTHETICAL 27.7 KD PROTEIN IN CPT1-SPC98 INTERGENIC REGION../0.00000032//67aa//31%/P53915
C-NT2RP4000150	C-NT2RP4000817//Homo sapiens mRNA for KIAA0470 protein, complete cds../0//1927bp//99%/AB007939
C-NT2RP4000151	C-NT2RP4000833
C-NT2RP4000159	C-NT2RP4000837//Homo sapiens mRNA for zinc finger protein SALL1../4.3E-94//810bp//65%/Y18265
C-NT2RP4000185	C-NT2RP4000839//VEGETABLE INCOMPATIBILITY PROTEIN HET-E-1../8.5E-21//271aa//28%/Q00808
C-NT2RP4000210//Homo sapiens mRNA for KIAA0700 protein, partial cds../0//4149bp//99%/AB014600	C-NT2RP4000855//AMINOPEPTIDASE B (EC 3.4.11.6) (ARGINYL AMINOPEPTIDASE) (ARGININE AMINOPEPTIDASE) (CYTOSOL AMINOPEPTIDASE IV) (AP-B)../5.7E-82//324aa//48%/Q09175
C-NT2RP4000212//ATRIAL GLAND-SPECIFIC ANTIGEN PRECURSOR (AGSA)../5.9E-15//104aa//40%/P15287	C-NT2RP4000865//ZINC FINGER PROTEIN ZFP-36 (FRAGMENT)../4.1E-85//174aa//55%/P16415
C-NT2RP4000243//Homo sapiens mRNA for cartilage-associated protein (CASP)../0//1932bp//99%/AJ006470	C-NT2RP4000878//MYELOID UPREGULATED PROTEIN../6.2E-91//173aa//87%/Q035682
C-NT2RP4000246//NPC DERIVED PROLINE RICH PROTEIN 1 (NDPP-1)../2.7E-84//208aa//76%/Q03173	C-NT2RP4000879//UBIQUITIN-ACTIVATING ENZYME E1 (A1S9 PROTEIN)../9.6E-96//513aa//42%/P22314
C-NT2RP4000259//GLUTATHIONE PEROXIDASE 2 (EC 1.11.1.9)../5.5E-29//153aa//43%/Q023968	C-NT2RP4000925//FIBROMODULIN PRECURSOR (FM) (COLLAGEN-BINDING 59 K D PROTEIN)../2.6E-26//227aa//36%/Q06828
C-NT2RP4000290//HYPOTHETICAL 116.5 KD PROTEIN C20G.09C IN CHROMOSOME 1../3.5E-297//1024aa//55%/P87115	C-NT2RP4000927//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE DUB-1 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE DUB-1) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE DUB-1) (DEUBIQUITINATING ENZYME 1)../1.5E-76//346aa//
C-NT2RP4000312//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATYLASE) (ADENYLYL CYCLASE)../1.5E-26//237aa//28%/Q01631	
C-NT2RP4000323//KERATIN, ULTRA HIGH-SULFUR MATRIX PROTEIN (UHS KER	

【0967】

【表664】

/43%/Q61068	0
C-NT2RP4000928//Homo sapiens mRNA for CDS2 protein.//0//2487bp//99%	C-NT2RP4001379//HYPOTHETICAL 49.1 KD PROTEIN C1103.06 IN CHROMOSOM E 1.//2E-53//436aa//30%/Q10085
%/Y16521	C-NT2RP4001407//Homo sapiens mRNA for KIAA0923 protein, complete c ds.//0//2716bp//99%/AB023140
C-NT2RP4000929//PUTATIVE ATP-DEPENDENT RNA HELICASE MJ1505.//0.000 00014//185aa//25%/Q58900	C-NT2RP4001414//SEPTIN 2 HOMOLOG (FRAGMENT).//7.7E-190//422aa//82% //Q14141
C-NT2RP4000955	C-NT2RP4001433//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.2E-138//419 aa//54%/Q99676
C-NT2RP4000973//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//1.4E-26//90aa//42%/P38660	C-NT2RP4001474//Xenopus laevis putative Zic3 binding protein mRNA, complete cds.//2.7E-66//738bp//71%/AF129131
C-NT2RP4000975	C-NT2RP4001483//2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT PRECURSO R (EC 1.2.4.2) (ALPHA-KETOGLUTARATE DEHYDROGENASE).//0//962aa//78% //Q02218
C-NT2RP4000979	C-NT2RP4001498//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//1E-27//37 4aa//29%/P39010
C-NT2RP4000984	C-NT2RP4001502
C-NT2RP4000989//UNC-47 PROTEIN.//0.0000082//173aa//25%/P34579	C-NT2RP4001507
C-NT2RP4000997//DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (EC 2.7.7.6) (RNA POLYMERASE I SUBUNIT 2) (RPA135).//0//838aa//87% //P70700	C-NT2RP4001524
C-NT2RP4001004//VACUOLAR PROTEIN 8.//3.7E-16//401aa//26%/P39968	C-NT2RP4001547//HYPOTHETICAL 45.0 KD PROTEIN IN NOT1/CDC39-HMR INT ERGENIC REGION.//5.7E-54//242aa//38%/P25656
C-NT2RP4001006	C-NT2RP4001551//Homo sapiens chromatin-specific transcription elon gation factor FACT 140 kDa subunit mRNA, complete cds.//0//3202bp/ //99%/AF152961
C-NT2RP4001010//Homo sapiens mRNA for KIAA0964 protein, complete c ds.//0//2482bp//99%/AB023181	C-NT2RP4001555//PUTATIVE ENDONUCLEASE VIII (EC 3.2.-.-).//4.7E-09/ //216aa//24%/P96902
C-NT2RP4001041//PROBABLE LEUCYL-TRNA SYNTHETASE (EC 6.1.1.4) (LEUC INE-TRNA LIGASE).//1.5E-92//443aa//44%/Q09996	C-NT2RP4001567//ARMADILLO SEGMENT POLARITY PROTEIN.//0.0000054//2 13aa//26%/Q02453
C-NT2RP4001057	C-NT2RP4001568//ZINC FINGER PROTEIN GC51.//1.8E-10//109aa//36%/P3 5197
C-NT2RP4001064//SYNAPTONEMAL COMPLEX PROTEIN SC65.//6.7E-51//335aa //37%/Q64375	C-NT2RP4001571
C-NT2RP4001079//CALCIUM-TRANSPORTING ATPASE 1 (EC 3.6.1.38) (GOLGI CA2+-ATPASE).//1.3E-123//563aa//46%/P13586	C-NT2RP4001574//Homo sapiens coat protein gamma-cop mRNA, complete cds.//0//3046bp//99%/AF100756
C-NT2RP4001080//Homo sapiens mRNA for Rod1, complete cds.//0//1439 bp//99%/AB023967	C-NT2RP4001575//Rattus norvegicus mRNA for ARE1 protein.//0//1087b p//87%/AJ223830
C-NT2RP4001086	C-NT2RP4001592//ISOLEUCYL-TRNA SYNTHETASE (EC 6.1.1.5) (ISOLEUCIN E-TRNA LIGASE) (ILERS).//1.7E-141//373aa//47%/P73505
C-NT2RP4001095//DOUBLE-STRANDED RNA-SPECIFIC EDITASE 1 (EC 3.5.-.-) (DSRNA ADENOSINE DEAMINASE) (RNA EDITING ENZYME 1).//2.6E-17//1 21aa//36%/P51400	C-NT2RP4001610//Homo sapiens mRNA for KIAA0869 protein, partial cd s.//0//1897bp//99%/AB020676
C-NT2RP4001100	C-NT2RP4001614
C-NT2RP4001117//PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT.//1. 9E-115//224aa//100%/P38378	C-NT2RP4001634
C-NT2RP4001122//TIPD PROTEIN.//1.4E-65//253aa//41%/Q15736	C-NT2RP4001638//DNA REPAIR/TRANSCRIPTION PROTEIN MET18/MMS19.//5.1 E-46//234aa//32%/P40469
C-NT2RP4001126//TRICHOHYALIN.//2.9E-18//380aa//26%/Q07283	C-NT2RP4001644//MYOSIN LIGHT CHAIN KINASE (EC 2.7.1.117) (MLCK).// 6.4E-19//1111aa//45%/P25323
C-NT2RP4001138	C-NT2RP4001677
C-NT2RP4001143//SUCCINYL-DIAMINOPIMELATE DESUCCINYLAISE (EC 3.5.1.1 8) (SDAP).//0.0000021//93aa//33%/P44514	C-NT2RP4001679
C-NT2RP4001148//SOF1 PROTEIN.//1.3E-104//236aa//52%/P33750	C-NT2RP4001696//CLEFTAGE AND POLYADENYLATION SPECIFICITY FACTOR, 1 00 KD SUBUNIT (CPSF 100 KD SUBUNIT).//4E-10//243aa//25%/Q10568
C-NT2RP4001149	C-NT2RP4001725//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT.// 3E-10//128aa//32%/Q10282
C-NT2RP4001150//NG-CAM RELATED CELL ADHESION MOLECULE PRECURSOR (N R-CAM) (BRAVO).//3.4E-29//385aa//29%/P35331	C-NT2RP4001730//UDP-GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECU RSOR (EC 2.4.1.-) (DUGT).//6.4E-170//1168aa//33%/Q09332
C-NT2RP4001174//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PR ECURSOR (CTPT).//4.7E-29//227aa//35%/P52178	C-NT2RP4001739
C-NT2RP4001206//Drosophila melanogaster strawberry notch (sno) mRNA A, complete cds.//4.4E-104//1460bp//65%/U95760	C-NT2RP4001753//ZINC FINGER PROTEIN 84 (ZINC FINGER PROTEIN HPF2). //3.9E-236//665aa//58%/P51523
C-NT2RP4001207	C-NT2RP4001760//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTO R (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN).//4.1E-16//263aa/ //27%/P98174
C-NT2RP4001210	C-NT2RP4001790//Homo sapiens mRNA for KIAA1015 protein, complete c ds.//0//3144bp//99%/AB023232
C-NT2RP4001219//PROBABLE PROTEIN DISULFIDE ISOMERASE P5 PRECURSOR (EC 5.3.4.1).//6.2E-27//90aa//42%/P38660	C-NT2RP4001803
C-NT2RP4001228//RING CANAL PROTEIN (KELCH PROTEIN).//1.8E-103//508 aa//43%/Q04652	C-NT2RP4001822//PLATELET-ENDOTHELIAL TETRASPAN ANTIGEN 3 (PETA-3) (GP27) (MEMBRANE GLYCOPROTEIN SFA-1) (CD151 ANTIGEN).//1.2E-30//24 1aa//30%/Q35566
C-NT2RP4001235	C-NT2RP4001823//MICROFIBRIL-ASSOCIATED GLYCOPROTEIN 4.//1.1E-19//7 7aa//54%/P55083
C-NT2RP4001256	C-NT2RP4001828
C-NT2RP4001260//Homo sapiens mRNA for KIAA0875 protein, partial cd s.//0//2876bp//99%/AB020682	C-NT2RP4001838//Homo sapiens CoREST protein (COREST) mRNA, complet e cds.//6.3E-99//555bp//73%/AF155595
C-NT2RP4001274//Human transporter protein (glt7) mRNA, complete cd s.//4.4E-58//1196bp//61%/U49082	C-NT2RP4001861//TRICHOHYALIN.//1E-35//307aa//34%/P37709
C-NT2RP4001276//TRICHOHYALIN.//7.9E-09//126aa//32%/Q07283	C-NT2RP4001893//Homo sapiens mRNA: cDNA DKFZp5640043 (from clone D XFP5640043).//0//1306bp//98%/AL050390
C-NT2RP4001313//MITOCHONDRIAL IMPORT RECEPTOR SUBUNIT TOM40 (MON38 PROTEIN) (TRANSLOCASE OF OUTER MEMBRANE 40 KD SUBUNIT).//5.9E-17/ //296aa//29%/P24391	C-NT2RP4001896//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//0.00 0000014//345aa//25%/Q0808
C-NT2RP4001315//Bos taurus mRNA for Rab5 GDP/GTP exchange factor, Rabex5.//8.5E-213//1129bp//92%/AJ001119	C-NT2RP4001901
C-NT2RP4001339//Homo sapiens mRNA for AMMERCI protein.//9.2E-160// 736bp//99%/AJ007014	C-NT2RP4001927//MICROTUBULE-ASSOCIATED PROTEIN YTM1.//1.3E-38//258 aa//32%/Q12024
C-NT2RP4001343	C-NT2RP4001938//TRANSCRIPTIONAL REPRESSOR CTCF.//9.8E-60//303aa//3 8%/P49711
C-NT2RP4001345//Homo sapiens mRNA for LCAT-like lysophospholipase (LLPL), complete cds.//2.7E-310//1400bp//100%/AB017494	
C-NT2RP4001351//Human ovarian cancer downregulated myosin heavy ch ain homolog (Docl) mRNA, complete cds.//1.4E-58//2425bp//59%/U534 45	
C-NT2RP4001353	
C-NT2RP4001372//IRREGULAR CHIASM C-ROUGHEST PROTEIN PRECURSOR (IRR EC PROTEIN).//1.6E-19//222aa//30%/Q08180	
C-NT2RP4001373	
C-NT2RP4001375//NON-RECEPTOR TYROSINE KINASE SPORE LYSIS A (EC 2. 7.1.112) (TYROSINE- PROTEIN KINASE 1).//9.2E-17//146aa//35%/P1816	

【表665】

C-NT2RP4001946//PROTEIN-L-ISOASPARTATE O-METHYLTRANSFERASE (EC 2.1.1.77) (PROTEIN- BETA-ASPARTATE METHYLTRANSFERASE) (PIMT) (PROTEIN L-ISOASPARTYL METHYLTRANSFERASE) (L-ISOASPARTYL PROTEIN CARBOXYL METHYLTRANSFERASE) //1.5E-13//211aa//28%/Q43209	C-OVARC1000465//PROTEIN TRANSPORT PROTEIN SEC7.//1.2E-25//227aa//25%/P11075
C-NT2RP4001950//GLUTAMIC ACID-RICH PROTEIN PRECURSOR.//1.2E-13//356aa//27%/P13816	C-OVARC1000466
C-NT2RP4001953	C-OVARC1000473//DUAL SPECIFICITY PROTEIN PHOSPHATASE 3 (EC 3.1.3.48) (EC 3.1.3.16) (DUAL SPECIFICITY PROTEIN PHOSPHATASE VHR) //3.1E-10//125aa//35%/P51452
C-NT2RP4001966	C-OVARC1000479//Homo sapiens mRNA for KIAA0829 protein, partial cds.//0//1919bp//99%/AB020636
C-NT2RP4001975	C-OVARC1000520//Homo sapiens supervillin mRNA, complete cds.//2.2E-15//892bp//91%/AF051850
C-NT2RP4002018//RING CANAL PROTEIN (KELCH PROTEIN) //6.9E-24//370aa//27%/Q04652	C-OVARC1000564
C-NT2RP4002052	C-OVARC1000576
C-NT2RP4002058//PUTATIVE PRE-MRNA SPLICING FACTOR RNA HELICASE (DEAH BOX PROTEIN 13) //1E-13//679aa//40%/Q43143	C-OVARC1000588
C-NT2RP4002071	C-OVARC1000605
C-NT2RP4002078//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7) //3E-150//722aa//39%/Q05481	C-OVARC1000640
C-NT2RP4002081//TRANSCRIPTION INITIATION FACTOR IIA ALPHA AND BETA CHAINS (TFIIA P35 AND P19 SUBUNITS) (TFIIA-42) (TFIIA) //0.0000067//250aa//31%/P52655	C-OVARC1000649//Human squamous cell carcinoma of esophagus mRNA for GRB-7 SH2 domain protein, complete cds.//0//1812bp//98%/D43772
C-NT2RP4002298	C-OVARC1000661
C-NT2RP4002408//PROTEIN KINASE CEK1 (EC 2.7.1.-) //1.5E-63//159aa//53%/P38938	C-OVARC1000771//RAS-RELATED PROTEIN RAB-2.//1.1E-46//121aa//79%/P08886
C-NT2RP4002791	C-OVARC1000959//HYPOTHETICAL PROTEIN MJ0933.//1.2E-17//127aa//33%/Q58343
C-NT2RP4002888//Homo sapiens mRNA: cDNA DKFZp434F172 (from clone D KFZp434F172) //0//2557bp//99%/AL080202	C-OVARC1001034//Mus musculus Fn54 mRNA, partial cds.//1.5E-178//113bp//86%/AF001533
C-NT2RP4002905	C-OVARC1001038//Homo sapiens mRNA for Ariadne-2 protein.//0//1172bp//97%/AJ130978
C-NT2RP5003461//RLR1 PROTEIN.//9.7E-22//177aa//27%/P53552	C-OVARC1001065//Homo sapiens CGI-12 protein mRNA, complete cds.//1E-215//1027bp//98%/AF132946
C-NT2RP5003477//VEGETABLE INCOMPATIBILITY PROTEIN MET-E-1.//5.5E-15//280aa//27%/Q00808	C-OVARC1001162
C-NT2RP5003492	C-OVARC1001243
C-NT2RP5003500	C-OVARC1001296
C-NT2RP5003506	C-OVARC1001360
C-NT2RP5003522//NADPH-CYTOCHROME P450 REDUCTASE (EC 1.6.2.4) (CPR) //3.3E-23//219aa//40%/P37116	C-OVARC1001381//Homo sapiens mRNA for candidate tumor suppressor involved in B-CLL.//6E-148//683bp//99%/AJ224819
C-NT2RP5003524	C-OVARC1001425
C-NT2RP5003534	C-PLACE1000005
C-OVARC1000008//HISTONE H2A.1.//1.1E-55//117aa//99%/P02262	C-PLACE1000066//SSU72 PROTEIN.//1.1E-39//206aa//43%/P53538
C-OVARC1000013//APOPTOTIC PROTEASE ACTIVATING FACTOR 1 (APAF-1) //0.0000042//102aa//32%/Q14727	C-PLACE1000142//3-HYDROXYBUTYRYL-COA DEHYDRATASE (EC 4.2.1.55) (CR OTONASE) //2.8E-29//134aa//43%/P52046
C-OVARC1000014//Homo sapiens GLE1 (GLE1) mRNA, complete cds.//2.6E-295//1393bp//97%/AF058922	C-PLACE1000184//Homo sapiens mRNA for KIAA0832 protein, complete cds.//5.5E-312//1411bp//99%/AB020639
C-OVARC1000035	C-PLACE1000185
C-OVARC1000060//EXTRACELLULAR RIBONUCLEASE LE PRECURSOR (EC 3.1.2.7.1) (RNASE LE) //0.0000032//60aa//45%/P80022	C-PLACE1000213//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//1904bp//99%/AB023194
C-OVARC1000087//HISTONE MACRO-H2A.1.//1.6E-12//174aa//26%/Q02874	C-PLACE1000347
C-OVARC1000091//HOST CELL FACTOR C1 (HCF) (VP16 ACCESSORY PROTEIN) (HFC1) (YCAF) (CF) //8.4E-14//259aa//30%/P51610	C-PLACE1000374
C-OVARC1000113	C-PLACE1000380//Homo sapiens mRNA for KIAA0853 protein, partial cds.//0//2208bp//99%/AB020660
C-OVARC1000139//Homo sapiens CGI-21 protein mRNA, complete cds.//0//1562bp//99%/AF132955	C-PLACE1000383//Homo sapiens mRNA for NTMR1 protein.//0//753bp//99%/AJ224979
C-OVARC1000148	C-PLACE1000401//POLIOVIRUS RECEPTOR PRECURSOR (CD155 ANTIGEN) //2.7E-30//352aa//31%/P15151
C-OVARC1000151//Homo sapiens partial mRNA for putative protein p38 interacting with transcription factor Spl.//2.5E-95//461bp//98%/AJ242975	C-PLACE1000406//PTB-ASSOCIATED SPLICING FACTOR (PSF) //1.2E-132//334aa//72%/P23246
C-OVARC1000168	C-PLACE1000420//7,8-DIHYDRO-8-OXOGUANINE TRIPHOSPHATASE (EC 3.1.6.-) (8-OXO-DGTPASE) //0.0000028//134aa//29%/P53368
C-OVARC1000209//Oryza sativa submergence induced protein 2A mRNA, complete cds.//1.8E-32//511bp//65%/AF068332	C-PLACE1000435
C-OVARC1000212	C-PLACE1000444
C-OVARC1000241//HYPOXIA-INDUCIBLE FACTOR 1 ALPHA (HIF-1 ALPHA) (AR NT INTERACTING PROTEIN) (MEMBER OF PAS PROTEIN 1) (MOP1) (HIF1 ALPHA) //8.2E-120//351aa//54%/Q16665	C-PLACE1000562
C-OVARC1000288//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE) (LEUCINE AMINOPEPTIDASE IV) (LAPIV) (AMINOPEPTIDASE III) (AMINOPEPTIDASE YSC1) //5.4E-53//384aa//30%/P14904	C-PLACE1000564
C-OVARC1000304//PROTEIN MOV-10.//1.1E-249//519aa//87%/P23249	C-PLACE1000588//INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1 (GU ANINE NUCLEOTIDE-BINDING PROTEIN 1) //1.6E-270//437aa//86%/P32455
C-OVARC1000309//THREONINE SYNTHASE (EC 4.2.99.2) //2.7E-40//154aa//38%/P29363	C-PLACE1000596//Homo sapiens mRNA for KIAA0850 protein, complete cds.//0//2393bp//99%/AB020657
C-OVARC1000321	C-PLACE1000611//Rattus norvegicus neural membrane protein 35 mRNA, complete cds.//2E-55//779bp//67%/AF044201
C-OVARC1000326	C-PLACE1000636//MALE STERILITY PROTEIN 2.//1.2E-39//261aa//27%/Q08891
C-OVARC1000335//HYPOTHETICAL 39.3 KD PROTEIN IN GCN4-WBP1 INTERGENIC REGION.//5.9E-14//200aa//27%/P40004	C-PLACE1000716
C-OVARC1000347	C-PLACE1000748
C-OVARC1000384	C-PLACE1000755//Homo sapiens mRNA for Helicase-MOI, complete cds.//4.6E-250//1189bp//97%/AB028449
C-OVARC1000411	C-PLACE1000785//Homo sapiens mRNA for KIAA0648 protein, partial cds.//0//2002bp//99%/AB014548
C-OVARC1000420	C-PLACE1000798
C-OVARC1000437//TENSIN.//7.9E-181//340aa//84%/Q04205	C-PLACE1000863//PUTATIVE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN YHR148.//2.5E-49//181aa//54%/P32899
C-OVARC1000443//Homo sapiens mRNA: cDNA DKFZp434A073 (from clone D KFZp434A073) //0//1216bp//99%/AL080126	C-PLACE1000909//ANKYRIN REPEAT-CONTAINING PROTEIN AKR1.//2.6E-19//404aa//26%/P39010
C-OVARC1000461	

【0969】

【表666】

C-PLACE1000948	C-PLACE1003353//Homo sapiens breast cancer antiestrogen resistance 3 protein (BCAR3) mRNA, complete cds.//0//2435bp//99%/U92715
C-PLACE1000972	C-PLACE1003369
C-PLACE1000977//BETA-CHIMAERIN (BETA-CHIMERIN).//4.4E-22//129aa//35%/Q03070	C-PLACE1003602//Homo sapiens mRNA expressed in placenta.//5.9E-278//1275bp//99%/D83200
C-PLACE1001000	C-PLACE1003611
C-PLACE1001092//Homo sapiens sorting nexin 4 mRNA, complete cds.//0//1500bp//99%/AF065485	C-PLACE1003625//ARMADILLO SEGMENT POLARITY PROTEIN.//3.2E-10//380aa//25%/P18824
C-PLACE1001257//RING CANAL PROTEIN (KELCH PROTEIN).//4.3E-54//257aa//46%/Q04652	C-PLACE1003704//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//8E-19//209aa//34%/Q08170
C-PLACE1001383//ZINC-FINGER PROTEIN UBI-D4 (APOPTOSIS RESPONSE ZINC FINGER PROTEIN REQUIEM).//3E-33//138aa//42%/Q61103	C-PLACE1003711
C-PLACE1001387//EPIDERMAL GROWTH FACTOR RECEPTOR KINASE SUBSTRATE EPS8.//2.3E-61//132aa//46%/Q12929	C-PLACE1003723
C-PLACE1001399//Homo sapiens chromosome 17, clone hRPK.22_M_12, complete sequence.//0//2118bp//99%/ACD05412	C-PLACE1003762
C-PLACE1001412	C-PLACE1003771
C-PLACE1001484//Homo sapiens chromosome 20 clone 387E22, WORKING DRAFT SEQUENCE, in unordered pieces.//0//1440bp//99%/AL031660	C-PLACE1003784
C-PLACE1001503	C-PLACE1003923
C-PLACE1001570	C-PLACE1003936
C-PLACE1001610	C-PLACE1003968//5'-AMP-ACTIVATED PROTEIN KINASE, GAMMA-1 SUBUNIT (AMPK GAMMA-1 CHAIN).//2.4E-124//326aa//73%/P80385
C-PLACE1001692//5'-ACYL FATTY ACID SYNTHASE THIOESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOESTERASE II).//4E-81//263aa//56%/P08635	C-PLACE1004104
C-PLACE1001729	C-PLACE1004114
C-PLACE1001739//PUTATIVE ATP-DEPENDENT RNA HELICASE PL10.//3.5E-75//439aa//41%/P16381	C-PLACE1004128//GUANINE NUCLEOTIDE-BINDING PROTEIN BETA SUBUNIT 4 (TRANSDUCIN BETA CHAIN 4).//6.1E-181//340aa//96%/P29387
C-PLACE1001781//PROBABLE PHOSPHOMANNOSUTASE (EC 5.4.2.8) (PMM).//5.4E-63//427aa//35%/Q57290	C-PLACE1004149
C-PLACE1001810	C-PLACE1004156
C-PLACE1001817//Homo sapiens ATP-specific succinyl-CoA synthetase beta subunit (SCS) mRNA, partial cds.//0//1995bp//99%/AF058953	C-PLACE1004161
C-PLACE1001869//L-RIBULOKINASE (EC 2.7.1.16).//2E-27//270aa//31%/P94524	C-PLACE1004183//Homo sapiens, for TONI-like protein.//0//1279bp//97%/AJ010071
C-PLACE1001912//Homo sapiens clone 24963 mRNA sequence, complete cds.//0//1196bp//99%/AF131737	C-PLACE1004197//BUTYROPHELIN PRECURSOR (BT).//4.5E-10//208aa//27%/Q62556
C-PLACE1001920//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//1729bp//99%/AF099935	C-PLACE1004203//Homo sapiens GPI-anchored membrane protein CDw108 precursor, mRNA, complete cds.//0//1882bp//99%/AF069493
C-PLACE1001928	C-PLACE1004258
C-PLACE1001989//PUTATIVE AMIDASE (EC 3.5.1.4).//1.4E-78//496aa//37%/Q49091	C-PLACE1004270//TRANSMEMBRANE PROTEASE, SERINE 2 (EC 3.4.21.-).//9.7E-36//389aa//31%/D15393
C-PLACE1002046//LIGATIN (FRAGMENT).//1.7E-240//560aa//80%/Q61211	C-PLACE1004277//Homo sapiens two pore domain K+ channel (TASK-2) mRNA, complete cds.//0//1498bp//99%/AF084830
C-PLACE1002072	C-PLACE1004289
C-PLACE1002073//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATYLASE) (ADENYL CYCLASE).//0.0000053//188aa//29%/P49606	C-PLACE1004302//SQF1 PROTEIN.//1.9E-110//325aa//48%/P33750
C-PLACE1002140	C-PLACE1004316//H. sapiens mRNA for apoptosis specific protein.//0//1767bp//99%/Y11588
C-PLACE1002163	C-PLACE1004358//Homo sapiens connector enhancer of KSR-like protein CNK1 mRNA, complete cds.//0//2512bp//99%/AF100153
C-PLACE1002170	C-PLACE1004376
C-PLACE1002433	C-PLACE1004388
C-PLACE1002438//ZINC FINGER PROTEIN 151 (MIZ-1 PROTEIN).//0.0000042//133aa//29%/Q13105	C-PLACE1004405
C-PLACE1002465	C-PLACE1004428//PRISTANOYL-COA OXIDASE (EC 1.3.3.-).//1.2E-39//385aa//33%/Q63448
C-PLACE1002529//Homo sapiens mRNA for KIAA0713 protein, partial cds.//6.7E-214//956bp//94%/AB018256	C-PLACE1004437//Human NAD+ specific isocitrate dehydrogenase beta subunit precursor, mRNA, nuclear gene encoding mitochondrial protein, complete cds.//0//985bp//99%/U49283
C-PLACE1002685//Homo sapiens B cell linker protein BLNK mRNA, alternatively spliced, complete cds.//0//1750bp//99%/AF068180	C-PLACE1004451
C-PLACE1002722//PROBABLE G PROTEIN-COUPLED RECEPTOR KIAA0001.//9E-45//305aa//33%/Q15391	C-PLACE1004460//MATERNAL TUDOR PROTEIN.//0.0000002//218aa//23%/P25823
C-PLACE1002794	C-PLACE1004473
C-PLACE1002815	C-PLACE1004510//Homo sapiens cofactor of initiator function (CIF150) mRNA, complete//1.3E-209//954bp//99%/AF026445
C-PLACE1002839	C-PLACE1004516
C-PLACE1002851	C-PLACE1004548
C-PLACE1002941	C-PLACE1004564//CLEAVAGE AND POLYADENYLATION SPECIFICITY FACTOR, 100 KD SUBUNIT (CPSF 100 KD SUBUNIT).//0//525aa//99%/Q10568
C-PLACE1002996	C-PLACE1004629//PROTEIN OS-9 PRECURSOR.//7.7E-18//264aa//32%/Q13438
C-PLACE1003045	C-PLACE1004645
C-PLACE1003092	C-PLACE1004646//B. taurus mRNA for retinal pigment epithelial membrane receptor p63.//4.4E-42//985bp//59%/X66277
C-PLACE1003100//HEP27 PROTEIN (PROTEIN D).//2.6E-79//253aa//60%/Q13268	C-PLACE1004664
C-PLACE1003108	C-PLACE1004672
C-PLACE1003145	C-PLACE1004674//PROBABLE CALCIUM-BINDING PROTEIN ALG-2 (PMP41) (ALG-257).//1.6E-95//191aa//96%/P12815
C-PLACE1003174//UBIQUITIN-CONJUGATING ENZYME E2-18 KD (EC 6.3.2.19) (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) (PM42).//3.8E-37//143aa//51%/P42743	C-PLACE1004691
C-PLACE1003190//SQF1 PROTEIN.//1.9E-110//325aa//48%/P33750	C-PLACE1004722
C-PLACE1003200	C-PLACE1004736
C-PLACE1003296//Homo sapiens mRNA: cDNA DKFp434G173 (from clone D KFP434G173).//0//1706bp//99%/AL080133	C-PLACE1004740
C-PLACE1003302//ZINC FINGER PROTEIN 83 (ZINC FINGER PROTEIN HPF1).//6.9E-206//396aa//86%/P51522	C-PLACE1004743//PROBABLE N-END-RECOGNIZING PROTEIN (UBIQUITIN-PROTEIN LIGASE E3 COMPONENT) (N-RECOGNIN).//4.4E-35//578aa//27%/Q60152
C-PLACE1003334	C-PLACE1004751//Homo sapiens mRNA for alpha2,3-sialyltransferase ST3Gal VI, complete cds.//7.1E-224//790bp//98%/AB022918
C-PLACE1003342	C-PLACE1004777//N-CHIMAERIN (NC) (N-CHIMERIN) (ALPHA CHIMERIN) (A-

【0970】

【表667】

CHIMAERIN).//1.9E-32//259aa//32%/P30337	98aa//37%/P43636
C-PLACE1004804//ADENYLATE CYCLASE (EC 4.6.1.1) (ATP PYROPHOSPHATE-LYASE) (ADENYLATE CYCLASE).//4.7E-65//695aa//29%/Q01631	C-PLACE1005955//VACUOLAR AMINOPEPTIDASE I PRECURSOR (EC 3.4.11.22) (POLYPEPTIDASE)//5.4E-54//455aa//32%/P14904
C-PLACE1004814//SPLICING FACTOR, ARGININE/SERINE-RICH 4 (PRE-MRNA SPLICING FACTOR SRP75).//5.9E-19//196aa//36%/Q08170	C-PLACE1005966//TRANSCRIPTION INITIATION FACTOR TFIID 90 KD SUBUNIT (TAFII-90).//0.00000014//254aa//25%/P38129
C-PLACE1004824	C-PLACE1005990
C-PLACE1004868//MALE STERILITY PROTEIN 2.//3.9E-39//261aa//27%/Q08891	C-PLACE1006011//Homo sapiens mRNA for poly(ADP-ribose) polymerase-2.//0//1564bp//99%/AJ236876
C-PLACE1004885	C-PLACE1006040//Homo sapiens mRNA for alpha endosulfine.//4.7E-161//744bp//99%/X99906
C-PLACE1004902//PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C.//9.3E-11//94aa//47%/Q42543	C-PLACE1006119//Homo sapiens Ran-GTP binding protein mRNA, partial cds.//1.5E-148//681bp//99%/AF039023
C-PLACE1004918//L-LACTATE DEHYDROGENASE M CHAIN (EC 1.1.1.27) (LDH-A).//4.9E-48//198aa//44%/P06151	C-PLACE1006139
C-PLACE1004930//Homo sapiens MDC-3.13 isoform 2 mRNA, complete cds.//0//1853bp//98%/AF099936	C-PLACE1006159
C-PLACE1004934	C-PLACE1006167
C-PLACE1004937//SEL-10 PROTEIN.//6.3E-125//357aa//58%/Q93794	C-PLACE1006170//Homo sapiens mRNA for KIAA0899 protein, partial cds.//4.5E-293//953bp//99%/AB020706
C-PLACE1004969//HYPOTHETICAL 55.1 KD PROTEIN B0416.5 IN CHROMOSOME X.//2E-14//205aa//26%/Q11073	C-PLACE1006195
C-PLACE1004982	C-PLACE1006196//PUTATIVE ATP-DEPENDENT RNA HELICASE C12C2.06.//2.7E-116//496aa//48%/Q09747
C-PLACE1005026	C-PLACE1006225
C-PLACE1005027	C-PLACE1006236
C-PLACE1005046	C-PLACE1006239//BONE PROTEOGLYCAN II PRECURSOR (PG-S2) (DECORIN).//2E-16//244aa//31%/P28675
C-PLACE1005077	C-PLACE1006246
C-PLACE1005101//Homo sapiens (clone zap128) mRNA. 3' end of cds.//1E-209//1031bp//96%/L40401	C-PLACE1006325//Homo sapiens mRNA: cDNA DKFp5564J142 (from clone D KFZp5564J142).//3.8E-278//1271bp//99%/AL080066
C-PLACE1005102//RING CANAL PROTEIN (KELCH PROTEIN).//2.6E-56//565aa//30%/Q04652	C-PLACE1006335
C-PLACE1005111	C-PLACE1006357
C-PLACE1005181	C-PLACE1006385//Homo sapiens epsin 2a mRNA, complete cds.//0//1168bp//99%/AF062085
C-PLACE1005187//APAG PROTEIN.//3.8E-13//122aa//36%/P05636	C-PLACE1006412
C-PLACE1005206	C-PLACE1006414
C-PLACE1005232	C-PLACE1006438//ZINC FINGER PROTEIN 165.//2.5E-45//122aa//43%/P49910
C-PLACE1005243//SERINE/THREONINE PROTEIN KINASE PKPA (EC 2.7.1.-).//1.3E-27//349aa//32%/Q01577	C-PLACE1006445
C-PLACE1005261	C-PLACE1006470
C-PLACE1005266	C-PLACE1006482//TRANSCRIPTION FACTOR MAFF.//7.7E-55//142aa//85%/Q90595
C-PLACE1005277//Homo sapiens mRNA for KIAA0510 protein, partial cds.//3.2E-297//1341bp//100%/AB011182	C-PLACE1006488//SIGNAL RECOGNITION PARTICLE 68 KD PROTEIN (SRP68).//1.1E-229//367aa//96%/Q00004
C-PLACE1005287//INNER CENTROMERE PROTEIN (INCENP).//2.3E-13//269aa//28%/P53352	C-PLACE1006492
C-PLACE1005305//GTP:AMP PHOSPHOTRANSFERASE MITOCHONDRIAL (EC 2.7.4.10) (AK3).//2E-111//226aa//92%/P08760	C-PLACE1006531
C-PLACE1005308	C-PLACE1006552
C-PLACE1005313	C-PLACE1006598//Homo sapiens clone NH0310K15, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0//2182bp//99%/AC007383
C-PLACE1005327	C-PLACE1006615
C-PLACE1005335	C-PLACE1006626//Homo sapiens mRNA for KIAA0928 protein, partial cds.//0//1760bp//99%/AB023145
C-PLACE1005373//TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE 55 SYNTHASE) (PS155 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE).//8.6E-09//194aa//27%/Q33335	C-PLACE1006673
C-PLACE1005374	C-PLACE1006678//Homo sapiens mRNA for type II membrane protein, complete cds, clone:HP10328.//5.8E-24//734bp//62%/AB015630
C-PLACE1005480	C-PLACE1006704
C-PLACE1005481	C-PLACE1006731//RIBOFLAVIN KINASE (EC 2.7.1.26) (FLAVOKINASE) / FMN ADENYLYLTRANSFERASE (EC 2.7.7.2) (FAD PYROPHOSPHORYLASE) (FAD SYNTHETASE).//6.9E-13//177aa//33%/Q59263
C-PLACE1005494//Homo sapiens mRNA for transient receptor potential protein TRP6.//0//1649bp//99%/AJ006276	C-PLACE1006782
C-PLACE1005530//HYPOTHETICAL 47.6 KD PROTEIN C16C10.5 IN CHROMOSOME E III.//5.6E-52//173aa//57%/Q09251	C-PLACE1006819//LINE-1 REVERSE TRANSCRIPTASE HOMOLOG.//9.8E-213//232aa//80%/P08547
C-PLACE1005550	C-PLACE1006829//UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 4 (EC 3.1.2.15) (UBIQUITIN THIOLESTERASE 4) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 4) (DEUBIQUITINATING ENZYME 4) (UBIQUITOUS NUCLEAR PROTEIN).//2E-15//188aa//29%/P35123
C-PLACE1005554	C-PLACE1006883
C-PLACE1005623	C-PLACE1006901
C-PLACE1005646//Homo sapiens RNA helicase-related protein mRNA, complete cds.//0//2130bp//99%/AF083255	C-PLACE1006917//HSH49 PROTEIN.//5.5E-12//97aa//35%/Q99181
C-PLACE1005656//RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE M2 CHAIN (EC 1.17.4.1) (RIBONUCLEOTIDE REDUCTASE).//2.1E-148//321aa//83%/P31350	C-PLACE1006932
C-PLACE1005730	C-PLACE1006935//HYPOTHETICAL 95.2 KD PROTEIN R144.6 IN CHROMOSOME III.//6.7E-48//278aa//41%/Q10000
C-PLACE1005755	C-PLACE1006956//ATP-DEPENDENT PERMEASE MDL1.//1.3E-86//522aa//36%/P97998
C-PLACE1005763//5-ACYL FATTY ACID SYNTHASE THIOLESTERASE, MEDIUM CHAIN (EC 3.1.2.14) (THIOLESTERASE II).//2.5E-79//209aa//53%/P08635	C-PLACE1006958//Homo sapiens mRNA for heat shock protein apg-1, complete cds.//0//1770bp//99%/AB023421
C-PLACE1005803	C-PLACE1006961
C-PLACE1005804//Homo sapiens alpha 1,2-mannosidase 1B mRNA, complete cds.//1.1E-217//994bp//99%/AF027156	C-PLACE1006962
C-PLACE1005851	C-PLACE1006966
C-PLACE1005921//AIG1 PROTEIN.//3E-31//284aa//31%/P54120	C-PLACE1007014//36 KD NUCLEOLAR PROTEIN HNP36 (DELAYED-EARLY RESPONSE PROTEIN 12) (DER12).//3.2E-35//180aa//33%/Q14542
C-PLACE1005923	C-PLACE1007021
C-PLACE1005925	C-PLACE1007105
C-PLACE1005934	
C-PLACE1005936	
C-PLACE1005951	
C-PLACE1005953//GLYCOSYLTRANSFERASE ALG2 (EC 2.4.1.-).//6.7E-30//1	

【0971】

【表668】

C-PLACE1007178	A, complete cds.//0//2252bp//99%/AF084530
C-PLACE1007226//PROBABLE OXYGEN-INDEPENDENT COPROPORPHYRINOGEN III OXIDASE (EC 1.-.-.-) (COPROPORPHYRINOGENASE) (COPROGEN OXIDASE).//1E-42//370aa//31%/P54304	C-PLACE1007958//Homo sapiens cAMP-specific phosphodiesterase 88 (PDE8B) mRNA, partial cds.//0//2300bp//99%/AF079529
C-PLACE1007238	C-PLACE1007969//HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN M (HNRNP M).//1.1E-36//202aa//48%/P52272
C-PLACE1007239//Homo sapiens mRNA for transcription elongation factor S-II, hS-II-TI, complete cds.//6.5E-216//1068bp//96%/D50495	C-PLACE1007990
C-PLACE1007242	C-PLACE1008000//CHANNEL ASSOCIATED PROTEIN OF SYNAPSE-110 (CHAPSY N-110) (SYNAPTIC DENSITY PROTEIN PSD-93).//6.1E-14//128aa//39%/Q63622
C-PLACE1007243//UNC-47 PROTEIN.//0.00000017//211aa//27%/P34579	C-PLACE1008002//Homo sapiens clone DJ0613C23, WORKING DRAFT SEQUENCE, 4 unordered pieces.//0//1833bp//99%/AC005628
C-PLACE1007257//Homo sapiens mRNA for dia-12c protein.//0//2052bp//99%/Y15908	C-PLACE1008044//NUCLEAR PORE COMPLEX PROTEIN NUP107 (NUCLEOPORIN NUP107) (107 KD NUCLEOPORIN) (P105).//4.6E-318//613aa//94%/P52590
C-PLACE1007274	C-PLACE1008095
C-PLACE1007282	C-PLACE1008122
C-PLACE1007301	C-PLACE1008129
C-PLACE1007317//Drosophila melanogaster Adrift (adrift) mRNA, complete cds.//4.1E-17//1037bp//56%/AF117649	C-PLACE1008132//HYPOTHETICAL 127.4 KD PROTEIN F07F6.4 IN CHROMOSOME E III.//1.3E-24//395aa//31%/Q09531
C-PLACE1007342	C-PLACE1008177//TRICHOHYALIN.//2.3E-29//487aa//26%/P37709
C-PLACE1007346//Homo sapiens estrogen-responsive B box protein (EBBP) mRNA, complete cds.//0//2366bp//99%/AF096870	C-PLACE1008209
C-PLACE1007367	C-PLACE1008273//COATOMER GAMMA SUBUNIT (GAMMA-COAT PROTEIN) (GAMMA A-COP).//1.3E-283//671aa//77%/P53620
C-PLACE1007375//PHORBOL ESTER/DIACYLGLYCEROL-BINDING PROTEIN UNC-13.//0.00000044//127aa//30%/P27715	C-PLACE1008275//DNA REPAIR PROTEIN REV1 (EC 2.7.7.-).//2.3E-18//162aa//37%/P12689
C-PLACE1007386	C-PLACE1008280
C-PLACE1007402	C-PLACE1008309
C-PLACE1007409//WHITE PROTEIN.//1.1E-64//428aa//32%/Q17320	C-PLACE1008329
C-PLACE1007416//DIPEPTIDYL PEPTIDASE IV (EC 3.4.14.5) (DPP IV) (T-CELL ACTIVATION ANTIGEN CD26) (TP103) (ADENOSINE DEAMINASE COMPLEXING PROTEIN-2) (ADABP).//8.8E-25//140aa//35%/P27487	C-PLACE1008356//Homo sapiens mRNA for KIAA0679 protein, partial cds.//0//1853bp//100%/AB014579
C-PLACE1007450	C-PLACE1008398//GENE 33 POLYPEPTIDE.//7.3E-114//243aa//87%/P05432
C-PLACE1007452	C-PLACE1008401
C-PLACE1007460	C-PLACE1008402//GENERAL VESICULAR TRANSPORT FACTOR P115 (TRANSCYTOSIS ASSOCIATED PROTEIN) (TAP).//0//698aa//95%/P41541
C-PLACE1007484	C-PLACE1008429//ANKYRIN HOMOLOG PRECURSOR.//3.1E-11//189aa//32%/Q06527
C-PLACE1007488//PUTATIVE RHO/RAC GUANINE NUCLEOTIDE EXCHANGE FACTOR (RHO/RAC GEF) (FACIOGENITAL DYSPLASIA PROTEIN HOMOLOG).//5.4E-53//426aa//33%/P52734	C-PLACE1008457
C-PLACE1007507	C-PLACE1008465
C-PLACE1007511//KERATIN, TYPE I CYTOSKELETAL 19 (CYTOKERATIN 19) (K19) (CK 19).//1.4E-85//385aa//45%/P08728	C-PLACE1008488
C-PLACE1007524	C-PLACE1008524//Human DNA sequence from clone 34821 on chromosome 6p12.1-21.1. Contains part of a gene for a novel protein with ZUS domain similar to part of Tight Junction Protein Z01 (TJPI) and UNC5 Homologs, the gene for a novel BZRP (peripheral benzodiazepine receptor).//0//1980bp//99%/AL031778
C-PLACE1007537//Homo sapiens ankyrin repeat-containing protein ASB-2 mRNA, complete cds.//8.9E-316//1485bp//98%/AF159164	C-PLACE1008531
C-PLACE1007544	C-PLACE1008532
C-PLACE1007547//HYPOTHETICAL 97.1 KD PROTEIN R0503.4 IN CHROMOSOME III.//1E-49//361aa//36%/P34537	C-PLACE1008533//101 KD MALARIA ANTIGEN (P101) (ACIDIC BASIC REPEAT ANTIGEN).//1.1E-09//62aa//48%/P22620
C-PLACE1007583	C-PLACE1008568
C-PLACE1007598//ZINC FINGER PROTEIN 184 (FRAGMENT).//1.6E-143//666aa//44%/Q99676	C-PLACE1008603//NUCLEAR PORE COMPLEX PROTEIN NUP155 (NUCLEOPORIN NUP155) (155 KD NUCLEOPORIN) (P140).//7.8E-236//453aa//96%/P37199
C-PLACE1007618//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//713bp//99%/AB023194	C-PLACE1008621
C-PLACE1007621	C-PLACE1008626
C-PLACE1007632//POLIOVIRUS RECEPTOR PRECURSOR.//0.0000001//228aa//31%/P32506	C-PLACE1008627//Homo sapiens mRNA for cysteine-rich protein.//0//850bp//99%/AJ006591
C-PLACE1007645	C-PLACE1008629
C-PLACE1007649//Homo sapiens mRNA for KIAA0977 protein, complete cds.//0//1952bp//99%/AB023194	C-PLACE1008650//Homo sapiens pleiotropic regulator 1 (PLRG1) mRNA, complete cds.//0//1548bp//100%/AF044333
C-PLACE1007688//LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA AUTO ANTIGEN HOMOLOG).//8.7E-09//279aa//28%/Q26457	C-PLACE1008693
C-PLACE1007690	C-PLACE1008696//Homo sapiens NADH dehydrogenase-ubiquinone Fe-S protein 8 23 kDa subunit (NDUFS8) gene, nuclear gene encoding mitochondrial protein, complete cds.//0//3002bp//99%/AF038406
C-PLACE1007697//GCN20 PROTEIN.//7.6E-119//717aa//38%/P43535	C-PLACE1008790//IMPORTIN ALPHA-6 SUBUNIT (KARYOPHERIN ALPHA-6 SUBUNIT) (IMPORTIN ALPHA S2).//3.1E-280//533aa//98%/Q35345
C-PLACE1007706//Homo sapiens metalloprotease 1 (MP1) mRNA, complete cds.//0//3431bp//99%/AF061243	C-PLACE1008808//Homo sapiens mRNA for cell cycle checkpoint protein rad1a.//2.3E-269//1225bp//99%/AJ004974
C-PLACE1007725	C-PLACE1008813
C-PLACE1007729//RETROVIRUS-RELATED PROTEASE (EC 3.4.23.-).//1.5E-44//231aa//42%/P10265	C-PLACE1008854
C-PLACE1007730//Homo sapiens mRNA for KIAA0685 protein, complete cds.//9.2E-294//1504bp//94%/AB014585	C-PLACE1008867
C-PLACE1007746	C-PLACE1008887
C-PLACE1007791//Homo sapiens IDN3-B mRNA, complete cds.//0//1836bp//99%/AB019602	C-PLACE1008902
C-PLACE1007810	C-PLACE1008925
C-PLACE1007843	C-PLACE1009020//NIFS PROTEIN.//3.9E-55//279aa//41%/P12623
C-PLACE1007846//Homo sapiens genomic DNA of 21q22.2 Down Syndrome region, segment 3/13.//0//1751bp//99%/AP000010	C-PLACE1009027//Homo sapiens mRNA for doublecortin.//0//1919bp//99%/AJ003112
C-PLACE1007858//Homo sapiens mRNA for KIAA0766 protein, complete cds.//0//3112bp//99%/AB018309	C-PLACE1009045
C-PLACE1007897	C-PLACE1009060//BRO1 PROTEIN.//6.7E-19//567aa//24%/P48582
C-PLACE1007946//MYOSIN HEAVY CHAIN, NON-MUSCLE (ZIPPER PROTEIN) (MYOSIN II).//2.6E-14//370aa//25%/Q99323	C-PLACE1009090
C-PLACE1007954	C-PLACE1009091
C-PLACE1007955//Homo sapiens cyclin-D binding Myb-like protein mRNA	C-PLACE1009094//FURIN-LIKE PROTEASE 2 PRECURSOR (EC 3.4.21.75) (FURIN 2).//1.9E-44//480aa//30%/P30432

【0972】

【表669】

C-PLACE1009099//ZINC FINGER PROTEIN 41 (FRAGMENT).//1.1E-179//452a a//67%/P51814	aa//44%/Q04652
C-PLACE1009110	C-PLACE1010106//Homo sapiens mRNA: cDNA DKFZp586M1418 (from clone DKFZp586M1418).//0//1974bp//99%/AL049385
C-PLACE1009111	C-PLACE1010134//TRANSCRIPTION REGULATORY PROTEIN SNF2 (SWI/SNF COMPLEX COMPONENT SNF2) (REGULATORY PROTEIN SWI2) (REGULATORY PROTEIN GAM1) (TRANSCRIPTION FACTOR TFE3).//1.7E-20//155aa//42%/P22082
C-PLACE1009130//UBIQUITIN-PROTEIN LIGASE E3A (EC 6.3.2.-) (ONCOGENIC PROTEIN-ASSOCIATED PROTEIN E6-AP).//2E-68//181aa//43%/Q05086	C-PLACE1010148//CYCLICIN I (MULTIPLE-BAND POLYPEPTIDE I).//0.00000046//431aa//23%/P35662
C-PLACE1009158	C-PLACE1010194//SPLICING FACTOR, ARGININE/SERINE-RICH 2 (SPLICING FACTOR SC35) (SC-35) (SPLICING COMPONENT, 35 KD) (PR264 PROTEIN).//9.8E-11//95aa//49%/Q01130
C-PLACE1009166	C-PLACE1010202
C-PLACE1009174	C-PLACE1010261//SEGREGATION DISTORTER PROTEIN.//1.6E-77//214aa//62%/P25722
C-PLACE1009186	C-PLACE1010274//Homo sapiens mRNA: cDNA DKFZp5640123 (from clone D KFZp5640123).//0//1964bp//99%/AL080122
C-PLACE1009190	C-PLACE1010293
C-PLACE1009230	C-PLACE1010321//NON-GREEN PLASTID TRIOSE PHOSPHATE TRANSLOCATOR PR ECURSOR (CTPT).//1.1E-09//350aa//22%/P52178
C-PLACE1009319//Rattus norvegicus outer membrane protein (OMP25) mRNA, complete cds; nuclear gene for mitochondrial product.//2.1E-132//1229bp//75%/AF107295	C-PLACE1010324
C-PLACE1009328	C-PLACE1010329
C-PLACE1009335	C-PLACE1010362//1-PHOSPHATIDYLINOSITOL PHOSPHODIESTERASE PRECURSOR (EC 3.1.4.10) (PHOSPHATIDYLINOSITOL-SPECIFIC PHOSPHOLIPASE C) (P1-PLC).//0.00000002//126aa//29%/P34024
C-PLACE1009338	C-PLACE1010364
C-PLACE1009368//METAL HOMEOSTASIS FACTOR ATX2.//2.5E-10//151aa//29%/Q12067	C-PLACE1010383
C-PLACE1009375	C-PLACE1010481//Homo sapiens mRNA for KIAA0836 protein, partial cds.//0//2121bp//99%/AB020643
C-PLACE1009388	C-PLACE1010491
C-PLACE1009404//HYPOTHETICAL 105.6 KD PROTEIN C16C9.06C IN CHROMOSOME 1.//0.000000047//165aa//33%/Q09820	C-PLACE1010492
C-PLACE1009434	C-PLACE1010522//Homo sapiens mRNA for DEPP (decidual protein induced by progesterone), complete cds.//0//1981bp//99%/AB022718
C-PLACE1009443	C-PLACE1010529
C-PLACE1009444//PHOSPHATIDYLINOSITOL 4-KINASE ALPHA (EC 2.7.1.67) (PI4-KINASE) (PTDINS-4-KINASE) (PI4K-ALPHA).//7.8E-71//82aa//89%/P42356	C-PLACE1010547//INTRACELLULAR PROTEIN TRANSPORT PROTEIN USO1.//0.0000012//616aa//24%/P25386
C-PLACE1009459	C-PLACE1010599//Homo sapiens Pex14 mRNA for peroxisomal membrane anchor protein, complete cds.//0//1904bp//99%/AB017546
C-PLACE1009468//PHOSPHOLIPASE A-2-ACTIVATING PROTEIN (PLAP).//3.1E-289//550aa//93%/P54319	C-PLACE1010616
C-PLACE1009476//PUTATIVE ATP-DEPENDENT RNA HELICASE T26G10.1 IN CHROMOSOME 11.//3.9E-40//179aa//37%/P34580	C-PLACE1010622//TROPOMIN T, CARDIAC MUSCLE ISOFORMS (TNTC).//0.0000016//120aa//28%/P02642
C-PLACE1009524//ARF NUCLEOTIDE-BINDING SITE OPENER (ARNO PROTEIN) (ARF EXCHANGE FACTOR).//8.1E-99//228aa//75%/Q99418	C-PLACE1010629
C-PLACE1009542	C-PLACE1010630
C-PLACE1009571	C-PLACE1010661//TESTIS-SPECIFIC PROTEIN PBS13.//5.7E-75//423aa//39%/Q01755
C-PLACE1009581	C-PLACE1010714
C-PLACE1009596//VEGETATIBLE INCOMPATIBILITY PROTEIN HET-E-1.//5.1E-54//291aa//40%/Q00808	C-PLACE1010720//Homo sapiens mRNA for chromosome-associated polypeptide-C, complete cds.//4E-299//1091bp//99%/AB019987
C-PLACE1009607	C-PLACE1010743//Homo sapiens myosin-IXb splice variant (Myo9b) mRNA, partial cds.//8.9E-91//668bp//82%/AF020267
C-PLACE1009621	C-PLACE1010771//Musculus musculus HCNGP mRNA.//7.4E-168//966bp//89%/X68061
C-PLACE1009622//WATERMELON EFFECT PROTEIN STAUFEN.//1.3E-60//209aa//41%/P25159	C-PLACE1010786
C-PLACE1009659//MEMBRANE-ASSOCIATED PROTEIN HEM-2 (NAP1 PROTEIN).//1.5E-285//538aa//99%/P55161	C-PLACE1010800
C-PLACE1009665	C-PLACE1010811
C-PLACE1009670//Homo sapiens genethonin 1 mRNA, complete cds.//0//1854bp//100%/AF062534	C-PLACE1010870//ZINC FINGER PROTEIN 91 (ZINC FINGER PROTEIN HTF10) (HPF7).//1.3E-143//407aa//58%/Q05481
C-PLACE1009708//HYPOTHETICAL 143.3 KD TRP-ASP REPEATS CONTAINING PROTEIN C12G12.13C IN CHROMOSOME 1.//7E-33//166aa//43%/Q09876	C-PLACE1010877//Homo sapiens mRNA for KIAA0610 protein, partial cds.//0//1885bp//99%/AB011182
C-PLACE1009721//NSF1 PROTEIN.//1.7E-22//176aa//33%/P35200	C-PLACE1010900
C-PLACE1009731//AIG1 PROTEIN.//1.6E-22//274aa//28%/P54120	C-PLACE2000050
C-PLACE1009763//Homo sapiens mRNA for Nedd8-activating enzyme HUBA3, complete cds.//4.3E-294//1329bp//100%/AB012190	C-PLACE4000522//NEUROGENIC LOCUS NOTCH PROTEIN HOMOLOG PRECURSOR (NOTCH PROTEIN).//2.4E-191//828aa//48%/P21783
C-PLACE1009794	C-PLACE4000590
C-PLACE1009845//Homo sapiens mRNA for KIAA0905 protein, complete cds.//0//2685bp//99%/AB020712	C-PLACE4000638
C-PLACE1009886	C-PLACE4000650//TUBERIN (TUBEROUS SCLEROSIS 2 HOMOLOG PROTEIN).//7.9E-177//201aa//34%/P49816
C-PLACE1009908//HYPOTHETICAL GTP-BINDING PROTEIN IN SEMI-PRP20 INTERGENIC REGION.//1.9E-108//277aa//43%/P53145	C-Y79AA1001647
C-PLACE1009971	
C-PLACE1009992//FIBRINUS CLOTTING FACTOR C PRECURSOR (EC 3.4.21.84).//4.6E-58//450aa//34%/P28175	
C-PLACE1009995//Homo sapiens mRNA: cDNA DKFZp5640123 (from clone D KFZp5640123).//0//1962bp//99%/AL080122	
C-PLACE1009997//Rattus norvegicus A-kinase anchoring protein AKAP220 mRNA, complete cds.//5.2E-70//736bp//73%/U48288	
C-PLACE1010023	
C-PLACE1010031	
C-PLACE1010053//Musculus musculus Spnr mRNA for RNA binding protein.//6E-279//1402bp//94%/X84692	
C-PLACE1010074//Homo sapiens sorting nexin 2 (SNX2) mRNA, complete cds.//0//2019bp//99%/AF065482	
C-PLACE1010076	
C-PLACE1010096//100 KD PROTEIN (EC 6.3.2.-).//1.4E-268//506aa//98%/Q62671	
C-PLACE1010102	
C-PLACE1010105//RING CANAL PROTEIN (KELCH PROTEIN).//7.3E-114//537	

【0973】

【配列表】

【図面の簡単な説明】

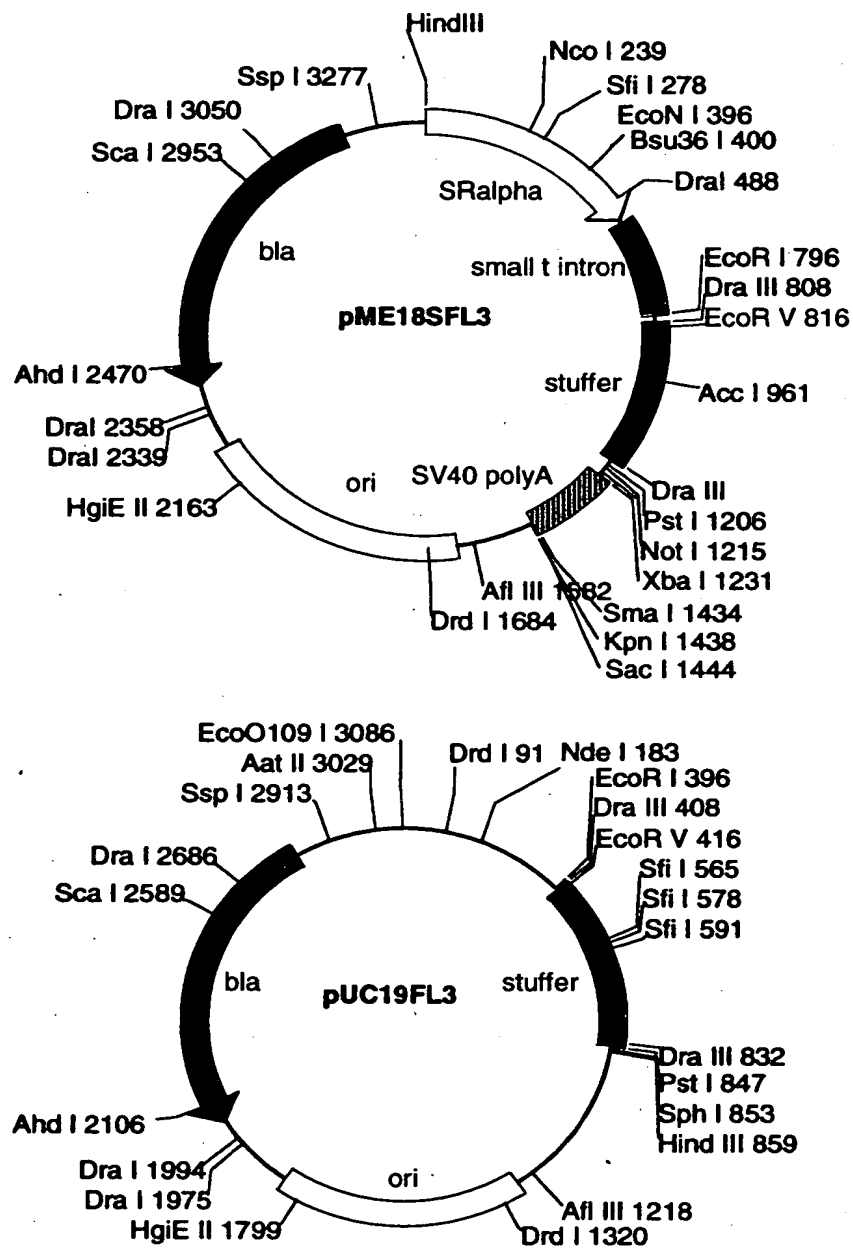
【図 1】 pME18SFL3とpUC19FL3のベクターのマップ

【図 2】 遺伝子発現解析の再現性を示すグラフ。縦軸と横軸はそれぞれ異なる実験によって得られた発現強度を示している。

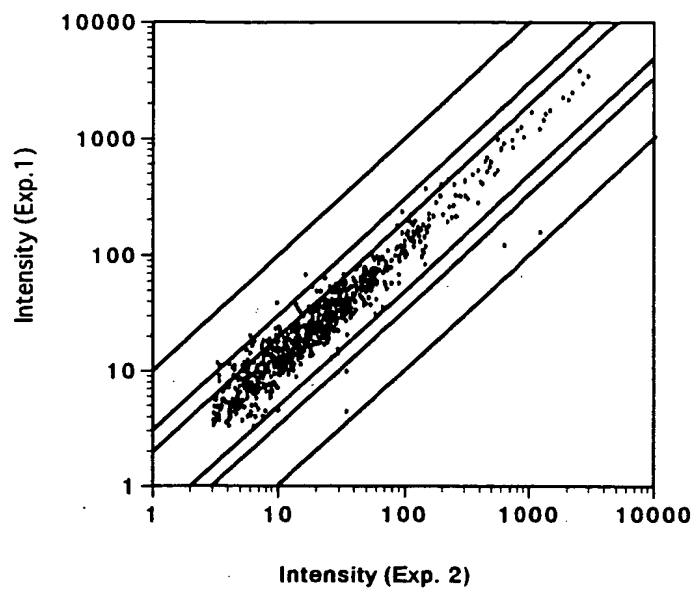
【図 3】 遺伝子発現解析における検出感度を示すグラフ。縦軸は発現強度を、横軸はプローブの濃度 ($\mu\text{g/ml}$) を示す。

【書類名】 図面

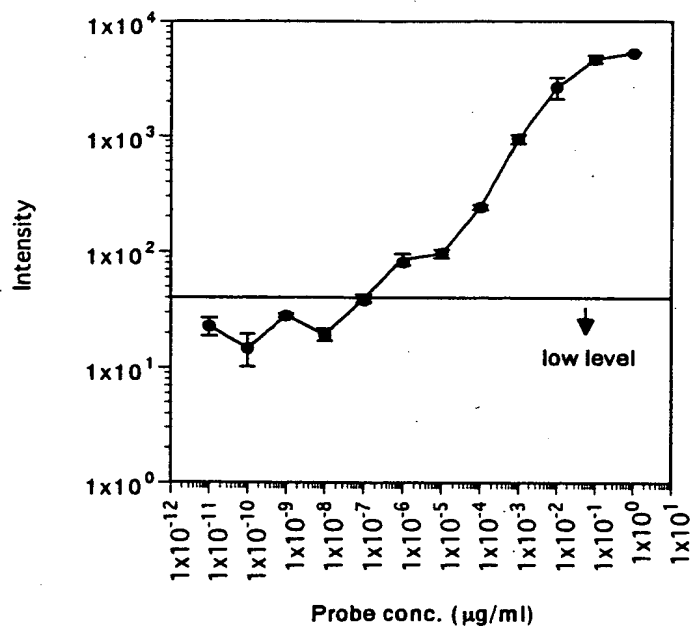
【図1】



【図2】



【図3】



【書類名】 要約書

【要約】

【課題】 全長cDNAを合成することができるプライマーとその用途の提供。

【解決手段】 ヒトのタンパク質をコードする5547のcDNAを単離した。そしてこのcDNAの5'側、および3'側の塩基配列を明らかにした。得られた塩基配列に基づいて、全長cDNA合成用プライマーを提供するとともに、cDNAによってコードされるタンパク質の機能を明らかにした。本発明のcDNAは全長であるため、翻訳開始点を含み、タンパク質の機能解析において有用な情報を与える。

【選択図】 なし

職権訂正履歴（書類修正）

特許出願の番号	特願2000-118776
受付番号	20008170003
書類名	特許願
担当官	宇留間 久雄 7277
作成日	平成13年 6月25日

<修正内容>

- ・「物件電子化フラグ（X083）」：' 2'（物件電子化無し・返還無し）
- ・「提出物件名（X081）」：' CD-R DNA配列表' としてください。

出 願 人 履 歴 情 報

識別番号 [597059742]

1. 変更年月日	1997年 4月28日
[変更理由]	新規登録
住 所	千葉県木更津市矢那1532番地3
氏 名	株式会社ヘリックス研究所